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SYMPOSIA AND ORAL SESSIONS

Late-Breaking Original Research

LB1 Identifying new biomarkers in liver for monitoring physiological imbalance and the response to feed restriction for cows during early lactation. K. L. Ingvartsen, E. Bendixen, M. C. Codrea, and K. M. Moyes*, *Aarhus University*, *Tjele, Denmark*.

The aim of this study was to identify new biomarkers in liver for monitoring physiological imbalance and to examine the different coping strategies used during feed restriction (FR) between cows in physiological imbalance and cows metabolically "normal" during early lactation. Twenty-two cows (22–55 DIM) were fed a standard TMR for ad libitum intake. After 5-d, all cows were FR to provide ~40% of NE_L requirements based on body weight, milk production and composition by supplementing the standard TMR with 60% wheat straw. After 4-d of FR, cows returned to full feed. Liver biopsies were collected −1 and 3 d relative to FR. Prior to FR, an index of degree of imbalance was calculated for all cows based on plasma fatty acid, ketone, and glucose concentration. A subset of 6 cows classified as having either the greatest (n = 3) or least (n = 3) degree of imbalance were used for iTRAQ-based quantitative profiling in liver using LC/MS/MS. Prior to FR, 8 proteins were differentially expressed ($P \leq 0.05$) due to physiological imbalance. Proteins upregulated (6) were involved in amino acid metabolism, gluconeogenesis, and β-oxidation of fatty acids. Feed restriction resulted in 20 proteins differentially expressed between cows in physiological imbalance and cows metabolically ′normal′. Upregulated proteins (8) were involved in β-oxidation of fatty acids and gluconeogenesis whereas downregulated proteins (12) were involved in antioxidant defense and glycine metabolism. This study is the first to identify new biomarkers in liver based on a physiological imbalance index and provide a better understanding of the differences in coping strategies used during FR for cows in physiological imbalance. Screening for relevant markers in more accessible samples (i.e., blood and milk) will help farmers identify cows at risk. Results provide new avenues for future management strategies relating to maintaining animal health and productivity during early lactation.

Key Words: physiological imbalance, cow, proteomics

LB2 A novel nonsense mutation of the *DMP1* gene is responsible for inherited rickets in Corriedale sheep. X. Zhao[1], K. E. Dittmer[2], S. Onteru[1], H. T. Blair[2], K. G. Thompson[2], M. F. Rothschild[1], and D. J. Garrick*[1,2], [1]*Iowa State University*, *Ames,* [2]*Massey University*, *Palmerston North, New Zealand*.

Inherited rickets of Corriedale sheep is a recently discovered skeletal disease of unknown prevalence characterized by decreased growth rate, thoracic lordosis and angular limb deformities. Previous outcross and backcross studies suggest it is a simple autosomal recessively inherited disorder. A genome-wide association study was conducted using the Illumina OvineSNP50 BeadChip on 17 sheep diagnosed as affected and an additional 3 known carriers descended from 1 carrier ram. Genomic regions showing association were scrutinized for possible candidate genes that were sequenced for causal polymorphisms concordant with disease status. A homozygous region of 199 consecutive single-nucleotide polymorphism (SNP) loci was identified in all the affected sheep, covering a region of 10 Mbp on ovine chromosome 6. Among 91 candidate genes in this region, exon 6 of the dentin matrix protein 1 (*DMP1*) gene was sequenced using DNA from the 3 carriers to reveal 10 novel SNPs including a nonsense mutation 253T/C. This T/C transition introduced a stop codon (R145X) that could truncate C-terminal amino acids. Genotyping by PCR-RFLP (restriction fragment length polymorphism) for this mutation showed that, all 17 affected sheep were "TT" genotypes and the 27 phenotypically normal sheep were either "CT" or "CC." This locus is not in complete linkage disequilibrium with the other 9 SNPs that can all be ruled out as candidates. Previous research has shown that mutations in *DMP1*gene are responsible for autosomal recessive hypophosphatemic rickets in humans. *Dmp1*_knockout mice also exhibit rickets phenotypes. We believe the *DMP1*_exon6_235T/C mutation to be responsible for the inherited rickets found in Corriedale sheep. A simple diagnostic test can be designed to identify carriers with the defective "T" alleles. Affected sheep could be used as animal models for this form of human rickets, and for further investigation of the role of DMP1 in phosphate homeostasis.

Key Words: rickets, DMP1, genome wide association

LB3 Association of polymorphisms in GPAT4 and SLC27A6 genes with bovine milk fat percentage and fatty acid composition. R. A. Nafikov*[1], J. P. Schoonmaker[2], K. T. Korn[2], K. Noack[1], D. J. Garrick[1], K. J. Koehler[1], J. Minick-Bormann[3], J. M. Reecy[1], D. E. Spurlock[1], and D. C. Beitz[1], [1]*Iowa State University*, *Ames,* [2]*Purdue University*, *West Lafayette, IN,* [3]*Kansas State University*, *Manhattan*.

The purpose of our study was to discover genetic polymorphisms to select animals producing milk with healthier fatty acid composition. The glycerol-3-phosphate acyltransferase-4 (GPAT4) and solute carrier family 27, isoform A6 (SLC27A6) involved in milk triacylglycerol biosynthesis and fatty acid transport into the mammary epithelial cells were candidate genes. We hypothesized that polymorphisms in GPAT4 and SLC27A6 will affect selectivity of fatty acid acylation onto glycerol-3-phosphate and of fatty acid uptake into the mammary epithelial cells, leading to variations in milk fatty acid composition. To test this hypothesis, milk samples were collected monthly over a 305-d lactation from 500 cows and analyzed for fatty acid composition by gas chromatography. After discovering single nucleotide polymorphisms (SNPs) in the genes of interest and genotyping animals for those SNPs, intragenic haplotypes were reconstructed and tested for associations with milk fat percentage and fatty acid composition by linear mixed models. Results showed that the haplotype effect of GPAT4 was associated significantly with concentrations of capric (10:0), lauric (12:0), palmitic (16:0), and oleic (18:1c9) acids, saturated fatty acids (SFA), unsaturated fatty acids (UFA), monounsaturated fatty acids (MUFA), polyunsaturated fatty acids (PUFA), and SFA/UFA. The haplotype effect of SLC27A6 was associated significantly with percentage of milk fat, concentrations of capric, lauric, myristic (14:0), and palmitic acids, SFA, UFA, MUFA, and SFA/UFA. The size of effects for some of the traits was numerically the same or greater than allelic effects of well known diacylglycerol

acyltransferase-1 (DGAT1) A232K mutation. Results of our study provide opportunity for selection for cows with healthier milk.

Key Words: milk fat percentage, milk fatty acid composition, SNP

LB4 Renneting properties of milk containing high molecular weight oat β-glucan. N. Sharafbafi*[1], S. M. Tosh[2], M. Alexander[1], and M. Corredig[1], [1]*Department of Food Science, University of Guelph, Guelph, Ontario, Canada*, [2]*Agriculture and Agri-Food Canada, Guelph Food Research Center, Guelph, Ontario, Canada*.

The effect of concentration and molecular structure of high molecular weight oat β–Glucan (BG) on renneting properties of concentrated skim milk gels were investigated. Incorporation of BG (0.15, 0.3, 0.6, and 0.9% w/w in permeate) into twice-concentrated skim milk resulted in bulk phase separation of gelling systems as shown by reduction in turbidity parameter (1/l*) and diffusion coefficient using diffusing wave spectroscopy (DWS). However, by controlling the kinetics of gelation and phase separation (using shear in renneted milk before BG addition), it was possible to create casein networks with entrapped BG. $CaCl_2$ was added to reduce time of gelation (TG), and increase textural properties, where high concentrations of BG (≥0.6%) resulted in weakening of protein gel network. The effects of shear and the presence of $CaCl_2$ on microstructure and rheological behavior of the renneted gels containing BG were monitored using DWS combined with small deformation rheology. In addition, BG distribution in the rennet gel network was observed by differential staining technique (Calcofluor and Rhodamine B, for BG and protein, respectively) using confocal laser scanning microscopy. The results showed that the onset of protein interactions, illustrated by the turbidity parameter, and the aggregation point, measured by the diffusion coefficient, were strongly affected by increase in BG concentration. BG-containing gels exhibited a significantly lower elastic modulus (G′) compared with their control counterparts ($P \leq 0.05$). Increase in BG concentration delayed the TG, and reduced gel firmness due to the non-interacting nature of the BG polymer. In contrast, the addition of $CaCl_2$ reduced the TG and produced a firmer gel in both control and BG added samples. BG addition could improve the texture and nutritional value of calorie-reduced cheeses, whose hard texture has traditionally been a barrier to their production.

Key Words: β-glucan, concentrated milk, renneting

LB5 Genome-wide association of a novel porcine stress-syndrome and isoflurane sensitivity to dystrophin. D. J. Nonneman*, T. M. Brown-Brandl, S. A. Jones, and G. A. Rohrer, *USDA, ARS, US Meat Animal Research Center, Clay Center, NE*.

Losses of slaughter-weight pigs due to transport stress are an economic concern to pork producers. Historically, the HAL-1843 mutation in the ryanodine receptor 1 gene was considered responsible for most of the losses; however, DNA testing has effectively eliminated this mutation from commercial herds. We identified 2 sibling barrows in the USMARC swine herd that died after transport to a research location at 8 weeks of age. The original mating was repeated along with sire-daughter matings to produce additional offspring. Pigs were challenged with isoflurane anesthesia (3% for 3 min) at 8 weeks. Heart rate and ECG were monitored during anesthesia and blood was collected one week before challenge and immediately after isoflurane administration. Four males from the original sire-dam mating and 2 males from a sire-daughter mating died after one minute of anesthesia. Animals from 6 other litters were identified as having a stress response, sometimes resulting in death, during regular processing and weighing. Their littermates were also challenged with isoflurane. Affected animals tended to have elevated plasma creatine phosphokinase (CPK) levels and cardiac arrhythmias, as determined by ECG. Pedigrees containing 58 pigs including 14 affected animals were genotyped with the Illumina Porcine 60K SNP Beadchip and 2 chromosomal regions were significantly associated with the syndrome at the genome-wide level. One is on SSC14 at position 82.7 to 88.9 Mbp, and the other is on SSCX at 25.1 to 27.7 Mbp over the dystrophin gene. In addition to muscular dystrophies, mutations in human dystrophin can cause dilated cardiomyopathy, rhabdomyolysis, and a malignant hyperthermia-like reaction in response to inhaled anesthesia, which supports this locus as a cause for the observed phenotypes in pigs. The identification of the causative mutation in these families will allow investigation of the prevalence of this disease in commercial populations.

Key Words: swine, stress, genotyping

LB6 Duration of maternal undernutrition differentially alters fetal development and metabolism in twin sheep pregnancies. M. Field*, R. Anthony, T. Engle, S. Archibeque, and H. Han, *Colorado State University, Fort Collins*.

Maternal undernutrition is known to impact fetal development and predispose the offspring to the metabolic syndrome later in life. We examined the impact of maternal undernutrition during early- to mid-gestation or from early gestation until near term on twin sheep pregnancies. Multiparous whiteface ewes (n = 19) were randomly assigned to one of 3 treatments beginning on 28 d of gestational age (dGA). Ewes were either fed 100% (Control; n = 7), or 50% of nutrient requirements from 28 to 78 dGA and readjusted to 100% beginning at 79 dGA (50-100; n = 5) or 50% of requirements from 28 to 110 dGA, followed by a 5% increase at 5 d intervals until 135 dGA (50-50; n = 7). Body weight of the Control (4.3 kg) fetuses were intermediate between the 50-50 (4.1 kg) and 50-100 (4.6 kg; $P < 0.05$). Organ weights differed between 50-50 and 50-100 fetuses ($P < 0.05$). Uterine artery glucose concentrations did not differ ($P = 0.35$), but 50-100 dams (98.8 mg/dL) were numerically higher than Control (76.6 mg/dL) and 50-50 (81.2 mg/dL) dams. The uterine artery:umbilical vein glucose gradient was numerically higher in 50-100 (50-100 = 65.5 mg/dL; Control = 52.3mg/dL; 50-50 = 53.2 mg/dL). The same trend was noted in umbilical vein glucose (50-100 = 34.4mg/dL; Control = 27.7 mg/dL; 50-50 = 25.7 mg/dL; $P = 0.23$). Interestingly, the umbilical vein:artery glucose gradient was less ($P < 0.05$) in 50-50 (4.68 mg/dL) fetuses compared with Control (6.84 mg/dL) and 50-100 (7.02mg/dL) fetuses. A similar trend was seen with umbilical vein:artery differences in O_2 content (50-100 = 4.43 m*M*; Control = 5.02 m*M*; 50-50 = 3.41 m*M*; $P = 0.10$). In conclusion, lower glucose and O_2 content gradients in 50-50 fetuses suggest lower metabolic rates resulting from long-term maternal diet restriction, while mid gestation realimentation may program maternal and placental glucose metabolism, providing for accelerated fetal growth.
Supported by USDA-NIFA-NRI grant 2009-35206-05273.

Key Words: undernutrition, pregnancy, sheep

LB7 Bovine mammary stem cells: Transcriptome profiling and the stem cell niche. R. K. Choudhary*[1], R. W. Li[2], C. M. Evock-Clover[2], and A. V. Capuco[2,1], [1]*Department of Animal and Avian Sciences, University of Maryland, College Park,* [2]*Bovine Functional Genomics Laboratory, USDA-ARS, Beltsville, MD*.

Identification and transcriptome analysis of mammary stem cells (MaSC) are important steps toward understanding the molecular basis of mammary epithelial growth, homeostasis and tissue repair. Our objective was to evaluate the molecular profiles of 4 categories of cells within

the bovine mammary epithelium, 2 subpopulations of putative stem cells and 2 subpopulations of control cells, with the goal of localizing and characterizing MaSC in situ. Putative MaSC were identified based upon their ability to retain the thymidine analog, bromodeoxyuridine (BrdU), for an extended period. Five Holstein calves were injected with BrdU, tissue was harvested 45 d later and label retaining epithelial cells (LREC) were identified in mammary cryosections by immunostaining. Using laser microdissection, LREC from basal (LRECb) and embedded (LRECe) layers of mammary epithelium were isolated along with adjacent control epithelial cells (EC). Cells (6–13) in each category per heifer were lysed, cDNA synthesized, amplified and labeled for microarray hybridization. Data analysis revealed 592 differentially expressed genes ($P \leq 0.05$; ≥2-fold change) between LRECb and basal EC, and 110 genes between LRECe and their embedded EC. Of these, 387 genes with enriched expression in LRECb were involved in cell growth and proliferation, cell cycle, and post-translational modifications. Low expression of estrogen receptor-β and high expression of aldehyde dehydrogenase 3B1 in LRECb were consistent with stem cell character. We found high expression of *NR5A2* (pluripotency transcription factor) and no expression of *XIST* (X-chromosome inactivation factor) in LRECb. Comparison between LRECb and LRECe showed downregulation of cell survival and proliferation factors (*IGF2, HSPB6, LAMC1*), nestin (stem cell marker), epigenetic modifiers (*JRID2, METTL33, SMARCC2*), and upregulation of apoptotic genes (*SFRS5, THAP3*) and *XIST* in LRECe. We conclude that BrdU label retention identifies stem and progenitor cells, wherein MaSC (LRECb) are located in the basal region of the mammary epithelium and committed progenitor cells (LRECe) are localized in more apical layers.

Key Words: mammary stem cell, progenitor, microarray

LB8 First metagenomic analysis of the rumen microbiome of dairy cows with subacute ruminal acidosis and identification of specific *Escherichia coli* virulence factors. E. Khafipour*[1], A. C. Little[1], N. C. Berard[1], P. C. Aikman[2], S. Li[1], S. E. Dowd[3], J. C. Plaizier[1], and D. O. Krause[1], [1]*University of Manitoba*, *Winnipeg, MB, Canada*, [2]*University of Reading*, *Earley Gate, Reading, United Kingdom*, [3]*Medical Biofilm Research Institute*, *Lubbock, TX*.

Subacute ruminal acidosis (SARA) is a metabolic disease in high-producing dairy cattle characterized by low rumen pH, reduced feed intake, lower milk fat, and systemic inflammation. We reproduced similar low rumen pH conditions of SARA with an alfalfa-pellet or a high-grain diet, but only the high-grain fed animals showed symptoms of SARA other than rumen pH depression. To further investigate rumen dynamics rumen DNA samples were subjected to next generation high-throughput pyrosequencing of 16S rRNA. A total of 81,416 sequences were generated of which 39,599 were unique. Sequences were converted to categorical data using a standard taxonomy by comparing the sequences to 16S rRNA databases. A negative binomial distribution was fitted to the data and analyzed using generalized linear mixed-model methodology (GLIMMIX) of SAS for categorical data. A total of 16 phyla were represented in the data set, with *Bacteroidetes*, *Firmicutes*, and *Proteobacteria* forming the most dominant phyla. Loss of *Bacteroidetes* was associated ($P < 0.05$) with grain-induced SARA suggesting that members of this phyla (*Prevotella* and *Bacteroides*) have a protective role in the rumen. Gram-negative *Proteobacteria* were associated ($P < 0.05$) with grain-induced SARA. To further evaluate the role of *Proteobacteria* we isolated *Escherichia coli* from rumen samples and performed PCR analysis on 25 *E. coli* virulence factors. *E. coli* were at least 3-logs ($P < 0.05$) higher in grain-induced SARA and curli fibers were highly associated ($P < 0.01$) with *E. coli* from grain induced, but not alfalfa pellet induced SARA. Curli fibers were first identified in *E. coli* isolated from bovine mastitis and attack tight junctions between cells potentially increasing permeability of the rumen epithelium to antigens. This is the most comprehensive metagenomic study of the rumen and the first in which specific virulence factors have been identified that potentially explain the etiology of SARA.

Key Words: subacute ruminal acidosis, rumen microbiome, *Escherichia coli*

ABSTRACTS

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Sunday, July 11, 2010
SYMPOSIA AND ORAL SESSIONS

Triennial Growth Symposium: Dietary Regulation of Growth and Development

1 Vitamin D mediated phosphate homeostasis—Implications for skeleton growth and mineralization. T. D. Crenshaw,* *University of Wisconsin*, *Madison.*

Foundational roles of vitamin D (D) in skeletal growth involve interrelationships between Ca, PTH, and conversion of D to the active hormone, 1α, 25-$(OH)_2$ D_3. Until the past decade relatively little research focused on these interrelationships and P homeostasis. A focus on Ca was driven, in part, by the limiting amount of Ca and abundance of P in human diets. Most ingredients used in monogastric animal diets are limiting in Ca and P. Ca and P have been typically supplied in excess of requirements from inorganic sources with minor incentives to improve nutrient efficiency. Constraints on amounts of supplemental P are driven by ingredient costs and environmental concerns. Thus P, not Ca, is typically more limiting in monogastric diets. The introduction of phytase supplements has only exasperated the need to understand P homeostasis. In the past 5 yr, discovery of novel pathways for P homeostasis offer opportunities to improve P efficiency without compromising skeletal growth and animal well-being. The objective of this review is to summarize interrelations of dietary P, D and the role of fibroblast growth factor 23 (FGF23) in P homeostasis. FGF23 directly affects P homeostasis via action on a renal Na-P transport protein and renal 1 α-hydroxylase activity. FGF23 is produced primarily in osteocytes which allow localized osteocyte regulation of osteoblast-mediated bone formation and regulation of systemic renal P excretion relative to needs for bone mineralization. In transgenic mice, overexpression of FGF23 led to hypophosphatemia and urinary P wasting. In contrast FGF23 knockout mice displayed hyperphosphatemia and renal P conservation. Current studies in our lab have shown that deletion of D supplements in diets fed to sows during gestation and lactation compromised ($P < 0.05$) skeletal bone mineral content in offspring at 13 wk of age and decreased the age at which pigs displayed kyphosis. These responses appear to be mediated by the efficiency of dietary P use. In summary, development of dietary inputs to balance both Ca and P homeostasis are needed to improve skeletal growth and nutrient efficiency.

Key Words: FGF23, kyphosis, Na-P transport

2 Effects of polymeric carbohydrates on growth and development. K. E. Bach Knudsen,* *Aarhus University, Faculty of Agricultural Sciences*, *Department of Animal Health and Bioscience, Tjele, Denmark.*

The main objective of the presentation is to provide insight into the role of polymeric carbohydrates in growth and development of pigs. Polymeric carbohydrates—starch and non-starch polysaccharides (NSP)—quantitatively represent the largest portion of the diets for pigs and are therefore the largest energy contributor. The 2 types of polysaccharides, however, have different fates and functions in the gastrointestinal tract and lead to different metabolites upon digestion. Pancreatic and mucosal enzymes in the small intestine break down the majority of starch, while NSP primarily are degraded by the microflora in the large intestine. Starch degradation leads to the release of glucose which is absorbed by an active absorption process that triggers the release of insulin from the pancreas, whereas the fermentation of NSP to short-chain fatty acids (SCFA: acetate, propionate and butyrate) occurs at a slower and more constant rate and with SCFA being absorbed by passive diffusion. Type and levels of polymeric carbohydrates influence growth and development through different mechanisms; first, the proportion of starch to NSP plays an important role for the content of available energy (digestible, metabolized and net energy); available energy relative to protein is crucial for performance and carcass quality; second, the proportion of starch to NSP will influence rate and type of metabolites (glucose vs. SCFA) deriving from carbohydrate assimilation, and finally, type of starch (types A, B, and C) and soluble NSP will influence the release of insulin, the hormone that facilitate nutrient uptake by tissues, organs and cells, and thus play a critical and essential role in protein synthesis and muscle growth as well as lipid synthesis and adipose tissue growth. In conclusion, polymeric carbohydrates influences growth and development through events in the gut and direct and indirect effects of different metabolites deriving from carbohydrate assimilation.

Key Words: polymeric carbohydrates, pigs, growth

3 Effect of feed additives on cattle growth and development. R. A. Zinn*[1], P. Garces-Yepez[2], and J. Salinas-Chavira[3],[1]*University of California*, *Davis,* [2]*UNAM*, *Mexico City, DF, Mexico*, [3]*UAT*, *Ciudad Victoria, Tam., Mexico*.

Feed additives are of themselves largely non-nutritive materials that are included in diet formulations to enhance health and growth performance. This presentation will focus on use of additives intended to enhance growth performance of feedlot cattle. They include: alkalizers (e.g., sodium bicarbonate, potassium carbonate, calcium carbonate, magnesium hydroxide), ionophores (e.g., laidlomycin, lasalocid, monensin, salinomycin), non-ionophore "mycin's" (e.g., bambermycins, virginiamycin), subtherapeutic antibiotics (e.g., chlortetracycline, tylosin), probiotics (e.g., *Lactobacillus*, *Bifidobacterium*, *Saccharomyces*), essential oils (e.g., cinnamonaldehyde, eugenol, limonene, terpinen, thymol, vanillin), enzymes (e.g., amylase, xylanase, cellulase), hormones (e.g., melengestrol acetate), and β-agonists (ractopamine, zilpaterol). This presentation will provide a brief overview of various additive classes, including possible modes of action, and practical measures of efficacy (growth performance and digestive function).

Key Words: additive, cattle, growth

4 Host targeted antibody strategies for preventing growth depression due to microbial colonization. M. E. Cook*[1,2] and S. M. Huebner[2], [1]*University of Wisconsin, Department of Animal Sciences*, *Madison,* [2]*University of Wisconsin, Department of Nutritional Sciences*, *Madison.*

The growth rate and feed efficiency of chicks and pigs colonized with commensal bacteria is only 80 to 90% of germ-free housed animals. Reduced growth of conventionally housed animals, when compared with germ-free animals, is the result of inflammatory processes. New information on the signaling pathways of inflammatory processes has provided scientists with new targets to improve animal growth and feed efficiency. It has become evident that inflammation can be regulated at the intestinal lumen/mucosa interface. Secretory phospholipase A2 (sPLA2) has emerged as a host target worthy of study. sPLA2 is secreted into the lumen of the gastrointestinal tract (GIT) during systemic inflammation. Following sPLA2 release, GIT permeability is increased, and sPLA2 action on phospholipids permit intracellular signal transduction for inflammatory mediator production (e.g., eicosanoids and cytokines). In addition, sPLA2 lipid products, such as lysophosphatidylcholine, can signal natural killer T cell (NKTC) cytokine production via the CD1d molecule on antigen presenting cells. Egg antibodies specific to host sPLA2 decreased lipopolysacchride-induced PGE2 and tumor necrosis factor release in macrophages and reduced cytokine production by NKTC. Egg anti-sPLA2 was tested in chick growth trials and found to improve growth and feed efficiency approximately 5%. Feeding anti-sPLA2 to pigs, calves, fish species resulted in improved growth. Studies were also conducted in animals with bacteria and protozoan challenges, and anti-SPLA2 was found to be protective in some diseased states or to have no beneficial or adverse effect on animal health. The anti-sPLA2 example suggests that inflammatory products and pathways are useful host targets for improving animal growth. Orally delivered antibodies, such as egg antibody, may serve as useful tools for discovering key mechanisms for increasing the efficiency for production of animal products.

Key Words: growth, inflammation, egg antibody

5 Neural regulation of feed intake: Modification by hormones, fasting and disease. J. L. Sartin*[1], B. K. Whitlock[2], and J. A. Daniel[3], [1]*Auburn University*, *Auburn, AL,* [2]*University of Tennessee*, *Knoxville,* [3]*Berry College*, *Mt. Berry, GA.*

Appetite is a complex process that results from the integration of multiple signals at the hypothalamus. The hypothalamus receives hormonal signals such as insulin, leptin and ghrelin to nutrient molecules such as glucose, free fatty acids, amino acids and volatile fatty acids. This effect is processed by a specific sequence of neurotransmitters beginning with the arcuate nucleus and orexigenic cells containing neuropeptide Y or agouti-related protein and anorexigenic cells containing proopiomelanocortin (POMC, yielding the neurotransmitter α-melanocyte stimulating hormone) or cells expressing cocaine amphetamine related transcript. These so called first order neurons end on second order orexigenic neurons containing either melanin concentrating hormone or orexin. The activity of these neuronal pathways are altered externally by nutritional alterations such as fasting or severe catabolic circumstances such as disease. In addition, there are other pathways from within the brain that may interact to dictate feed consumption patterns in farm animals. This review will begin with the central hypothalamic pathways and then discuss the ways in which hormones and metabolites may alter the process to impact on feed intake.

Key Words: appetite, leptin, NPY

6 Leucine acts as a nutrient signal to stimulate protein synthesis. T. A. Davis,* A. Suryawan, R. A. Orellana, and M. L. Fiorotto, *USDA/ARS Children's Nutrition Research Center, Department of Pediatrics, Baylor College of Medicine.*

The postprandial rise in amino acids and insulin independently stimulates protein synthesis in skeletal muscle of piglets. Leucine is an important mediator of the response to amino acids. We have shown that the postprandial rise in leucine, but not isoleucine or valine, acutely stimulates muscle protein synthesis in piglets. Leucine increases muscle protein synthesis by modulating the activation of signaling components of translation initiation. Thus, leucine increases the phosphorylation of mammalian target of rapamycin (mTOR), 70-kDa ribosomal protein S6 kinase, eukaryotic initiation factor (eIF)4E-binding protein-1, and eIF4G, decreases the phosphorylation of eIF2 α, and increases the association of eIF4E with eIF4G. However, leucine does not affect the canonical upstream activators of mTOR, i.e., protein kinase B, AMP-activated protein kinase, and tuberous sclerosis complex 1/2, or the translation elongation regulator, eukaryotic elongation factor 2. The acute leucine-induced stimulation of muscle protein synthesis is not maintained for prolonged periods, despite continued activation of the mTOR signaling pathway, because circulating essential amino acids fall as they are utilized as substrates for protein synthesis. However, if circulating amino acids levels are maintained, the leucine-induced stimulation of muscle protein synthesis can be maintained for prolonged periods. The activation of the mTOR signaling pathway by leucine does not appear to be affected by the circulating levels of other amino acids. Supplementation of low protein diets with leucine stimulates protein synthesis in muscle and most visceral tissues to a rate similar to that achieved by feeding high protein diets and this stimulation involves activation of the mTOR downstream effectors. Together, these studies indicate that leucine acts as a nutrient signal to stimulate translation initiation but whether this translates into a sustained increase in protein synthesis depends on the sustained availability of dietary amino acids.

Key Words: muscle, protein synthesis, amino acids

7 Important roles for L-glutamine in swine nutrition and growth. G. Wu,* F. W. Bazer, G. A. Johnson, R. C. Burghardt, D. A. Knabe, T. E. Spencer, X. L. Li, and J. J. Wang,*Texas A&M University*, *College Station.*

L-Glutamine (Gln) has traditionally not been considered as a nutrient needed in diets for livestock species or even mentioned in animal nutrition textbooks. This is due to previous technical difficulties in the analysis of Gln (free and protein-bound) and the unsubstantiated assumption that animals can synthesize sufficient amounts of Gln to meet their needs. Consequently, the current 10th version of NRC (1998) does not recommend dietary Gln requirements for growing, gestating or lactating swine. This lack of knowledge about Gln nutrition has contributed to suboptimal efficiency of global pig production. Because of recent advances in analytical methods and biochemical research, Gln is now known to be an abundant amino acid in physiological fluids (e.g., milk and fetal fluids) and proteins (both plant and animal), as well as a major fuel for rapidly dividing cells (including enterocytes and lymphocytes) and a key regulator of gene expression. Additionally, Gln participates in cell signaling via the mammalian target of rapamycin pathway, AMP-activated protein kinase, extracellular signal-related kinase, Jun kinase, mitogen-activated protein kinase, and nitric oxide. Exquisite integration of these regulatory networks has profound effects on cell proliferation, differentiation, metabolism, homeostasis, survival, and function. As a result of translating basic research into practice, dietary supplementation with 1% Gln maintains gut health and prevents intestinal dysfunction in low-birth-weight piglets and early-weaned piglets, while increasing their growth performance and survival. Also, supplementing 0.6% Gln to a corn- and soybean meal-based diet between d 30 and 114 of gestation ameliorates fetal growth retardation in gilts. Furthermore, adding 1% Gln to a conventional diet enhances milk production by lactating sows. Thus, adequate amounts of Gln in diets are necessary to support maximum growth, development and production performance of swine.

Key Words: growth, physiology, requirement

8 Feedlot performance and carcass quality of conventionally raised lambs implanted with zeranol versus naturally raised lambs. S. R. Eckerman*[1,2], G. P. Lardy[1], M. M. Thompson[2], B. W. Neville[1], M. L. Van Emon[1,2], P. T. Berg[1], and C. S. Schauer[2], [1]*North Dakota State University, Department of Animal Sciences*, *Fargo,* [2]*Hettinger Research Extension Center*, *Hettinger, ND*.

Our objectives were to compare feedlot performance and carcass quality of conventional and naturally raised lambs. Two-hundred 88 crossbred lambs (34 ± 0.1 kg) were assigned randomly to one of 12 pens (6 pens/treatment) and fed a finishing ration for 112 d. Treatments were conventional (CONV) or naturally raised (NAT). Naturally raised lambs were fed 80% corn and 20% commercial supplement ad libitum (DM basis; 87.9% TDN and 15.8% CP) with decoquinate included. The NR lambs were not treated with antibiotics nor given growth promoting implants. Conventional lambs were fed a similar ration, with decoquinate, chlortetracycline and lasalocid included in the ration and were implanted with 36 mg zeranol on d 28 and treated with antibiotics as necessary, primarily for treatment of prolapse. Lambs were weighed and feed refusals collected every 28 d. Lambs were harvested on d 117 and carcass data collected 24 h post chill. Data were analyzed using the mixed procedures of SAS. Repeated measures was used to analyze period effects for ADG, DMI, and G:F. Treatment x period interactions were observed for ADG, DMI, and G:F ($P < 0.01$). From d 29 to 56, CONV lambs had increased ADG, DMI, and G:F ($P \leq 0.01$) compared with NAT lambs. However, ADG, DMI, and G:F were not different between treatments ($P \geq 0.06$) for d 0 to 112. Naturally raised lambs had greater rib eye area ($P = 0.03$), decreased body wall thickness ($P = 0.05$), and a greater percentage boneless, closely trimmed retail cuts ($P = 0.05$). More CONV lambs prolapsed rectally or vaginally ($P = 0.001$; 8.3 vs 0%) which increased mortality ($P = 0.01$; 2.8 vs 0%). Lambs managed utilizing antibiotics, implants, and ionophores may have increased growth performance compared with lambs raised naturally, but may have diminished carcass quality and are more susceptible to prolapse and mortality.

Key Words: lamb, zeranol, naturally raised

9 Effects of rumen protected arginine supplementation on ewe serum amino acid concentration, circulating progesterone, and ovarian blood flow. C. S. Saevre*[1,2], J. S. Caton[1], J. S. Luther[3], A. M. Meyer[1], D. V. Dhuyvetter[4], R. Musser[5], J. D. Kirsch[1], M. Kapphahn[1], D. A. Redmer[1], and C. S. Schauer[2],[1]*Department of Animal Sciences, North Dakota State University*, *Fargo,* [2]*Hettinger Research Extension Center, North Dakota State University*, *Hettinger,*[3]*University of Wisconsin River Falls*, *River Falls*,[4]*Ridley Block Operations*, *Mankato, MN,* [5]*SODA Feed Ingredients, LLC*, *Mankato, MN*.

Objectives were to determine if rumen-protected arginine supplemented to ewes on d 8 to 13 of the estrous cycle affected serum amino acid concentration, ovarian blood flow, and circulating progesterone. Nineteen multiparous Dorset ewes (63.8 ± 1.1 kg initial BW) were individually housed and randomly allocated to 1 of 4 rumen-protected arginine treatments: 0 (CON, n = 5), 90 (90 ARG, n = 4), 180 (180 ARG, n = 5), or 360 mg/kg BW supplemental arginine (360 ARG, n = 5). Following estrous synchronization, ewes were individually fed rumen-protected arginine blended into 150 g ground corn, which was immediately followed with 650 g of a pelleted diet (2.40 Mcal ME/kg and 12.9% CP, DM basis) on d 8 to 13 of the estrous cycle. Jugular blood samples were taken for amino acid and progesterone analysis. On d 12, color Doppler ultrasonography was used to determine ovarian hemodynamics. Ewes fed 360 ARG had greater serum arginine concentration than CON, 90 ARG, and 180 ARG on d 11 (175.5 vs. 153.2, 132.3, and 145.4 ± 8.6 nmol/mL, respectively; $P = 0.01$) and d 12 (166.4 vs. 142.7, 121.7, and 128.2 ± 7.4 nmol/mL, respectively; $P = 0.002$). On d 11, arginine as a percent of total amino acid concentration was increased in 360 ARG compared with CON and 90 ARG (7.16 vs. 6.19, 5.70 ± 0.34 nmol/mL, respectively; $P = 0.04$). Total essential amino acid concentration was elevated in 360 ARG compared with 90 ARG and 180 ARG ($P = 0.08$) on d 12. Arginine supplementation increased peak systolic velocity in the corpus luteum for 360 ARG and 90 ARG compared with CON (30.53 and 32.59 vs. 22.63 ± 2.48 cm/s, respectively; $P < 0.07$). Flow time (milliseconds) in the ovarian hilus and corpus luteum was increased in 360 ARG compared with all other treatments ($P \leq 0.02$ and $P \leq 0.06$, respectively). Supplemental rumen-protected arginine had no effect on serum concentration of progesterone ($P > 0.50$). Results indicate that rumen-protected arginine supplemented to ewes at the rate of 360 mg/kg BW may increase circulating serum arginine concentration, in addition to increasing ovarian blood flow.

Key Words: arginine, ovarian hemodynamics, sheep

10 Effect of wet distillers grains with solubles on rumen bacterial community profiles in individually fed cattle. L. N. Tracey*[1], J. Browne-Silva[1], C. H. Ponce[2], J. B. Osterstock[3], J. C. MacDonald[2,3], M. Brown[2,3], and S. L. Lodge-Ivey[1],[1]*New Mexico State University*, *Las Cruces,* [2]*West Texas A&M*, *Canyon,* [3]*Texas AgriLife Research*, *Amarillo.*

Despite the growing use of wet distillers grains with solubles (WDGS) in the US, very few data are available that describe potential rumen fermentation and microbial ecology alterations that may occur by feeding higher concentrations of WDGS. The objective of this experiment was to evaluate the effects of WDGS on ruminal bacterial communities. Twenty-three steers that had been acclimated to steam-flaked corn finishing ration (average BW = 340 ± 29.6 kg) were randomized and assigned to one of 3 treatment groups. Cattle were individually fed via calan gates once per day. Treatments were replacement of steam-flaked corn with 0, 30, or 60% WDGS (DM basis; n = 7, 8, and 8, respectively). Ruminal fluid was collected once per wk for 5 wk via esophageal tubing before feeding. Samples were frozen and stored at −20°C for further analysis. Ruminal fluid community DNA and 16S rDNA was amplified and analyzed by denaturing gradient gel electrophoresis (DGGE). Clustering of DGGE banding patterns was normalized to an external standard and compared based on binary and numerical coefficients of Dice and Pearson, respectively. Binary banding patterns for all samples were 59.8% similar and total number of bands per sample was not influenced by treatment ($P = 0.96$). Analysis of treatment dendrograms for binary banding pattern revealed a decrease in similarity from 30 to 60% WDGS, with 0% being intermediate (68.5, 71.2, and 59.2 ± 7.09% for 0, 30, and 60% WDGS, respectively). Banding pattern similarity decreased during the duration of the experiment (73.4, 80.4, 72.8, 60.0, and 61.9 ± 8.65% for wk 1–5, respectively). Construction of dendrograms based on band intensity resulted in a dramatic reduction (19.2 ± 12.32%) of similarity across treatments. These results indicate feeding high levels of WDGS does not decrease the richness of the bacterial population but shifts in individual bacterial community members do occur.

Key Words: wet distillers grains with solubles, cattle, bacteria

11 Forage selection preferences by multiparous and primiparous beef cows grazing native tallgrass range during winter. N. A. Sproul,* L. W. Murray, J. R. Jaeger, D. A. Blasi, L. N. Edwards, G. J. Eckerle, L. A. Pacheco, and K. C. Olson, *Kansas State University*, *Manhattan.*

Our objective was to evaluate diet selection preferences of 18 experienced multiparous and 20 naive primiparous beef cows (9 and 2 yr old, respectively) grazing dormant, native tallgrass pastures during winter. The study was analyzed as a 4-period, 8-pasture (average size = 28 ha) Latin rectangle. Predominant pasture forage species were *Andropogon geradii* and *Schizachyrium scoparium*, which were grouped together for analysis (BL); *Bouteloua curtipendula* (SO); *Bouteloua gracillis*, (BG); *Panicum virgatum* (SG); *Sorghastrum nutans* (IG); *Amorpha canescensi* (LP); *Symphyotrichum ericoides* (HA); *Liatris punctata* (DG); and *Dalea purpurea* (PP). Animals were grouped randomly by parity status (n = 4 or 5) and grazed 1 of 4 assigned pastures during 4 consecutive 48-h periods. Fecal samples were collected from each animal at the end of each period. Range-plant fragments in fecal samples were quantified using a modified microhistological technique; plant fragment prevalence in fecal material was assumed to be equivalent to diet composition on a DM basis. Primiparous cows selected more forbs and fewer grasses (main effect of parity; $P = 0.09$) than multiparous cows. Multiparous cows ate more ($P = 0.07$) BL and less DG ($P = 0.05$) than primiparous cows. Consumption of all forbs, PP, LP, and DG by both classes of cows declined ($P \leq 0.04$) over time, while consumption of all grasses, BL, and BG increased over time ($P \leq 0.02$), possibly indicating that forb availability diminished over time. Occasional differences in consumption of IG, SG, SO, and HA between primiparous and multiparous cows occurred; however, differences were inconsistent (parity × period effect; $P \leq 0.02$) over time. Differences in diet selection patterns between multiparous and primiparous cows during a short-term winter grazing period could be indicative of differences in long-term foraging strategies. We interpreted these data to suggest that foraging strategies associated with cow stayability may be related to selection preferences during periods of poor forage quality.

Key Words: botanical composition, beef cows, grazing

12 Dry matter intake is repeatable over parities and residual feed intake is negatively correlated with dry matter digestibility in gestating cows. T. J. McDonald,* B. M. Nichols, M. M. Harbac, T. M. Norvell, and J. A. Paterson, *Montana State University*, *Bozeman*.

Feed costs account for approximately two-thirds of total cash inputs for cow/calf producers. Selecting cows that consume less DM, but maintain production, would lower breakeven costs. The objectives of these 2 experiments were to determine repeatability of DMI over parities, calculate residual feed intake (RFI), and examine the relationships between RFI and diet DM digestibility. Nichols et al. (2010, these proceedings) previously determined individual DMI for 120 gestating, primiparous heifers in 2008. Twenty-four of these heifers that had the highest and lowest DMI were selected for this 2009 experiment. Cows (3-yr-old, BW = 593 ± 50 kg, second trimester gestation) were fed a diet composed of 74% grass hay and 26% grain-based supplement (104% of MP requirement) to determine the correlation of DMI per $BW^{.75}$ between 2008 and 2009 when cows were in a similar gestational state. Diets were limit fed at 12.7 kg DM•cow^{-1}•d^{-1} using a GrowSafe system. Cows were adapted to the diet for 10 d, followed by a 70-d trial to determine individual feed intakes and weight gain. Residual feed intake was calculated as the residual from the linear regression of DMI on $BW^{.75}$ and ADG. Dry matter intake per $BW^{.75}$ was highly correlated (r = 0.71, $P < 0.01$) between first and second parities. Residual feed intake ranged from 4.46 kg/d to −4.58 kg/d. Immediately following Exp. 1, cows were fed for an additional 5 d for collection of feces (Exp. 2). Grab samples were collected daily at 0600 and 1800, and indigestible ADF was used to estimate DM digestibility. Residual feed intake was negatively correlated with DM digestibility (r = −0.51, $P = 0.03$, range = 62.6% to 74.2%) but had no relationship with digestible DMI ($P = 0.32$). Results showed that DM intakes were repeatable over parities, and as RFI increased, DM digestibility of a forage-based diet decreased.

Key Words: residual feed intake, gestation, digestibility

13 The relative importance of weaning management and vaccination history on performance by ranch-direct beef calves during weaning and receiving. M. J. Macek*[1], J. W. Iliff[1], K. C. Olson[1], J. R. Jaeger[2], T. B. Schmidt[3], D. U. Thomson[1], and L. A. Pacheco[1], [1]*Kansas State University*, *Manhattan,* [2]*Western Kansas Agricultural Research Center*, *Hays,* [3]*Missisippi State University*, *Starkville.*

Angus × Hereford calves (n = 437; average initial BW = 208 ± 25 kg) were stratified by BW, sex, and age and assigned randomly to 1 of 3 treatments that corresponded to length of time between weaning and shipping to a feedlot: 45, 15 or 0 d. Within each weaning period length, calves were assigned randomly to 1 of 2 bovine respiratory disease (BRD)-vaccination treatments: vaccinated 14 d before weaning and again at weaning (PRE) or vaccinated on the d of arrival at the feedlot and again 14 d later (POST). On a common shipping date, calves were transported 3 h to an auction market and held for 12 h. Calves were then transported 1 h to a feedlot. Calves were fed the same diets ad libitum throughout the study. Incidence of undifferentiated fever 15 d after weaning was greater ($P < 0.01$) for calves weaned 45 d before shipping than for calves weaned 15 d before shipping; however, ADG before shipping was greater ($P < 0.01$) for calves weaned 45 d than those weaned 15 d. Incidence of undifferentiated fever and ADG before shipping were similar ($P > 0.66$) between PRE and POST. Average DMI before shipping by 45-d calves was less ($P < 0.01$) than that by 15-d calves. Also, DMI by PRE calves was less ($P = 0.03$) than that by POST calves. Incidence of undifferentiated fever during receiving was similar ($P \geq 0.73$) between weaning and vaccination treatments. Calf ADG during receiving tended to be greater ($P < 0.07$) for 45- and 15-d calves than for 0-d calves. Receiving DMI increased ($P < 0.01$) as number of d between weaning and shipping increased. Conversely, the timing of vaccination did not affect ($P \geq 0.51$) ADG or DMI during receiving. Growth efficiency was similar ($P \geq 0.36$) among weaning and vaccination treatments. Weaning more than 15 d before shipping did not improve health or growth of cattle that were moved from their ranch of origin to a feedlot within 16 h and were not commingled with market-sourced cattle. Pre-shipment BRD vaccination may not change health or performance of ranch-direct cattle relative to BRD vaccination deferred until feedlot arrival.

Key Words: health, preconditioning, weaning

14 Effects of sun-curing and harvest maturity on concentration and protein-binding capacity of condensed tannins in sericea lespedeza (*Lespedeza cuneata*). G. J. Eckerle*[1], K. C. Olson[1], J. R. Jaeger[2], J. L. Davidson[3], T. K. Kraft[1], and L. A. Pacheco[1], [1]*Kansas State University*, *Manhattan,* [2]*Western Kansas Agricultural Research Center*, *Hays,* [3]*Greenwood County Extension*, *Eureka, KS.*

A study was conducted to evaluate the effects of sun-curing and harvest maturity on concentrations of condensed tannins (CT) and protein-precipitable phenolics (PPP) in sericea lespedeza (SL). Samples of SL (n = 200 plants/sample) were collected from a single native tallgrass pasture at 1 to 4-wk intervals from June 24 to October 11 that corresponded to

single-stem, branched-stem, budding, flowering, and senescent stages of plant phenology. Samples were divided randomly into 2 equal portions that were either dried via sun-curing or were frozen immediately after harvest and later freeze-dried. Total phenolics were extracted from dried, ground SL samples using a modified methanol-extraction technique and were analyzed for CT and PPP. Concentrations of CT in sun-cured SL were less (main effect of treatment, $P < 0.01$) than that in fresh SL. Concentration of CT in SL responded cubically ($P < 0.01$) over time; CT was least during June and October and peaked from late July to mid September. Peak CT concentration corresponded to the budding and flowering stages of the SL life cycle. Concentrations of PPP in SL also changed over time but the magnitude of the effect was influenced by treatment (treatment × period, $P < 0.01$). Concentrations of PPP in sun-cured SL responded cubically ($P < 0.01$) as the growing season advanced; PPP was least during June and October and peaked during July and August. In contrast, PPP in fresh SL increased quadratically ($P < 0.01$) over time, indicating that significant concentrations of PPP remained in SL late into the growing season. Concentration of CT and PPP in SL decreased dramatically during drying and storage. These data may explain why sharp avoidance of SL by grazing livestock is not generally observed when SL is fed in the form of sun-cured hay. Understanding how drying and plant growth stage influence tannins in SL could lead to more effective research models for the study of SL intake by ruminants.

Key Words: condensed tannin, noxious weed, sericea lespedeza

15 Effects of gestational dietary metabolizable protein level and dry matter intake on subsequent production traits in primiparous heifers. B. M. Nichols*[1], T. J. McDonald[1], M. M. Harbac[1], A. J. Roberts[2], and J. A. Paterson[1], [1]*Department of Animal and Range Sciences, Montana State University*, *Bozeman,* [2]*USDA-ARS, Fort Keogh Livestock and Range Research Laboratory*, *Miles City, MT.*

The objective of this experiment was to determine if feeding 2 levels of dietary metabolizable protein (102% vs. 119% of NRC requirements) and biological variation in feed intake during the second and third trimesters of gestation influenced subsequent production traits in primiparous heifers. Two-yr-old Angus and Simmental x Angus heifers (n = 120, initial BW = 448 ± 36 kg) had individual DMI determined using a GrowSafe feeding system. Dietary treatments were based on approximately 85% grass hay and 15% supplement. Supplements contained whole soybeans plus corn (102% MP) or dried distillers grains plus soybean meal (119% MP) and each supplement was assigned to 2 pens. Heifers were randomly assigned to one of 3 periods (P; 40 heifers/P) followed by random assignment to one of 4 pens (10 heifers/pen). Diets were fed at approximately 10.3 kg DM•heifer^{-1}•d^{-1}. After 35 d of intake measurement, heifers were placed into adjacent pens and fed their diets for an additional 50 (P1 and 2) or 82 d (P3). The next 40 heifers (P2) were placed in the facility and DMI was again determined over 35 d. Upon completion of the feeding trial, heifers were returned to the ranch, managed as a single group, and production data were measured. Level of dietary MP had no effect ($P > 0.17$) on calf birth weight, adjusted 205 d weight, ADG, age at weaning, cow BW at calving, proportion of cows cycling at bull turnout, or proportion of cows which conceived. Dry matter intake per unit of BW$^{0.75}$ (range = 0.057 - 0.187 kg/kg) did not affect ($P > 0.17$) any of the variables measured. Under the conditions of this study, feeding MP in excess of NRC recommendations during mid- to late-gestation did not enhance subsequent heifer productivity. Heifers that consumed less DM/kg BW$^{0.75}$ produced similarly to heifers that consumed more DM/kg BW$^{0.75}$.

Key Words: metabolizable protein, dry matter intake

16 Sampling bias when estimating adipocyte cellularity. G. D. Cruz*[1], J. A. Oliveira[2], T. R. Famula[1], and J. G. Fadel[1], [1]*University of California*, *Davis,* [2]*Universidade Federal de Goiás*, *Goiânia, Goiás, Brazil*.

The objective of this study is to determine if a random adipose sample would represent the overall cellularity mean within the *Longissimus dorsi* at the 12th rib. Marbling is a major factor in the determination of beef quality grades and is evaluated by appraisal of the *Longissimus dorsi* at the 12–13th rib interface in the United States. Thus, a goal is to increase marbling without negatively affecting carcass characteristics. A common measurement of the development and distribution of adipocytes is through cellularity, which involves measurements of size and number of adipocytes. Current estimates rely on one sample obtained from the muscle. To evaluate sampling bias, one muscle (2.54cm thick) was divided horizontally into halves of 1.22cm and each half was vertically divided in approximately 10 strips of various lengths for a total of 20 strips. These 20 strips were placed next to each other and 10 were selected by choosing every other one. These strips were evenly divided horizontally into a total of 89 samples. Twenty-five milligrams of marbling fat were dissected from each sample and osmium tetroxide technique was applied to estimate adipocyte cellularity. A random number generator was used to choose 5 samples to represent the muscle. The mean diameters of the samples were 72.4, 90.7, 77.0, 93.4, and 94.2 µm and the overall mean diameter was 81.6 µm. The mean number of cells for each sample was 2.73, 6.36, 1.38, 5.41, and 1.40 cells/g × 10^{-5} and the overall mean number was 2.59 cells/g × 10^{-5}. The mean diameter of each of the 5 samples was different ($P < 0.01$) from the overall mean. Also, 3 of the 5 samples were different (($P < 0.01$) from the overall mean number of cells. In conclusion, sampling bias is the major source of variation when estimating adipocyte size and number. A sampling technique should be developed to reduce sampling bias and increase the precision when estimating adipocyte cellularity. Currently our laboratory is developing such technique.

Key Words: adipocyte cellularity, sampling bias, beef cattle

17 Effect of forage energy intake and supplementation on marbling deposition in growing beef cattle. E. D. Sharman,* P. A. Lancaster, G. G. Hilton, C. R. Krehbiel, and G. W. Horn, *Oklahoma Agricultural Experiment Station*, *Stillwater*.

Glucose is the primary carbon source for fatty acid synthesis in intramuscular fat, whereas, acetate is primarily utilized by subcutaneous fat. Our objective was to examine the effect of forage energy intake and type of fermentation on marbling deposition by stocker cattle grazing dormant native range (DNR) or winter wheat pasture (WP). Angus steer calves (n = 68; 258 ± 29 kg) were used in a completely randomized design comparing 4 winter grazing treatments: (1) control, 1.02 kg•hd^{-1}•d^{-1} of a 40% CP supplement to meet their DIP requirement while grazing DNR; (2) control plus corn-based supplement at 1% BW while grazing DNR; (3) WP at a high stocking rate (3.2 steers/ha) to achieve a low rate of BW gain; and (4) WP at a low stocking rate (2.2 steers/ha) to achieve a high rate of BW gain. Supplements were fed individually 5 d/wk during the 138-d winter grazing phase. Following winter grazing, 3 steers per treatment were randomly selected for intermediate harvest. The remaining wheat pasture steers were transitioned to the finishing phase, while the DNR treatments remained on summer pasture for 115 d before finishing. Steers were fed to a predicted backfat end point of 1.27 cm. During winter grazing, ADG was 0.19, 0.52, 0.68, and 1.37 ± 0.03 kg/d ($P < 0.01$) for treatments 1–4, respectively. Steers that grazed WP had heavier HCW and larger REA ($P < 0.01$) at intermediate harvest than steers supplemented on DNR. Backfat was 0.03, 0.10, 0.17, and

0.85 ± 0.07 cm ($P < 0.01$) and marbling scores were 180, 217, 280, and 340 ± 11.67 ($P < 0.01$) for treatments 1–4, respectively. At harvest after finishing, treatment 3 had a thicker backfat and smaller REA resulting in higher YG ($P < 0.02$) compared with the other treatments. There were no differences in final marbling scores (423, 428, 427, and 425 ± 14.92; $P = 0.99$, respectively). These data indicate that growing programs differing in forage energy intake and type of fermentation can influence marbling deposition at the end of winter grazing; however, final marbling scores may not be affected when cattle are fed to a common fat end point.

Key Words: growing beef cattle, forage energy intake, marbling deposition

18 Grazing patterns of Angus, Brangus and Brahman cows in the Chihuahuan Desert. M. L. Russell,* D. W. Bailey, M. G. Thomas, B. K. Witmore, and C. C. Bailey, *New Mexico State University*, *Las Cruces.*

In extensive pastures, forage utilization may decrease due to limited water sources. However, adapted breeds of cattle may facilitate an improvement in grazing distribution by utilizing distant portions of extensive pastures. A 2-yr study was conducted to evaluate grazing distribution and quality of diet for Angus, Brangus and Brahman cows in the Chihuahuan Desert during 3 seasons (winter, early summer and late summer) using 3 pastures varying in terrain. Cows were tracked with GPS technologies every 10 min for 10- to 14-d periods in each pasture (3 periods per season). Pooled data from 7 cows of each breed were evaluated in 2008 utilizing a Latin square design with breed as the treatment and period and pasture as blocking factors (n = 9). Breeds were kept together during 2009 and evaluated for 10 to 14 d in each of 3 pastures during each season using breed and pasture as fixed effects. When cows were rotated among pastures, fecal samples were collected and analyzed using near infrared spectroscopy (NIRS) to estimate diet quality. In 2008, CP content of diets was similar ($P > 0.31$) among breeds during all seasons. Brahman cows regularly traveled greater distances per day than Angus or Brangus cows during early and late summer seasons in 2008 and 2009 ($P < 0.05$). Brahman cows traveled 12.4 ± 0.6 km/d while Angus and Brangus traveled 7.2 ± 0.6 and 8.3 ± 0.6 km/d, respectively, during late summer 2009. In contrast, average distance from water was similar ($P > 0.59$) among breeds during both 2008 and 2009, which suggests that distribution patters were similar. Diurnal movement patterns sometimes differed among breeds. In late summer 2009, Brahman cows (1.81 ± 0.11) made more ($P = 0.03$) trips to water each day than Angus (1.15 ± 0.11) or Brangus (1.36 ± 0.11); however, during the winter and early summer in 2008 and 2009, trips to water each day were similar ($P > 0.48$) among breeds. Spatial movement patterns of Brahmans appeared to differ from Angus and Brangus, however, no clear advantage in grazing distribution was observed for any breed.

Key Words: breed, distribution, telemetry

19 Arginine supplementation does not alter nitrogen metabolism of beef steers during a lipopolysaccharide challenge. B. H. Carter*[1], C. A. Löest[1], G. G. Gilliam[1], B. C. Graham[1], J. A. Carroll[2], C. T. Collier[2], and D. M. Hallford[1], [1]*New Mexico State University*, *Las Cruces,* [2]*USDA ARS*, *Lubbock, TX.*

Demand for Arg is reported to increase during immune challenges. This study evaluated effects of lipopolysaccharide (LPS) and abomasal Arg infusion on N metabolism and immune response of 20 ruminally cannulated steers (369 ± 46 kg BW) in a randomized block design. Each block consisted of a 14-d adaptation, 1-d blood collection, and 5-d fecal and urine collection. Steers were fed a diet (12.9% CP, 0.99 Mcal/kg NEg) at 1.5% BW. Treatments (2 × 2 factorial) were AA solutions with no Arg (-ARG) or 10 g/d Arg (+ARG), and sterile saline with no LPS (-LPS) or 1 µg LPS (+LPS; *E. coli* 055:B5) per kg BW. The AA solutions were abomasally infused (720 mL/d) from d 7 to 20; LPS solutions (100 mL) were intravenously infused (1 mL/min) on d 15. Rectal temperature (RT) and blood samples were collected 0, 2, 4, 8, 12, and 24 h after LPS infusion on d 15. No LPS × Arg × h or LPS × Arg interactions occurred ($P > 0.24$). Cortisol, IL-6, and RT were greater (LPS × h, $P < 0.01$) for +LPS vs -LPS at 2, 4 (peak), 8 and 12 h (cortisol, IL-6). Tumor necrosis factor-α was greater at 2 h, and haptoglobin was greater at 24 h in +LPS vs -LPS steers (LPS × h, $P < 0.01$). Plasma Ala was greater (LPS × h, $P = 0.04$) for +LPS vs -LPS at 2, 12, and 24 h. Plasma Met, Leu, Val, Gln, and Orn of +LPS vs -LPS steers were greater (Met, Leu) or not different (Val, Gln, Orn) at 0 h, not different at 2 and 4 h, lower at 8 (all) and 12 h (Met, Val, Gln, Orn), and either not different (Met, Val, Orn) or greater (Leu, Gln) at 24 h (LPS × h, $P < 0.01$). Plasma Thr, Ser, Asp, Asn, and Glu were lower (LPS × h, $P \leq 0.02$) for +LPS vs -LPS at 2 (Asn), 4, 8, 12, and 24 h (Thr, Ser, Asp, Glu). Plasma Ile and Pro were lower (LPS × h, $P < 0.01$) for +LPS vs -LPS at 4, 8, and 12 h (Ile). Plasma Lys, Tyr, and Trp were lower ($P < 0.05$) for +LPS vs -LPS, and plasma Ala, Pro, and Orn were greater ($P < 0.05$) for +ARG vs -ARG. The +LPS vs -LPS steers tended to have greater ($P = 0.13$) urinary N excretion and lower ($P = 0.11$) N retention, and steers infused with Arg had greater ($P < 0.01$) digested N and tended to have greater ($P = 0.15$) N retention. Abomasal infusion of Arg does not alter the effects of LPS on N metabolism.

Key Words: arginine, lipopolysaccharide, steer

20 Calcium and phosphorus metabolism in finishing steers supplemented with vitamin D_3. J. S. Schutz*[1], M. R. Genho[2], J. A. Scanga[3], K. E. Belk[1], G. C. Smith[1], and T. E. Engle[1], [1]*Colorado State University*, *Fort Collins,* [2]*Ascendant Partners, Inc.*, *Greenwood Village, CO,* [3]*Elanco Animal Health*, *Greenfield, IN.*

Twelve Angus steers (435kg ± 5.01) were used to determine the effect of high dietary vitamin D_3 (Vit D_3) on Ca and P metabolism in feedlot cattle. Steers were randomly assigned to one of 2 treatments: 1) 0.5×10^6 IU of Vit D_3•hd^{-1}•d^{-1} (0.5 Vit D_3) or 2) 5.0×10^6 IU of Vit D_3•hd^{-1}•d^{-1} (5.0 Vit D_3) for 8 consecutive days. Steers were maintained on a basal ration for 7 d, followed by 8 d of Vit D_3 supplementation and then 5 d of basal ration. Vitamin D_3 was administered via a premix carrier immediately before feeding the basal diet to assure complete consumption of Vit D_3. Individual daily DMI, 24-h urine volume and fecal excretion were recorded and sub-sampled daily for subsequent Ca and P apparent absorption and retention determination. Jugular blood samples were obtained before initiation of Vit D_3 supplementation, at the end of Vit D_3 supplementation, and 5 d following Vit D_3 supplementation. Vitamin D_3 supplementation increased ($P < 0.05$) serum concentrations of 25-OH_2-Vit D_3 in both treatments. Steers supplemented with 5.0 Vit D_3 had greater ($P < 0.05$) serum concentrations of 25-OH_2-Vit D_3 than 0.5 Vit D_3 supplemented steers. Serum Ca concentrations were higher in steers supplemented with 5.0 Vit D_3 compared with 0.5 Vit D_3 supplemented steers. Relative to baseline measurements for each treatment, apparent absorption and retention of Ca were reduced ($P < 0.05$) in steers supplemented with 5.0 Vit D_3 but not altered in steers supplemented with 0.5 Vit D_3. Apparent absorption and retention of dietary P were similar for both treatments. Daily urine excretion increased ($P < 0.05$) from the pre-supplementation period to the end of the Vit D_3 supplementation period and remained greater ($P < 0.05$) throughout the subsequent 5 d non-Vit D_3 supplementation period relative to baseline excretion volumes in

5.0 Vit D_3 supplemented steers. Supplementation of feedlot steers with 5.0 million IU of Vit D_3•hd^{-1}•d^{-1} increased serum Ca concentrations, decreased Ca absorption, and decreased retention of Ca.

Key Words: vitamin D, calcium, phosphorus

21 Genetic and environmental influences on distribution patterns of beef cattle grazing foothill rangeland. D. W. Bailey[1], S. Marta*[1], D. Jensen[2], D. L. Boss[2], and M. G. Thomas[1], [1]*New Mexico State University*, *Las Cruces,* [2]*Montana State University*, *Havre.*

A study was conducted in foothill rangelands of northern Montana to determine the relative effects of genotype and environment (or early learning) on grazing distribution. Based on 5 years of observations, 5 of 180 Hereford and Tarentaise crossed cows that used the highest and steepest terrain (hill climbers) and 5 cows that used the most gentle terrain near water (bottom dwellers) were used as donors for embryo transfer. A single AI sire was used in these matings. Crossbred recipient cows were classified as hill climbers (HC) and bottom dwellers (BD) based on 4 years of observation from a separate herd of 98 cows. This resulted in 2x2 factorial study with donor and recipient as the 2 factors and HC and BD as the 2 levels within each factor. A total of 28 of these cows were observed in late summer of 2009 when they were mature (4 to 6 years of age). Horseback riders recorded positions of cows during the early morning when they were gazing for 10 d during the 6 weeks cows were in the 336 ha study pasture. Elevation in the pasture ranged from 1184 to 1398 m and the average slope was 34%. Horizontal distance to water, elevation, and slope of the recorded positions of each cow were averaged together resulting in one value for each trait for each cow. Donor (genotype), recipient (environment) and the donor*recipient interaction were used as fixed effects in the statistical analyses. Distance from water and slope use were not affected by donors, recipients or the donor*recipient interaction ($P > 0.20$). Daughters of HC donors (1314 ± 7 m) used higher elevations ($P = 0.04$) than those from BD (1290 ± 8 m), and cows raised by HC recipients (1315 ± 7 m) also used higher elevations ($P = 0.04$) than cows from BD recipients (1290 ± 8 m). Cattle use of higher elevations in foothill rangeland appears to be influenced to at least some degree by both genetic (donor dam -daughter relationships) and environmental factors such as early learning (recipient dam - daughter relationships).

Key Words: genotype, early learning, behavior

22 *Propionibacterium acidipropionici* P169 and glucogenic precursors to improve rumen parameters associated with low quality forage. P. H. Sanchez,* L. Tracey, J. Browne-Silva, and S. L. Lodge-Ivey, *New Mexico State University*, *Las Cruces.*

Cattle grazing dormant western rangelands tend to have a high ruminal acetate to propionate ratio (A:P) and may have low tissue clearance of acetate. Two studies were conducted to evaluate the effects of *P. acidipropionici*, P169 (P169) on VFA production, forage digestibility, and rumen bacterial ecology. In Exp. 1, in vitro effect of P169 on IVDMD and VFA production was evaluated in a 2 × 2 factorial arrangement of treatments. Factors were substrate (dormant warm-season grass extrusa or 50:50 Sudan:corn, DM basis) and P169 (with or without). In Exp. 2, 12 2-yr old, pregnant Brangus heifers (BW = 416 ± 85 kg) were assigned to 1 of 3 treatment (n = 4). All cattle were fed a basal ration consisting Old World Blue stem hay at 1.5% BW 10 d before initiation of treatment and for the duration of the experiment. Treatments were 1) protein supplement (36% CP, 35% UIP of CP, DM basis, fed at 454 g/hd per d; CON), 2) CON plus P169 (6×10^{10} cfu/hd, twice per d; P169), 3) calcium-propionate supplement fed at 454 g/hd per d (36% CP, 53% UIP of CP + 80 g calcium propionate; PROP). Ruminal fluid was collected and analyzed for VFA, ammonia, pH and community DNA was extracted for denaturing gradient gel electrophoresis (DGGE). Glucogenic potential of treatment was evaluated with an acetate tolerance test on d 49. In Exp. 1, IVDMD, total VFA, acetate, propionate, and A:P increased ($P < 0$ 0.001) in both extrusa and 50:50 with P169 addition. In Exp. 2, the only effect of P169 on rumen parameters was a 4.3% increase in propionate ($P < 0.02$) over CON. Calcium-propionate supplement increased propionate and decreased A:P by 7.8% and 5.9% respectively ($P < 0.004$) over CON. Similarity of bacterial populations between treatments was evaluated with construction of a DGGE dendrogram using the Dice coefficient and samples were 73.9 ± 6.38% similar. Acetate half-life did not differ by treatment ($P = 0.49$). These data indicate that addition of propionate-producing bacteria to low quality forage diets could be as beneficial as supplementing with a propionic salt.

Key Words: cattle, propionate, *Propionibacterium acidipropionici*

23 Effects of supplemental docosahexaenoic acid to ewes on lamb production, immunocompetence, serum metabolites, and thermogenesis. J. I. Keithly,* R. W. Kott, J. G. Berardinelli, S. Moreaux, and P. G. Hatfield, *Montana State University*, *Bozeman*.

Eighty twin-bearing Targhee ewes (ages 2 to 5 yr; 68.5 ± 3 kg) were stratified by age and assigned randomly to 1 of 2 supplemental treatments to determine the effects of feeding algae containing docosahexaenoic acid (DHA) to ewes during late gestation and early lactation on lamb growth (from birth to 38 d), passive immunity (anti-Parainfluenza Type 3 titers), serum metabolites, and thermogenesis. Treatment supplements were formulated to be isocaloric and isonitrogenous, and when fed at the rate of 0.9 kg daily with a 10% CP and 58.1% TDN hay met the CP and TDN requirements of a 70-kg twin-bearing ewe during late gestation. Supplement treatments were: 1) 12 g/ewe daily of DHA Gold (Advanced Bionutrition Corporation, Columbia, MD), in the form of algal biomass (ALGAE), and 2) no DHA (CONTROL). Diets were individually fed (40 ewes/treatment) daily during the last 30 d of gestation and pen fed (6 pens/treatment, and 6 or 7 ewes/pen) during the first 38 d of lactation. One hour after lambing, twin-born lambs were weighed, bled via jugular puncture, and placed in a 0°C dry cold chamber for 30 min. Lamb rectal temperature was recorded every 1 min. After cold exposure, lambs were removed from the cold chamber, bled via jugular puncture, and returned to their dam. Lambs were weighed and bled via jugular puncture on the final day of the trial (38 d of age ± 7 d). Lamb sera were assayed for glucose, NEFA, cortisol, and anti-Parainfluenza Type 3 (PI_3) titers. There was a treatment by time interaction ($P < 0.01$) for lamb rectal temperature. Lambs born to ALGAE ewes had higher ($P = 0.09$) rectal temperatures at 0 min compared with CONTROL lambs, but rectal temperature did not differ ($P \geq 0.11$) at any other time during cold exposure. Glucose, cortisol, NEFA, anti-PI_3 titers, and birth weights did not differ between treatments. Lamb 38-d BW was greater ($P = 0.03$) in lambs born to CONTROL ewes than in lambs born to ALGAE ewes. Supplementation of DHA during late gestation and early lactation did not appear to benefit lamb production, or factors that may impact production.

Key Words: docosahexaenoic acid, lamb production, thermogenesis

24 Sustainability implications of feedlot management practices. K. L. Cooprider,* F. M. Mitloehner, and A. L. Van Eenennaam, *University of California*, *Davis*.

There is an increased consumer demand for animal products that have been raised sustainably. This term has many definitions, but generally

refers to some balance of environmental, social, and economic goals. The use of biotechnologies that increase units of output (e.g., pounds of meat) with the same or fewer inputs should be included in sustainability assessments. The objective of this project was to quantify the inputs (days on feed, kg feed fed and refused, ADG, health treatments) and outputs (carcass measurements, greenhouse gas emissions) associated with 2 feedlot cattle management regimens: Never Ever 3 (NE3) and conventional cattle (CON). The former treatment group received no feed additives or implants, whereas the latter were implanted with Synovex Choice (Fort Dodge) on d 1 and d 70, and were additionally fed Elanco's Rumensin (330 mg/head/day), Tylan (90 mg/head/day), and for the 29 d before shipping Optaflexx β-agonist (254 mg/head/day). Angus-cross steers were stratified by BW (n = 104; 337 kg ± 17) and randomly assigned to 4 pens per treatment group. Amount of feed fed per pen and refusals were recorded daily. Animals were shipped on a constant average pen weight basis (Target 590 kg; actual 596 kg ± 32 BW). The CON cattle had higher ADG (1.81 vs. 1.35 kg, $P < 0.01$), and were on feed fewer days (146 vs. 188 d, $P < 0.01$) than NE3. No significant differences were observed in HCW or dressing percentage between groups ($P > 0.05$), however CON carcasses had larger ribeyes (87 vs. 80 cm^2, $P < 0.01$), lower USDA marbling score (5.4 vs. 6.2, $P < 0.01$), backfat thickness (1.64 vs. 1.84 cm, $P < 0.05$) and yield grade (3.38 vs. 3.95, $P < 0.01$) as compared with NE3. Overall, CON cattle consumed 393 kg less feed in the feedlot (1250 vs. 1643 kg, $P < 0.05$). Although additives resulted in additional costs in CON steers, cost of feed per kg of gain was significantly lower ($1.12 vs. $1.35/kg, $P < 0.05$) relative to NE3. The use of implants and feed additives reduced feed inputs and production resources required to produce a fixed amount of output, with resultant environmental and economic sustainability advantages.

Key Words: feedlot, sustainability, biotechnology

25 Effect of ram exposure on temporal patterns of progesterone and metabolic hormones concentrations in 18-mo-old virgin Targhee ewes during the transition into the breeding season. R. B. McCosh*[1], E. M. Berry[1], M. E. Wehrman[1], R. R. Redden[1], R. W. Kott[1], D. Hallford[2], and J. G. Berardinelli[1], [1]*Montana State University*, *Bozeman,* [2]*New Mexico State University*, *Las Cruces.*

The objective was to determine if ram exposure during the transition into the breeding season altered progesterone (P4), cortisol, triiodothyronine (T3), thyroxine (T4), T3:T4 ratios, prolactin (PRL) or IGF-1 concentrations in 18-mo-old Targhee ewes. Anestrous ewes were stratified by residual feed intake (RFI) score (efficient; n = 12); middle; n = 12; inefficient; n = 12) and assigned randomly to be exposed to rams (RE; n = 18) or wethers (NE; n = 18). Ewes within exposure type were assigned to one of 2 pens (1 male/9 ewes/pen); with 33 m separation between RE and NE pens. Blood samples were collected from each ewe by jugular venipuncture every other day for 20 d, beginning on the first d of exposure. Samples were assayed for P4, cortisol, T3, T4, PRL, and IGF-1. Resumption of luteal activity began earlier ($P < 0.05$) in RE than in NE ewes. There were no differences in patterns of cortisol, T3 or IGF-1 concentrations, or T3:T4 ratios between RE and NE ewes or among ewes with efficient, middle, or inefficient RFI scores. There was a treatment by day interaction ($P < 0.05$) for T4 and PRL concentrations. Concentrations of T4 in RE ewes decreased less rapidly and over a longer interval before increasing by the end of the sampling period than those in NE ewes. Concentrations of PRL were greater in RE than in NE ewes 4 d after exposure but decreased over the next 12 d; whereas, PRL decreased in NE ewes during the first 6 d then increased over the next 14 d. There was an exposure type by RFI score interaction ($P < 0.05$) for BW change. Change in BW did not differ among NE and RE ewes with medium or inefficient RFI scores. However, RE ewe with efficient RFI scores showed a greater increase in BW over the 20-d experiment than NE ewes with efficient RFI scores. Exposing 18-mo-old ewes to rams accelerated resumption of luteal activity and altered T4 and PRL concentrations during the transition into the breeding season. Furthermore, the ram effect appears to alter BW change in ewes with efficient RFI scores differently than in ewes of lower RFI scores.

Key Words: ram biostimulation, seasonal anestrus, metabolic hormones

26 Conjugated linoleic acid decreases prostaglandin synthesis in bovine luteal cells. K. C. P. May,* G. Bobe, C. J. Mueller, and M. J. Cannon, *Oregon State University*, *Corvallis*.

Feeding conjugated linoleic acids (CLA) improves reproductive performance in dairy cows; however, the molecular mechanisms by which CLA improves reproduction are not well understood. Therefore, we evaluated whether the CLA isomers, *trans*-10, *cis*-12 CLA and *cis*-9, *trans*-11 CLA altered synthesis of steroidogenic hormones in bovine luteal cells by measuring concentrations of progesterone, PGE_2, and $PGF_{2\alpha}$ in conditioned medium and expression of genes involved in their synthesis. Confluent luteal cells from each of 4 cows were cultured in 0 μM (control) or 0.1 μM solutions of *trans*-10, *cis*-12 CLA and *cis*-9, *trans*-11 CLA in varying ratios (1:0, 0:1, 1:1, 2:1, 1:2, 5:1, 1:5, 9:1, or 1:9) for 48 h in the presence and absence of 1 μM of the adenylate cyclase activator forskolin. Independent of CLA isomer and ratio, CLA decreased, compared with control, hormone concentrations of prostaglandin $F_{2\alpha}$ (62.6 ± 10.5 vs. 50.4 ± 9.9 pg/mL; $P = 0.003$) and, in the absence of forskolin, prostaglandin E_2 (61.2 ± 11.3 vs. 36.1 ± 10.1 pg/mL; $P < 0.001$) in cultured luteal cells, while no effect was observed for progesterone ($P = 0.94$). Compared with control, CLA decreased relative levels of COX-2 mRNA, a rate limiting enzyme in prostaglandin synthesis, by 1.7 fold ($P < 0.001$) and 3 β-hydroxysteroid dehydrogenase mRNA, a rate limiting enzyme in progesterone synthesis, by 1.4 fold ($P = 0.008$). Relative levels of PGE synthase and PGE_2 9-keto-reductase mRNA, both involved in prostaglandin synthesis, and steroid acute regulatory protein and cytochrome P450 side chain cleavage mRNA, both involved in progesterone synthesis, were not significantly altered by CLA. In conclusion, a potential mechanism by which *trans*-10, *cis*-12 CLA and *cis*-9, *trans*-11 CLA may improve reproductive performance in dairy cows, is by suppressing $PGF_{2\alpha}$ synthesis in luteal cells through attenuating COX-2 gene expression.

Key Words: cattle, corpus luteum, progesterone

27 Camelina meal and crude glycerin as feed supplements for developing replacement beef heifers. P. Moriel,* B. I. Cappellozza, V. Nayigihugu, K. M. Cammack, and B. W. Hess, *University of Wyoming*, *Laramie*.

Two hundred and 4 (n = 99, yr 1; n = 105, yr 2) Angus × Gelbvieh rotationally crossbred heifers were used in a 2-yr randomized complete block designed (RCBD) experiment to determine the effect of feeding camelina biodiesel co-products (meal and crude glycerin) on serum concentrations of thyroid hormones and glucose, as well as on growth and reproductive performance. Heifers were stratified by BW (297 ± 5.8 kg) and randomly allocated to a pen that received bromegrass hay plus 1 of 3 supplements (12.6% CP): control (50% ground corn and 50% soybean meal, as-fed); camelina meal (mechanically extracted); glycerin (50% soybean meal, 33% ground corn, 15% crude glycerin, 2% corn gluten meal; as-fed) for a 60-d period. Preprandial blood samples

were collected via the jugular at d 0, 30 and 60 of the experimental feeding period. On d 60, heifers were synchronized for estrus using a 2-shot PGF2α protocol; any heifer exhibiting estrus was bred via AI 12 h after standing heat. Heifers not exhibiting estrus were given GnRH and bred by AI on d 74. Data were analyzed as a RCBD using the MIXED procedure of SAS with pen as a random effect for BW and reproduction traits; serum parameters were analyzed as repeated measures. Dietary treatment × sampling period interactions were not detected ($P = 0.17$ to 0.87). Dietary treatment did not affect serum T_4 ($P = 0.96$), glucose ($P = 0.59$) or BW at d 30 or 60 ($P \geq 0.40$), but increased ($P = 0.05$) T_3 in heifers fed camelina meal. Additionally, dietary treatment did not affect the percentage of heifers detected in estrus before timed AI ($P = 0.82$), first service conception rates of those heifers detected in estrus ($P = 0.87$), conception rates to timed AI ($P = 0.19$), or overall first conception rates ($P = 0.65$). Heifers fed camelina co-products maintained growth and reproductive performance comparable to heifers fed the control supplement. Therefore, camelina co-products can replace conventional corn-soybean meal supplements.

Key Words: beef heifers, supplementation, biodiesel co-products

28 Use of a portable near infrared spectrophotometer to predict nutrient composition of feces from Holstein cattle fed high-concentrate diets. J. D. Allen,* D. R. Tolleson, L. W. Hall, C. D. Burrows, G. Xie, and G. C. Duff, *University of Arizona*, *Tucson*.

Our objective was to evaluate the application of a chute-side near infrared spectrophotometer (NIRS) analysis to predict nutrient composition of feces from Holstein cattle. Growing Holstein cattle (42 steers and 2 freemartin heifers; average initial BW = 220 kg) were fed either 86 or 90% steam-flaked corn-based concentrate diets (3 pens/diet with 7 to 8 animals/pen). Fecal samples were collected in plastic bags and scanned within 2 h after collection using an ASD Field Spec NIRS unit (Boulder, CO). Spectra were collected under ambient conditions using a contact probe. Samples were then dried at 60°C, ground in a Wiley mill to pass a 1 mm screen and analyzed for DM, CP, NDF and ADF. Calibrations were developed using samples collected on d 0 and 28 with log 1/R spectra in the 1,100 to 2,400 nm range. Partial least squares (PLS) regression in SAS was used to develop calibrations. Cross validation was employed to determine the number of PLS factors to use. Simple regression was used to evaluate the relationship between observed and predicted constituent values. Although regression values were moderate for predicting CP ($R^2 = 0.88$) and fair for DM ($R^2 = 0.68$) and NDF ($R^2 = 0.62$), prediction regression values for ADF were statistically significant ($P < 0.01$) but not predictive ($R^2 = 0.34$). Our data indicate that while our calibrations were variably successful, validations were mostly unsuccessful ($R^2 < 0.4$). Lack of validation success is most likely due to small sample number and limited range of values. However, this project has illustrated a relationship between NIR spectra and the observed laboratory values for these constituents, and that the use of a portable NIRS on-site may improve the nutritional management of a commercial feedlot.

Key Words: NIRS, Holstein, nutrient composition

29 Effects of implant type and protein source on growth performance of steers grazing summer pasture. C. P. McMurphy,* E. D. Sharman, D. A. Cox, G. W. Horn, and D. L. Lalman, *Oklahoma State University*, *Stillwater*.

Implants consistently increase performance 10 to 15% in grazing cattle and supplemental protein is necessary in late summer when forage is maturing and rumen ammonia-N is first limiting. Therefore, a split-plot design was used to investigate the effects of implant type and protein source on performance of steers grazing summer pasture. Crossbred steers (n = 392; BW = 212 ± 24 kg) were ranked by weight and randomly assigned to 1 of 15 pastures and then randomly allotted to implant treatment, within pasture. Supplement treatments were control (no supplement), dried distillers grains with solubles (DDGS; 33% CP), and cottonseed meal (CSM; 33% CP). Implant treatments were control (no implant), Ralgro and Component TE-G. The grazing season was 126 d with supplementation beginning in late July. Steers were group fed, within pasture, each wk on Monday, Wednesday and Friday at a rate of 0.95 kg•steer^{-1}•feeding^{-1}. Data were analyzed using PROC MIXED procedure of SAS where supplement treatment served as the whole-plot and implant treatment served as the sub-plot. Orthogonal contrasts were used to determine the effects of supplementation, supplement type, implantation and implant type. Protein supplementation increased ($P < 0.05$) BW and ADG by 12 and 0.16 kg, respectively. Compared with CSM, DDGS improved ($P < 0.05$) ADG by 0.05 kg resulting in improved supplement efficiency (2.39 vs. 3.49 kg of supplement per kg of additional ADG for DDGS and CSM, respectively). Implantation increased final BW ($P = 0.02$) and improved ADG 8.1% ($P < 0.05$) during the first ~95 d, but implant type had no influence on rate of BW gain during this period. During the final ~31 d of the grazing season there was no difference in ADG for Ralgro and non-implanted steers, while Component TE-G increased ($P < 0.05$) ADG by 0.08 kg. Steer performance was enhanced when supplemental CSM was replaced by DDGS. Furthermore, Component TE-G implants enhanced weight gain further into the grazing season than Ralgro.

Key Words: implants, supplementation, grazing steers

30 The effect of morbidity on feedlot performance and carcass quality in feedlot steers. K. J. Austin*[1], J. L. Seabrook[1], T. E. Engle[1], R. K. Peel[1], C. M. McAllister[1], B. W. Brigham[1], R. M. Enns[1], R. L. Weaber[2], H. Van Campen[1], G. H. Loneran[3], J. L. Salak-Johnson[4], and C. C. L. Chase[5], [1]*Colorado State University*, *Fort Collins,* [2]*University of Missouri*, *Columbia*, [3]*West Texas A & M University*, *Canyon*, [4]*University of Illinois*, *Urbana*, [5]*South Dakota State University*, *Brookings*.

The objective of this project was to examine the effects of morbidity in feedlot cattle on animal performance, carcass quality, and subsequent carcass value. Performance and morbidity data were collected over a 2 year period (year 1 n = 1551; year 2 n = 1319). Steers were randomly assigned to 9-head pens and fed a commercial feedlot ration for 230 ± 5 d (year 1 and year 2) with an average entry weight of 224 kg or 219 kg for year one or 2, respectively. Body weight and ultrasound measurements of ribeye area (REA), intramuscular fat (IMF) and backfat (BF) were collected at 6day intervals between d0 and d180. Animal performance data in conjunction with yield and quality grade measurements at the time of slaughter were analyzed to determine impacts on performance resulting from feedlot morbidity. Morbidity was defined as behavioral and/or physical abnormalities observed during daily rounds (between 0700 and 0900), severe enough to warrant pharmaceutical treatment and/or isolation pens from designated treatment pens. For year one, morbidity was a source of variation for ultrasound BF and REA measurements ($P < 0.01$, $P = 0.02$, respectively), and resulted in lower final live body weight ($P = 0.01$). For year 2, morbidity was a source of variation for final live body weight and hot carcass weight (HCW) ($P < 0.01$), and calculated yield grade was marginally lower in morbid steers ($P = 0.08$). Feedlot morbidity was a factor in reducing the performance and ultimate carcass yield from the steers in this experiment.

Key Words: carcass characteristics, feedlot performance, morbidity

31 Changes in hepatic gene expression in steers administered high-S water with or without supplemental Mo. K. L. Kessler*[1], K. C. Olson[2], C. L. Wright[2], K. J. Austin[1], and K. M. Cammack[1], [1]*University of Wyoming*, *Laramie*, [2]*South Dakota State University*, *Brookings*.

High-S water is associated with reduced performance, poor health, and an increased incidence of polioencephalomalacia (PEM) in ruminant livestock. Changes in expression of immune function and inflammatory response genes have been shown in steers administered high-S water. Our objective was to determine changes in hepatic gene expression in steers administered low-S water or high-S water with or without supplemental Mo. Yearling steers (n = 96) were randomly assigned to a low-S water (LS; 375 mg SO_4/L), high-S water (HS; 2,218 mg SO_4/L), or high-S water plus Mo (HSMO; 2,218 mg SO_4/L; 100 mg Mo/kg DM) treatment for 56 d. Body weights were recorded on d −1, 29, and 57, and liver biopsies were conducted on d 57. Feed intake (as-fed basis) was lower in HSMO steers than HS ($P = 0.018$) and LS ($P = 0.002$) steers. Also, ADG was lower ($P < 0.001$) in HSMO steers than LS and HS steers, with HS steers being intermediate. For real-time RT-PCR analysis, RNA was extracted from liver tissues of 8 randomly selected steers within each treatment. Genes selected for analysis included *Reg1*, *TGFβ1*, *INHβA*, *Iβ2*, *TG2*, and *APP*, all of which were affected by high-S water in a previous study. Relative expression values were tested for treatment differences using the GLM procedure of SAS. Expression of *TG2* tended to be greater in HS steers than LS ($P = 0.08$) and HSMO ($P = 0.06$) steers. However, *TG2* expression was not different between LS and HSMO steers, indicating that Mo prevented the change in *TG2* expression induced by high-S water. Expression of *APP* was lower in HSMO steers than both LS ($P < 0.001$) and HS ($P = 0.04$) steers. No differences in *APP* expression were detected between LS and HS steers, indicating that the downregulation of *APP* in the HSMO steers was due to the Mo treatment, not the high-S water. No other changes in gene expression were observed. Results from this study indicate that hepatic gene expression is altered in response to high-S water and possibly Mo treatment. Further work is needed to determine other genes and metabolic pathways affected by high-S water consumption in ruminant livestock.

Key Words: gene expression, sulfate water, beef cattle

Symposium: National Extension Workshop: The Impact of Major Food Policy Shifts on the US Food Supply and its Producers: Animal Welfare Issues

32 Washington Update. R. D. Reynnells,* *USDA/NIFA/PAS*, *Washington, DC*.

The 2010 Extension Special Recognition Award is presented to Greg Martin, The Pennsylvania State University. Greg has been an integral part of the planning for the Poultry Science Association (PSA) National Extension Workshop, member and Chair of the PSA Extension Committee and made significant other contributions to extension programming. On October 1, 2009 the National Institute of Food and Agriculture replaced the Cooperative State Research, Education and Extension Service. Multi-state research committees are creating innovative programs: the NCCC209 (Agricultural Bioethics) and NC1029 (Applied Animal Behavior and Welfare) collaborated on a USDA educational grant. A 5 year portfolio review for Plant and Animal Systems was completed in 2009, but otherwise are conducted internally each year. Areas of primary responsibility are: (Knowledge Area (KA) 306, Environmental Stress in Animals; KA308, Improved Animal Products (Before Harvest); KA315, Animal Welfare). The 2009 Southern Region (Quadrennial) Poultry Extension Workshop, was held in Raleigh, NC, (contact Ken Anderson, NC). Edgar Oviedo (NC) is the coordinator of the 2010 National Poultry Waste Management Symposium. The 2009 Future Trends in Animal Agriculture symposium provided a balanced discussion on what animal production and processing would and should look like in 2030, and other animal welfare (AW) issues. The Council for Agricultural Science and Technology scheduled their Food Animal Agriculture Symposium for June, 2010. The annual Animal Welfare Assessment Contest is open to undergraduate, graduate and veterinary students at Land Grant and other universities, and was held at Michigan State University. The contest focuses on AW and animal behavior areas, and emphasizes the importance of collaboration between disciplines and commodities to address AW and related issues. Bioethics (ethics as applied to biological systems) is an important component of discussions of AW and animal rights concepts and issues. Bioethics discussions help us understand value-driven perspectives of members of society, and proposed mandated restrictions regarding animal use.

Key Words: special recognition award, animal welfare, bioethics

33 The impact of major food policy shifts on the US food supply and its producers: Animal welfare issues. J. Reynolds,* *University of California*, *Davis*.

Major governmental policy shifts that have impacted the welfare of farm animals in the US have included changes in farm subsidy programs, milk price supports, subsidizing ethanol production and increasing environmental regulations. These have had effect on the consolidation of farm production and subsequent changes in animal housing and management. In the US many policies are determined by the private sector, not the government. This has been the case with farm welfare issues. Because our society prefers industries to set standards or regulations the trend in the US has been for retailers of food products to work to develop welfare standards tolerated by consumers. Examples using the housing of poultry and sows and cattle tail docking and dehorning will be discussed to illustrate the effects of governmental policy driving consolidation and production efficiency and the attempts by retailers to counteract the dissonance in animal welfare experienced by animals and consumers.

34 Animal agricultural conflict as competing worldviews. W. Jamison,* *Cornerstone Public Relations, LLC*, *Tequesta, FL*.

Animal Agriculture in industrialized nations has become the locus of intense conflict regarding the proper role and treatment of animals. Most analysis of the related animal welfare issues involves physiological, behavioral, or economic research focused on confinement systems and their impacts on the animal. Nonetheless, all of these analytic constructs are socially derived in that the larger social and political context defines what constitutes acceptable research and valid questions. However, this paper argues that animal welfare can be better understood as a social conflict between the competing worldviews regarding animals and their roles in human life. Consumptive-instrumentalist worldviews accept that animals and animal products will be slaughtered and consumed for human benefit; hence animal welfare becomes a function of that reality. Aesthetic-instrumentalist worldviews conversely understand the role of animals as companions or in other aesthetic roles for human benefit, hence animals are protected from consumptive uses. These 2 views are irreconcilable in that consumptive-instrumentalism results in animal death, while the goal of aesthetic-instrumentalism is the perpetuation of animals for human benefit.

35 Update on the *Guide for the Care and Use of Agricultural Animals in Research and Teaching*. J. J. McGlone*[1] and J. Swanson[2], [1]*Texas Tech University*, *Lubbock*, [2]*Michigan State University*, *East Lansing*.

In January 2010, the third edition of the Ag Guide was published. The first edition was in 1988 and the first revision was in 1999. The third edition of the Ag Guide had 62 authors with expertise in each common species of farm animal and from each major discipline of the animal sciences. In addition, the authors represented the diversity of the FASS membership and Veterinarians and Agricultural Engineers. This updated Ag Guide is different in some meaningful ways. Previous editions used the title of agricultural animals in agricultural teaching and research. The title was changed by deleting the second use of the word agricultural. The authors concluded that this Guide applies to care of agricultural animals in any type of research and teaching (biomedical or agricultural). Two new chapters were added: farm animal handling and transport, and environmental enrichment. The husbandry and animal health chapters were reorganized and expanded. Information on biosecurity and genetically engineered animals was added. The scientific literature was updated in each species chapter. The veal chapter was deleted and information in calf husbandry was added to the beef and dairy chapters. The revised Ag Guide suggests that all animal uses be understood and managed by the institution, including field studies on commercial farms. The revised Ag Guide will be a useful resource to people that conduct and oversee research and teaching using agricultural animals.

Key Words: animal care, animal welfare, animal research

36 Update on horse slaughter. K. Martinson*[1] and T. Lenz[2], [1]*University of Minnesota*, *St. Paul,* [2]*Pfizer Animal Health*, *Louisburg, KS.*

Slaughter is the humane ending of an animal's life under federal regulation when the carcass is processed for food. Legislation surrounding horse slaughter began in 2001 when a bill prohibiting the transport of horses to slaughter was introduced. This bill was never taken up by the House. In 2003 and 2004, The American Horse Slaughter Prevention Act

(HR 857) was introduced to prohibit the slaughter of horses for human consumption. A similar bill was introduced in the Senate (S 2352). Both limited the methods available for euthanasia of horses, including penetrating captive bolt, the method used at processing plants. Neither bill moved out of committee. The Horse Slaughter Prohibition Bill (HR 503) was introduced in the House in 2005 and aimed to prohibit the sale or transportation of horses to slaughter for human consumption. A similar bill was introduced in the Senate (S 1915). In 2006, HR 503 passed the House, but was not taken up by the Senate. In 2007, HR 503 was reintroduced along with a new Senate bill (S 311). Both bills aimed to end slaughter of the US horse for human consumption and prohibited export to other countries. Neither bill has moved forward. In 2007, a 1949 TX law that prohibited the slaughter of horses was discovered and enforced. That same year, IL bill HB 1711 was passed and banned slaughter of horses for human consumption in IL. Both bills closed the remaining horse processing plants in the US. In 2008, The Prevention of Equine Cruelty Act (HR 6598) was introduced and aimed to impose a fine or prison term for possessing, shipping, or transporting horses or horse parts for human consumption. The bill was reintroduced in 2009 (HR 503) but has not been taken up by the House. In 2009, the Senate ordered an investigation into the impact that banning US horse slaughter has had on horse welfare and farm income. The study should be released by March 2010. Some states have also introduced horse slaughter bills. A consequence of banning equine processing has been an increase in unwanted horses. In MN, the number of horses involved in humane cases increased 411% between 2003 and 2008. This issue is likely to influence development and content of future equine Extension programs across the US.

Key Words: horse, slaughter, legislation

Monday, July 12, 2010

POSTER PRESENTATIONS

Animal Behavior and Well-Being: Livestock

M1 Rubber flooring impact on health of dairy cows. S. D. Eicher*[1], D. C. Lay Jr.[1], J. D. Arthington[2], and M. M. Schutz[3], [1]*USDA-ARS*, *West Lafayette, IN,* [2]*University of Florida*, *Ona,* [3]*Purdue University*, *West Lafayette, IN*.

Rubber flooring in dairies has become popular because of perceived cow comfort. The objective of this longitudinal study was to evaluate locomotion, stress, and immunity over the first 180d of each of the 1st and 2nd lactations of cows assigned to free-stall housing with either rubber (RUB) or concrete (CON) at the feed-alley of their housing. Cows entered the experiment at d −60 before 1st (n = 30) lactation and were observed over 2 lactations. Between lactations cows remained in a straw bedded-pack dry-cow pen. Locomotion scores and blood samples were obtained at approximately −60, −30, 0, +7 and weekly through d +189 relative to calving throughout 2 lactations. Data were analyzed as a completely randomized design with repeated measures. Chi Square analysis was used to evaluate hoof pathologies. Cortisol responses were only affected by d ($P = 0.05$). White blood cell (WBC) counts increased for CON cows compared with RUB cows after d 63 through 182. WBC counts returned to similar counts of RUB cows over the dry period, but quickly became greater than those of CON cows after parturition (9.0, 9.5, and 7.8, and 11.0, 8.8, and 13.0×10^6 cells/mL for RUB and CON cows at d 142, parturition, and d 142 of 2nd lactation; treatment by d interaction, $P < 0.01$). Neutrophil counts only tended to be affected by d ($P = 0.10$) and a weak trend ($P = 0.13$) for a treatment by d interaction was detected. Lymphocyte counts followed the pattern of WBC counts, but only had a trend ($P = 0.08$) for a treatment by d effect (4.9, 5.1, and 5.3, and 6.8, 5.1, and 8.4×10^6 cells/mL for RUB and CON cows at d 142, parturition, and d 142 of 2nd lactation; treatment by d interaction, $P < 0.01$). Monocytes counts were not affected by treatment or time ($P > 0.10$). Haptoglobin (treatment by d interaction, $P = 0.15$) and ceruloplasmin (week effect, $P = 0.08$) were not affected by treatment. Hoof pathology was different by number of treatments that were required (RUB = 2.1 and CON = 1.4; $P = 0.03$). Lame and sound classifications were not different between treatments ($P = 0.13$). These data show that flooring affected cow hoof and leg health and altered immune cell counts, which may indicate an underlying chronic inflammation.

Key Words: innate immunity, rubber flooring, stress

M2 Rubber flooring impact on production and herdlife of dairy cows. M. M. Schutz*[1] and S. D. Eicher[2], [1]*Purdue University*, *West Lafayette, IN,* [2]*USDA- ARS*, *West Lafayette, IN*.

Use of rubber flooring in dairies has become popular because of perceived cow comfort. The overall objective of this longitudinal study was to evaluate production, reproduction, and retention of first and second lactations of cows assigned to either rubber (RUB) or concrete (CON) flooring at the feed alley. Feeding system included headlocks; and cows were fed once daily, with feed pushed up 5 times daily. Grooved concrete cow alleys provided access to 2 rows of free stalls in each pen. Cows entered the experiment at d −60 before 1st (n = 13 for CON and n = 17 for RUB) lactation and were observed over 2 lactations. Between lactations cows remained in a straw bedded-pack dry-cow pen. Production and health data were recorded throughout both lactations. Date left was recorded for each cow or considered to be 4 years after first calving for cows still in the herd. Milk, fat, and protein; somatic cell scores (SCS); and numbers of days open and inseminations were analyzed as linear models using Proc Mixed of SAS. Explanatory variables in models included fixed effects of treatment, age and year-season of calving, and number of days open. Days from calving to exiting the herd were analyzed separately by parity. RUB increased mature equivalent (ME) fat (488 vs 432 kg), ME protein (364 vs 326 kg), and protein % (2.99 vs 2.81%) and persistency of the milk lactation curve (114 vs 106%) ($P < 0.04$) and tended to increase fat % (4.02 vs 3.70%) ($P < 0.10$) in first parity. However, for second parity, CON increased ME fat (524 vs 432 kg) ($P < 0.04$) and tended to increase fat % (3.95 vs 3.49%) ($P < 0.08$). Treatment did not affect days of herd life from first calving, but those cows calving a second time tended to remain in the herd more days after second calving on CON (660 vs 368 d) ($P < 0.08$). Treatment by parity interactions were confirmed in repeated records analyses. These data indicate that flooring can influence production and herd life. Rubber flooring for cow comfort may not be justified solely in terms of yields and herd life.

Key Words: housing, production, rubber flooring

M3 Motivation to walk affects speed but not gait score in dairy cattle. A. K. Barrientos*, M. A. G. von Keyserlingk, and D. M. Weary, *University of British Columbia*, *Vancouver, Canada*.

Gait scoring systems have been developed as a tool to improve early detection and treatment of lameness; however, a variety of confounding factors including motivation to walk to toward an attractive resource (such as fresh feed) may affect the way cows walk. Our aim was to vary motivation to walk (by providing a food reward) testing the prediction that increased motivation will a) increase walking speed and b) reduce gait score (i.e., make lame cows appear sound). Eleven cows, scored for presence and severity of hoof lesions and balanced for lameness, were trained to walk individually down a 16 m test alley. Cows received 4 training sessions per day; during each session cows were randomly assigned to either receive a food reward (from a feed bin visible from the end of the alley) or not. After 5 d of training cows were tested using the same procedure. Walking speed (m/s) was recorded electronically using light sensors. Gait was scored using a 1-to-5 numerical rating system (NRS; 1 = sound, 5 = severely lame) and a continuous 100-unit visual analog scale (VAS) of 6 gait attributes (back arch, head bob, tracking-up, joint flexion, asymmetric steps, and reluctance to bear weight). Cows walked faster when they were given a reward than when they were not rewarded (1.22 ± 0.02 m/s vs. 1.01 ± 0.02 m/s, $P < 0.001$). This increase in walking speed tended to be lower for cows with sole ulcers, interdigital hyperplasia or both than for cows without these conditions (0.16 ± 0.04 m/s vs. 0.28 ± 0.05 m/s, $P = 0.08$). Provision of a reward had no effect on NRS (3.26 ± 0.04 vs. 3.34 ± 0.04, $P = 0.20$). However, the food reward affected certain gait characteristics; cows had greater back arch (54 ± 1 vs. 50 ± 1, $P = 0.01$), but better tracking up (44 ± 3

vs. 53 ± 3, $P = 0.05$), when provided a food reward. These results show that motivation to walk affects walking speed and gait attributes likely affected by speed (back arch and tracking up), but that overall gait score remains consistent.

Key Words: lameness, locomotion, reliability

M4 Resting patterns of dairy cows and housing characteristics. A. Bach*[1,2] and I. Guasch[1], [1]*Department of Ruminant Production, IRTA, Caldes de Montbui, Spain*, [2]*ICREA, Barcelona, Spain*.

One hundred and 41 lactating Holstein cows (milk yield = 37.1 ± 7.6 kg/d, DIM = 136 ± 67 d) wearing a pedometer able to record daily number of lying bouts and lying time were monitored for a period of 6 mo to evaluate whether resting behavior was affected by the characteristics of different pens within a farm. Cows were distributed in 8 different pens holding an average of 67 ± 14 cows with about 25% of the cows in each pen wearing a pedometer. All cows received the same ration and were milked 3 times daily. Average ratios of stalls and feedbunk per cow were 1.0 ± 0.22 and 1.12 ± 0.17, respectively. Average distance from the neck rail to end the of the stall was 186 ± 12.2 cm, and the diagonal from the top of the neck rail to rear of the stall was 226 ± 7.3 cm. Stall design was not confounded with DIM, as several pens with different stall designs had the same number of DIM. Resting activities were averaged within pen, and a weighted regression analysis (including the proportion of animals wearing a pedometer in each pen as a weighting variable) with DIM as a covariate was used to determine associations between different housing parameters and lying time across pens. Average resting time was 11.4 ± 0.98 h/d distributed in 15.5 ± 2.2 bouts/d. Lying time tended ($P < 0.10$) to be positively correlated with DIM. The numbers of stalls and feed bunk spaces per cow were positively correlated (r = 0.98 and 0.74, respectively) with resting time. The distance between the neck rail and the end of the stall and the diagonal from the top of the neck rail to the end of the stall were also positively correlated (r = 0.69 and 0.72, respectively) with lying time. Stall curb height was negatively correlated (r = −0.87) with lying. Cows lying on stalls with 25 cm or lower curb heights (50% of the pens) rested for 12.3 ± 0.67 h/d and those on stalls with curb heights above 25 cm rested 10.3 ± 0.33 h/d. Providing sufficient number of stalls and feedbunk space should improve lying time. In addition, when designing stalls, an attempt should be made to minimizing curb height and maximizing the diagonal between the end the top of the neck rail and the rear end of the cubicle.

Key Words: behavior, lying, housing

M5 Short-term overcrowding did not affect the feed intake, hygiene, or stress response of Holstein dairy cows. **P. D. Krawczel*[1,2], L. B. Klaiber[1], R. E. Butzler[1], L. M. Klaiber[1], M. P. Carter[1], H. M. Dann[1], C. S. Mooney[1], and R. J. Grant[1], [1]***William H. Miner Agricultural Research Institute***, *Chazy, NY*, [2]***The University of Vermont, Department of Animal Science***, *Burlington*.**

Access to feeding and resting resources is critical to the welfare of dairy cows. The objective of this study was to determine whether housing Holstein dairy cows at stocking densities of 100 (1 cow per stall and headlock), 113, 131, and 142% would affect the well-being (assessed from dry matter intake (DMI), fecal cortisol metabolites and udder and leg hygiene). Multiparous cows (n = 96) and primiparous cows (n = 40) were assigned to 1 of 4 pens (34 cows per pen) in a 4-row freestall barn. Pens were balanced for parity, milk production, days in milk, and somatic cell count. Treatments were imposed for 14 d using a 4 × 4 Latin square design. DMI was assessed at the pen-level over the final 3 d of each period. Fecal cortisol metabolites were measured from samples collected from the focal cows (n = 12) in each pen on d 13 and d 14 of each period. Udder and leg hygiene was assessed using a scale of 1-to-4 on the focal cows, who were groomed on d 1 of each period and scored on d 14. Data were analyzed using MIXED procedure of SAS. DMI (26.4 ± 0.6 kg/d) was unaffected by treatment ($P > 0.10$). Cortisol metabolites (3.2 ± 0.2 ng/g; $P = 0.21$) and udder hygiene score (1.8 ± 0.1; $P = 0.99$) did not differ among treatments. Leg hygiene scores differed between 131 (2.5 ± 0.2) and 142% (2.8 ± 0.2; $P = 0.03$). The mean score when housed at 100 and 113% (2.6 ± 0.2) indicated this observed difference was not biologically meaningful. Overall, the results suggest that well-being, as defined within this experiment, was not affected by short-term overcrowding. However, further research is needed to determine if the same responses are observed over longer durations.

Key Words: dairy cow, overcrowding, well-being

M6 Greater feed bin stocking density increases the social aggression of postpartum dairy cows. P. D. Krawczel*[1,2], D. M. Weary[3], R. J. Grant[1], and M. A. G. von Keyserlingk[3], [1]*William H. Miner Agricultural Research Institute*, *Chazy, NY*, [2]*The University of Vermont, Department of Animal Science*, *Burlington,* [3]*Animal Welfare Program, University of British Columbia*, *Vancouver, BC, Canada*.

Beyond dry matter intake, feed bunk management practices that affect feeding-related behaviors may influence the welfare of postpartum dairy cows. The objective of this study was to determine the effects of feed bin stocking densities of 100% (1:1, bin:cow), 133% (1: 1.33), 150% (1:1.5), and 200% (1:2) on the feeding and social behavior of dairy cows during the 3 wk after parturition. Two groups of multiparous, Holstein cows (n = 24) with no clinical illness were housed sequentially in a pen containing 36 freestalls (freestall stocking density was 67%) and 18 feed bins. The pen was managed as a dynamic group to keep stocking density constant. Daily visits to the feed bin were recorded by an electronic feeding system. Meals and total meal time (defined as time feeding from bin plus time of within meal intervals) were calculated from the bimodal distribution of the frequency of the intervals between visits to the feed bins. Social behavior was defined as the number of successful displacements from the feed bin. Displacements were recorded for 3 h following 6 consecutive deliveries of a total mix ration during wk 2 of each cow's lactation. Data were analyzed as a randomized design using the mixed procedure of SAS. The model included week as the repeated measure for feeding behavior. Feed bin visits decreased after wk 1 ($P < 0.001$) and a treatment by week interaction was evident ($P = 0.03$). Meals decreased (from 8.4 ± 0.2 to 7.5 ± 0.2 per day; $P < 0.001$) and total meal time increased (from 3.8 ± 0.1 to 4.9 ± 0.1 h/d; $P < 0.001$) from wk 1 to wk 3, but were not affected by treatment ($P > 0.80$) or treatment by day interaction ($P > 0.10$). At 200%, cows initiated more displacements ($P < 0.03$) and were involved in a greater total number of interactions ($P \leq 0.05$) than the other treatments, but were only displaced more ($P = 0.04$) than the 100% cows. These results are consistent with earlier work on transition cows showing increased aggressive interactions with overcrowding. Future work should consider the role of freestall overcrowding or clinical illness on the response to feed bunk competition.

Key Words: dairy cow, behavior, competition

M7 Lying and standing behavior on farms using deep-bedded versus mattress freestalls. K. Ito*, M. A. G. von Keyserlingk, and D. M. Weary, *University of British Columbia*, *Vancouver, BC, Canada*.

Freestall dairy herds using mattresses experience a higher prevalence of lameness than do herds using deep-bedded stalls. This difference may be due to reduced comfort of mattresses as a lying surface, but the effects of mattresses on lying and standing behaviors are not well understood. The aim of this study was to compare lying and standing behavior on commercial farms using mattresses with minimal bedding (MAT; n = 17) versus those using deep-bedded stalls with sand or sawdust bedding (DB; n = 12). We have previously reported lameness prevalence for these 29 freestall herds: 10.3% severe lameness (score ≥4 on a 5-point gait scoring system) on MAT farms versus 4.6% on DB farms. Using electronic data loggers attached to the hind leg, lying behavior of 48 ± 2 focal cows/farm were recorded at 1-min intervals for 5 d, from which mean lying time (h/d) and the SD of lying time (h/d) among cows within farm were calculated. Numbers of cows that were standing fully inside stall, perching with only 2 feet inside stall, lying down in stall, and feeding were counted on each farm during one farm visit 2 h before afternoon milking. Stall Standing Index (SSI) was calculated as the percentage of cows in the pen not feeding that are standing or perching in the freestall. Effect of stall base on each behavioral variable was tested using a *t*-test. Lying time averaged 11.0 ± 0.7 (mean ± SD) h/d, and did not differ with stall base ($P = 0.5$). However, the variation (SD) in lying time was greater on MAT farms compared with DB farms (2.1 ± 0.07 h/d vs. 1.8 ± 0.08 h/d, respectively, $P = 0.005$). SSI at the time of assessment was 21.6 ± 1.9% on MAT farms compared with 12.0 ± 1.2% on DB farms ($P < 0.001$). In summary, farms using mattresses have more variable lying times, and cows on these farms spend more time standing and perching in the freestall.

Key Words: lameness, cow comfort, stall design

M8 Limit-feeding dairy heifers: Effects of feed bunk space and provision of a low nutritive feedstuff. K. Stevenson, B. L. Kitts, A. M. Greter, and T. J. DeVries*, *Dept. Animal and Poultry Science, University of Guelph, Kemptville Campus*, *Kemptville, ON, Canada*.

The objective of this study was to examine the effects of feed bunk space and provision of a low nutritive feedstuff on the behavior of limit-fed dairy heifers. Twelve Holstein dairy heifers (391.1 ± 44.8 d of age; 415.4 ± 47.2 kg), divided in groups of 3, were exposed to each of 3 treatments in a Latin square design with 7-d periods. The treatments were: 1) 0.68m of feed bunk space/heifer (TMR-0.68), 2) 0.34m of feed bunk space/heifer (TMR-0.34), and 3) 0.34m of feed bunk space/heifer with straw (up to 2kg/animal/d) provided (TMR-S). All heifers were fed a TMR at a restricted level (1.9% of BW), which contained (DM basis) 19.9% haylage, 20.1% corn silage, 49.6% high moisture corn, and 10.4% protein supplement. Group DMI was recorded daily. Feeding behavior and displacements from the feed bunk were recorded for the last 4 d of each period. Data were analyzed in a general linear mixed model. Heifers consumed more DM on the TMR-S treatment provided compared with the TMR-0.68 and TMR-0.34 treatments (9.4 vs 7.8kg/d; SE = 0.07, $P = 0.001$). Feeding time was also longer on the TMR-S treatment (147.7 min/d) compared with the TMR-0.68 and TMR-0.34 treatments (64.5 min/d; SE = 5.5; $P = 0.005$). Within the TMR-S treatment, feeding time on straw was 80.4 min/d, thus the rate of consumption of only the TMR was similar across all treatments. During the first 90 min following feed delivery, when all TMR consumption occurred, very little time (4.0 ± 1.6 min) was spent consuming straw on the TMR-S treatment. During that 90-min time period, the frequency of displacements from the feed bunk was similar (SE = 2.4; $P = 0.5$) between the TMR-0.68 (13.0), TMR-0.34 (13.2), and TMR-S (15.1) treatments. For the TMR-S treatment, heifers displaced each other 8.7 times per day during the rest of the day while consuming straw. As result, there was more competition at the feed bunk on the TMR-S treatment over the course of the day as compared with the other treatments (23.8 vs. 13.1; SE = 2.9; $P = 0.05$). The results suggest that neither increased feed bunk space, nor provision of a low nutritive feedstuff, will reduce competition for, or slow consumption rates of, a limit-fed TMR.

Key Words: limit-feeding, dairy heifer, feed bunk space

M9 Effect of feed type exposure on diet selection behavior of dairy calves. E. K. Miller-Cushon* and T. J. DeVries, *Dept. of Animal and Poultry Science, University of Guelph, Kemptville Campus*, *Kemptville, ON, Canada*.

Dairy cattle exhibit characteristic feeding behavior patterns which may be influenced by early experiences. The objective of this study was to determine how early exposure to different feed types affects diet selection behavior (sorting) of dairy calves once fed a mixed ration. Eight Holstein bull calves were randomly assigned at birth to a feed exposure treatment: 1) concentrate (CONC) or 2) hay (HAY), offered ad libitum. All calves received 8L/d of milk, incrementally reduced after 4 weeks to enable weaning by the end of wk 7. After milk weaning, all calves were fed a mixed ration containing 60% concentrate and 40% chopped hay (as is basis) for 9 weeks. Intake was recorded and calves were weighed 3x/week. Daily samples of fresh feed and orts from each calf were taken biweekly to determine dry matter intake (DMI), and duplicate samples were taken on wk 8, 12, and 16 for particle size analysis. The separator had 3 screens (19, 8, and 1.18mm), producing long, medium, short, and fine particle fractions. Sorting of each fraction was calculated as actual intake as a percentage of predicted intake. Sorting values >100% indicate sorting for, while values <100% indicate sorting against. Data were analyzed using a repeated measures mixed model. CONC calves tended to have higher DMI than HAY both pre-weaning (0.49 vs. 0.16kg/d; SE = 0.12; $P = 0.09$) and post-weaning (3.3 vs. 2.6 kg/d; SE = 0.21; $P = 0.06$). Pre-weaning weights were similar ($P = 0.4$) but CONC calves had higher weights post-weaning (118.1 vs. 104.6 kg; SE = 4.0; $P = 0.05$). Initially after weaning, calves sorted for familiar feed; CONC calves sorted for short particles (126.4 ± 4.6%; $P < 0.01$), which were mainly concentrate, while HAY did not (94.2 ± 8.5%; $P = 0.3$). HAY calves tended to sort for long particles (113.4 ± 10.6%; $P = 0.08$), which were solely hay, while CONC calves sorted against them (56.4 ± 12.6%; $P < 0.01$). By wk 12, sorting was similar between treatments ($P > 0.15$), with both CONC and HAY calves sorting ($P < 0.01$) for short (117.4 ± 3.0, 120.5 ± 2.7%) and against long particles (62.4 ± 6.8, 54.4 ± 4.9%). The results indicated that feed familiarity affected initial diet selection post-weaning, but did not have any lasting effect.

Key Words: feed selection, dairy calves

M10 Lying time and animal activity after surgical castration of Holstein bulls recorded with pedometers. S. Marti*[1], M. Devant[1], and A. Bach[1,2], [1]*Department of Ruminant Production, IRTA*, *Barcelona, Spain*, [2]*ICREA*, *Barcelona, Spain*.

The aim of this study was to evaluate the effect of surgical castration on lying time and animal activity. A pedometer was placed in the left hind leg of 86 animals (27 bulls, 29 steers castrated at 3 mo of age, and 30 bulls castrated at 8 mo of age during the study) randomly chosen from a total of 132 animals (initial age = 232 ± 4.4 d). Animals were allocated in 6 pens (2 pens for each treatment). The study started 5 d before bulls were surgically castrated and finished 10 d after. Each pen had one

computerized concentrate feeder (GEA SurgeWestfalia, Germany), one straw feeder, and one drinker. Animals received concentrate and straw *ad libitum*. Daily lying time and average number of steps per hour were automatically recorded using a pedometer (E.N.G.S. Systems, Almagor, Israel). The statistical model included gender, day and their 2-way interaction, as fixed effects, and pen as a random effect. An interaction ($P < 0.05$) was observed between treatment and day in lying time. From castration day until 5 d later, surgically castrated bulls spent a lesser amount of time lying (10.1 ± 1.88 h) than bulls and steers (12.7 ± 0.65 h and 13.2 ± 0.89 h, respectively). Steers activity (48 ± 5.0 steps/h) was 54% lesser ($P < 0.01$) than that of bulls (106 ± 5.0 steps/h). Activity was also affected ($P < 0.001$) by an interaction between treatment and day. Bulls castrated at 8 mo of age showed a reduced activity above the first 3 d after castration (69 ± 5.5 steps/h) being lesser than that of bulls (109 ± 22.7 steps/h) but greater than that of steers castrated at 3 mo of age (43 ± 6.2 steps/h). Lying time is reduced during the 5 d following surgical castration. Bulls are more active (steps/h) than steers, and activity of steers decreases immediately after castration and for at least 10 d after castration remains lesser than that of bulls.

Key Words: beef, behavior, pedometers

M11 Dairy cattle welfare assessment in 25 farms in southern Brazil. G. B. Bond*[1], A. Ostrensky[2], R. Almeida[1], and C. F. M. Molento[1], [1]*Universidade Federal do Paraná*, *Curitiba, PR, Brazil*, [2]*Pontifícia Universidade Católica do Paraná*, *Curitiba, PR, Brazil*.

The objective of this study was to assess the main welfare indicators for lactating cows in 25 dairy farms in southern Brazil. The participating farms used confined or semi-confined systems, and had a median of 164 (min. 78, max. 480) lactating Holstein cows with a mean daily production of 28.5 ± 4.1 kg/cow. The visits occurred during the morning or afternoon milking, when a sample of 20% of the lactating cows was selected for locomotion scoring for locomotion scoring (0-good, 1-imperfect, 2-impaired, 3-severely impaired). After milking, other sample of 20% of the lactating cows was selected at the free stall. The animals were then observed for claw overgrowth (0 = normal, 1 = mildly overgrown, 2 = severely overgrown), hock lesions (0 = healthy, 1 = hair loss, 2 = abrasion), hock swelling (0 = healthy, 1 = mildly swollen, 2 = severely swollen) and hygiene score (1 = clean, 2 = slight manure splashes, 3 = demarcated plaques of manure, 4 = confluent plaques of manure). The data was analyzed through descriptive statistics using the FREQ procedure of SAS. Most animals (47.7%, min. 0, max. 63.9%) had imperfect locomotion and 7.6% (min. 0, max. 20%) presented the most severe degree. Some of them (6.1%, min. 0, max. 30%) had overgrown claws, and hock lesions were observed in 41.7% (min. 15%, max. 65.4%) of the cows; 7.2% (min. 0, max. 34,8%) of the animals had severely swollen hocks. Regarding the hygiene score, 10.7% (min.0, max. 52.9%) had excessively dirty sides (scores 3 and 4), 40.9% (min. 0, max. 81%) had excessively dirty hind limbs and 19.3% (min. 0, max. 50%) of the cows showed excessively dirty udders. The welfare indicators recognized internationally can also be used in Brazilian intensive dairy farms. The animals studied face important animal welfare issues, and preventive measures should be taken to avoid them. Further studies are needed investigating the causes of the specified problems to improve animal welfare assessment.

Key Words: cows, lameness, incidence

M12 Correlations between production traits and dairy cattle welfare indicators in 19 farms in southern Brazil. G. B. Bond*[1], A. Ostrensky[2], R. Almeida[1], and C. F. M. Molento[1], [1]*Universidade Federal do Paraná*, *Curitiba, PR, Brazil*, [2]*Pontifícia Universidade Católica do Paraná*, *Curitiba, PR, Brazil*.

The objective of this study was to analyze the correlation between animal welfare and production indicators for lactating cows in 19 dairy farms in southern Brazil, during the winter of 2009. The studied farms used confined or semi-confined systems, and had a median of 211 (max. 480, min. 80) lactating Holstein cows with a mean daily production of 33.6 ± 10.4 kg/cow. The visits occurred during the morning or afternoon milking. A sample of 50 lactating cows per herd was selected, according to their position in the milking parlor, for locomotion scoring (0-good, 1-imperfect, 2-impaired, 3-severely impaired). After milking, another sample of 50 lactating cows was selected at the free stall. The animals were then scored for claw overgrowth (0–normal, 1–mildly overgrown, 2-severely overgrown), hock lesions (0–healthy, 1–hair loss, 2-abrasion), hock swelling (0–healthy, 1–mildly swollen, 2-severely swollen) and hygiene score (1–clean, 2-slight manure splashes, 3-demarcated plaques of manure, 4-confluent plaques of manure). The correlations were analyzed through Kendall Tau-b correlations in SAS (the CORR procedure). The correlations show that low BCS was associated to overgrown claws and to higher milk yield (−0.153, $P < 0.01$ and −0.186, $P < 0.01$). Also, later lactation was associated to higher BCS (0.184, $P < 0.01$). Severe hock lesions were associated to swollen hocks (0.402, $P < 0.01$). The cow hygiene indicators for 3 separate body parts are highly correlated. The correlations between cow dirtiness (side, hind limb and udder) and milk production were positive (0.132, 0.164 and 0.136, respectively, $P < 0.01$). Later lactation was associated to less milk yield (−0.308, $P < 0.01$) and to cleaner sides and hind limbs (−0.123 with sides, −0.124 with hind limbs, $P < 0.01$). There was no clear association between lameness and milk production. Higher locomotion scores were associated to more lactations in lifetime (0.229, $P < 0.01$). The correlations between animal welfare indicators and productive traits were generally low, but many are statistically significant. Other studies are needed, correlating indicators such as lameness and cow hygiene.

Key Words: dairy cows, milk yield, lameness

M13 Effect of food restriction on the behavior of penned goats kids. D. Oliveira, I. A. M. A. Teixeira*, S. F. Souza, M. J. R. Paranhos da Costa, K. T. Resende, A. G. Pascoa, O. Boaventura Neto, and T. F. V. Bompadre, *Universidade Estadual Paulista/UNESP*, *Jaboticabal, SP 14884900, Brazil*.

The aim of this study was to evaluate the behavior and welfare of preweaned goat kids submitted to feed restriction. To adjust the period of observation, a preliminary trial was carried out to evaluate the circadian rhythm of 3 male Saanen kids. Direct way (video cameras) observations were conducted to evaluate the frequency and length of the behaviors. Data were analyzed using Rayleigh's Test of Uniformity (Oriana software). Based on the analyses of the circadian rhythm trial, 6 h of observation were defined per day: 10 a.m., 11 a.m., 12 a.m., 1 p.m., 3 p.m., and 4 p.m. Once established the hours for behavioral evaluation, 27 35 d-old goat kids (males, females, castrates) were subjected to 3 nutritional levels: without restriction (ad libitum), intermediate restriction (25%) and severe restriction (50%). The individual feed intake was daily recorded and the behavior observations were determined considering 11 categories (feeder, water drinker and pen interaction; reaction to human; active and passive social interaction; standing; lying; movement; bipedal and self-grooming). The evaluations were based on the frequency and length of the behaviors, totalizing 702 h

of observation. Data were analyzed as a 3x3x3 factorial arrangement (period of observation x nutritional level x sex) using PROC MIXED. DMI was lower than what is commonly reported for kids at similar age (8 g/day of DM), and there were not significant differences between nutritional levels ($P = 0.47$) and sex ($P = 0.27$). Kids subjected to severe feed restriction were less reactive to human and showed less reaction to external stimuli, staying in standing position for longer periods ($F = 3.71$; $P = 0.04$). Kids in this treatment also showed apathy and depression, indicating impaired welfare. All animals presented stereotypes. However, females were more sensitive to restrictive conditions, biting pen bars more often and for longer periods than other animals. This study showed that feed restriction affected animal welfare, which calls attention to the consequences in adopting such technique.

Key Words: behavior stereotype, chronobiology, dairy goat

M14 Effect of metabolizable energy levels on the feeding behavior of Santa Inês sheep. R. M. Fontenele*, E. S. Pereira, P. G. Pimentel, M. S. de Souza Carneiro, A. B. Selaive Villarroel, and J. G. L. R. Filho, *Federal University Ceará*, *Fortaleza, Ceará, Brazil*.

The objective of this study was to evaluate the feeding behavior of Santa Inês sheep fed different levels of energy (2.08, 2.28, 2.47 and 2.69 Mcal/kg DM) in diets. Twenty lambs, average weight of 13 kg ± 0.56 kg and age 50 d, confined in individual pens with concrete floor and provided with feeders and drinkers. The animals were weighed, identified and treated for ecto and endoparasites, then distributed in 4 experimental treatments with different levels of metabolizable energy (2.08, 2.28, 2.47 and 2.69 Mcal/kg DM) in a randomized block design with 5 replications. The roughage used was the Tifton 85 hay. Since the experimental variables were subjected to ANOVA and regression using the Statistical Analysis System and Genetic - SAEG. Feeding time, expressed in h/day, decreased linearly ($P = 0.02$) with the increase in energy levels of experimental diets (5.83, 5.87, 4.85 and 4.77 min/day, levels 2.08, 2.28, 2.47 and 2.69 Mcal/kg DM, respectively). With regard to leisure time, there was a linear increase ($P = 0.03$), recording the values of 5.10, 5.65, 6.14 and 6.50 min/day, to levels 2.08, 2.28, 2.47 and 2.69 Mcal/kg DM, respectively. However, rumination, feeding efficiency (g DM/h and g NDF/h), and rumination efficiency (g NDF/h), were not affected ($P > 0.05$) by levels of energy in diets. However, the efficiency of rumination (g DM/h), decreased linearly ($P = 0.007$) with increasing energy levels in diets, recording values of 5.10, 5.65, 6.14 and 6.50 h/day, for the levels of 2.08, 2.28, 2.47 and 2.69 Mcal/kg DM, respectively. It was observed that the total mastication time (min/day), too, was influenced ($P = 0.02$) the energy levels of the experimental diets, with linear effect, with values of 15.56, 14.63, 13, 78 and 13.08 min/day, for the levels 2.08, 2.28, 2.47 and 2.69 Mcal/kg DM, respectively. As for variables such as frequency of regurgitation, frequency of mastication, frequency of mastication and regurgitation of mastication time per regurgitation were not affected ($P > 0.05$) by levels of energy in the diets.

Key Words: lamb, roughage:concentrate ratio, ruminants

M15 Evaluation of feed behavior traits in beef heifers using a GrowSafe intake measurement system. E. Mendes*, G. Cartens, and L. Tedeschi, *Texas A&M University*, *College Station*.

The objective of this study was to evaluate the use of an electronic feed intake system to quantify feeding behavior traits in beef heifers. Feed intake and feeding behavior data were recorded in 32 heifers (initial BW = 285 kg) fed a high grain diet (3.1 Mcal ME/kg DM) for 81 d while confined to a pen equipped with 4 GrowSafe 4000E feedbunks (2-s read rate). Time-lapse video was used to record observations of individual bunk visits for 10 heifers over 3 consecutive d. Bunk visit frequency (BVF) and duration (BVD) were computed using software (DAQ4000E ver. 9.22) at parameter settings (PS) of 30, 60, 100, 150 and 300 s, which defines maximum duration between transponder hits for a new event (default = 300 s). Meal frequency (MF) and duration (MD) were computed from BV data using a meal criteria as 5 min. Daily BVF and BVD data were split into 4 6-h periods for statistical comparison with observed video data using r^2, mean square error of prediction (MSEP), mean bias (MB), accuracy (Cb), and corrected Akaike's Information Criterion (AIC). Observed BVF and BVD (mean ± SD) were 12.8 ± 9.1 events and 18.0 ± 12.1 min/6-h period. As PS increased from 30 to 300 s, BVF decreased (16.6, 12.7, 11.9, 11.6 and 11.4 events/6-h, respectively) and BVD increased (13.4, 16.0, 17.0, 17.7 and 18.3 min, respectively). Statistical analyses revealed that PS of 60 and 100 s generated predicted BVF data most similar to observed data (0.91 and 0.88, 0.1 and 0.2, 0.01 and 0.13, 1.0 and 0.9, and −218 and −192 for r^2, MSEP, MB, Cb, and AIC, respectively), while PS of 100 and 150 s generated predicted BVD data that were most similar to observed data (0.91 and 0.91, 0.2 and 0.2, 0.13 and 0.01, 1.0 and 1.0, and −203 and −201 for r^2, MSEP, MB, Cb, and AIC, respectively). Meal frequency and duration computed from BV data was minimally affected by PS. These results suggest that BVF and BVD computed with a PS of 100 s most accurately predicted observed feeding behavior traits, which were on average 94 and 95% of observed BVF and BVD, respectively.

Key Words: feeding behavior, intake

M16 Feeding behavior and ruminal acidosis in beef cattle offered a total mixed ration or dietary components separately. D. Moya*[1], A. Mazzenga[2], L. Holtshausen[3], G. Cozzi[2], L. González[4], S. Calsamiglia[1], D. Gibb[3], T. McAllister[3], K. Beauchemin[3], and K. Schwartzkopf-Genswein[3], [1]*UAB*, *Barcelona, Spain*, [2]*UP*, *Padova, Italy*, [3]*Agriculture Canada*, *Lethbridge, Canada*, [4]*U of Manitoba*, *Winnipeg, Canada*.

Eighty continental crossbred beef heifers (414.9 ± 37.9 kg BW), including 16 ruminally cannulated, were used in a 52-d experiment conducted as a complete randomized block design, to asses if, when allowed to select their own diet, heifers would choose a proportion of ingredients that prevents drops in ruminal pH and improves the rumen environment. Treatments were: TMR (85% barley-grain, 10% corn silage); free-choice diet (FCD) (BGCS) of barley-grain (BG) and corn silage (CS); FCD (BGDG) of BG and wheat distillers grain (DG); and FCD (CSDG) of CS and DG. Animals were housed in groups of 10 in 8 pens equipped for automatic recording of feeding events 24 h/d, allowing for the calculation of individual feeding behavior. Cannulated heifers were fitted with an indwelling pH probe to record ruminal pH every 60s. Data were summarized as mean pH, and area under the curve (AUC) with pH lower than 5.8. Ruminal samples were taken from cannulated animals 2 h post-feeding on d 4 and 42, for determination of VFA. Data were analyzed with a mixed model which included treatment, time and their interactions as fixed effects and pen as a random factor. Heifers fed TMR had lower ($P < 0.05$) meal length, time, and size than those fed FCD. Cattle fed BGCS and BGDG increased ($P < 0.05$) the proportion of BG intake over the trial up to 80 and 70%, respectively, by increasing ($P < 0.05$) eating rate and maintaining ($P > 0.10$) feeding duration of BG, and increasing ($P < 0.05$) eating rate but decreasing ($P < 0.05$) feeding duration of either CS or DG. Even with these changes, ruminal pH and VFA profile was not different ($P > 0.10$) over the trial or compared with TMR. Cattle fed CSDG ($P > 0.10$) maintained DG intake at 60% over the trial, and had greater ($P < 0.05$) mean ruminal pH, AUC, and acetate to propionate ratio than those fed other treatments. Finishing feedlot cattle fed FCD including BG as an option consume

similar ingredients and have intake and ruminal fermentation profiles similar to those fed TMR.

Key Words: beef cattle, acidosis, feeding behavior

M17 Association between facial hair whorl and temperament in noncastrated male cattle *Bos taurus* and *Bos indicus*. R. Rivas*[1,2], A. Schmidek[2], E. N. Andrade[3,2], F. D. Resende[2], G. R. Siqueira[2], M. H. Faria[2], and R. O. Roça[3], [1]*Centro Universitário da Fundação Educacional de Barretos - UNIFEB*, *Barretos, SP, Brazil*, [2]*Agência Paulista de Tecnologia do Agronegócio - APTA*, *Colina, SP,Brazil*, [3]*Universidade Estadual Paulista Júlio de Mesquita Filho - UNESP*, *Botucatu, SP, Brazil*.

Studies have associated cattle temperament with the presence and location of facial hair whorls in these animals. The objective of this work was to investigate the relationship between facial hair whorl and temperament during weighing crate. Seventy-three noncastrated males were used (*Bos taurus* and *Bos indicus* – Angus and Nelore), aged between 20 to 22 mo. The animals were classified into 4 categories according to the location and presence of hair whorl: above the eye, at eye level, below the eye or absent upon entry into a handling crush. All animals were submitted to the same type of housing and handling. The first weighing crate was done 21 d after at the beginning of feedlot. Later, they were done every 21 d, always after a 12 h fasting period. Temperament was evaluated during weighing crate, according to the tension shown in the first 5 s after closing the gates to the scale. The animals were classified as relaxed or tense, based on the speed of movements and muscle tone. Response variables of hair whorl and temperament were evaluated through Spearman correlation in SAS. There was no significant association between facial hair whorl and temperament ($P \geq 0.05$). Most animals (90.4%) were classified as tense during evaluations. The absence of whorl was observed in 57.1% of relaxed animals and 43.9% of tense animals did not show hair whorls. Hair whorl at eye level was observed in 42.9% of relaxed animals and 31.8% of tense animals. There were no relaxed animals among those with hair whorls above and below the eye. The location of facial hair whorls did not prove to be an applicable tool in the identification of temperament in noncastrated male cattle (*Bos taurus* and *Bos indicus*).

Key Words: bovine, Nelore and Angus, temperament

M18 Comparison of adrenal responsiveness to corticotropin-releasing hormone (CRH) in Angus and Brahman steers of divergent temperament. K. O. Curley Jr.*[1,2], J. A. Carroll[3], R. C. Vann[4], R. D. Randel[1], and T. H. Welsh Jr.[1], [1]*Texas AgriLife Research*, *College Station,* [2]*Texas AgriLife Research*, *Overton,* [3]*USDA ARS*, *Lubbock, TX,* [4]*MAFES*, *Raymond, MS*.

The objective of this study was to compare adrenal activity after pituitary stimulation with exogenous CRH, in cattle of differing temperament and breedtype. Using a combination of exit velocity, the rate at which cattle exit a squeeze chute and traverse a fixed distance (1.83 m), and pen score, a subjective assessment of cattle's behavior toward a handler, we identified the 10 calmest (C) and 10 most temperamental (T) weaned calves from a Brahman (B) and an Angus (A) herd. Blood samples were collected via indwelling jugular cannula for a period of 6 h pre- and 6 h post- administration of CRH (0.1 μg/kg BW). Sampling intervals were 15 min throughout the 12 h except for the initial 30 min of the post-challenge period when the sampling intervals were 5 min. Serum cortisol concentrations were determined by RIA. MIXED model repeated measures ANOVA was conducted for a factorial analysis of (1) time and breed, within temperament, or (2) time and temperament, within breed, effects on hormone concentrations throughout the duration of blood sampling. Additionally, the GLM was utilized for ANOVA of adrenal response parameters. During the initial 3 h of sampling an effect ($P < 0.01$) of breed was present in only the calm animals, as the A steers maintained higher cortisol concentrations than the B steers. Baseline cortisol concentrations were affected ($P < 0.01$) by both breed (A = 16.7 ± 2.7; B = 9.7 ± 1.2 ng/ml) and temperament (t = 18.2 ± 2.5; C = 8.7 ± 1.3 ng/ml); no breed by temperament interaction was present. During the post-challenge sampling period there was a time by temperament interaction ($P < 0.005$) observed within each breed. Only a breed effect ($P < 0.005$) on peak stimulated-cortisol concentrations (A = 35.1 ± 1.7; B = 28 ± 1.3 ng/ml) was observed. However, only temperament influenced ($P < 0.01$) the amplitude of the cortisol response (C = 22.3 ± 2.1; t = 14.1 ± 2.0 ng/ml). Thus, cattle characterized as temperamental exhibit an endophenotype of a higher basal secretion of cortisol coupled with a blunted adrenal response to exogenous CRH. The genetic bases of variation in endophenotype and temperament warrant investigation in cattle.

Key Words: adrenal, cortisol, temperament

M19 Evaluation of temperament on pregnancy rate in beef embryo recipient cows. S. S. Jennings*[1], K. J. Stutts[1], C. R. Looney[2], and T. H. Welsh Jr.[3], [1]*Sam Houston State University*, *Huntsville, TX*, [2]*OvaGenix, Inc.*, *Bryan, TX*, [3]*Texas AgriLife Research*, *College Station*.

The objective of this study was to determine if temperament had an effect on pregnancy rate (PR) of recipient females to embryo transfer (ET). Multiparous cows (n = 57) of various breed compositions were used as recipient females. Donor and recipient females were synchronized using a vaginal insert containing progesterone in combination with estradiol 17β and prostaglandin $F_2\alpha$. Embryos were non-surgically collected 7 d after insemination and transferred to recipients the same day as fresh embryos, or were frozen-thawed embryos preserved in ethylene glycol. At the time of ET, cows were assigned a temperament score of 1 to 5 (1 = docile and 5 = aggressive) based on the cow's behavior while being confined in the chute. Following transfer of the embryo, 10 mL of blood was collected via coccygeal venipuncture to determine serum cortisol concentration to assess each cow's stress response to handling at the time of ET. Serum concentration of cortisol was quantified by RIA. Pregnancy exams were conducted using transrectal ultrasonography at least 21 d post transfer to determine PR. Cortisol data were analyzed using one-way ANOVA and PR was analyzed by chi-squared analysis using the frequency procedure. Pearson correlation coefficients were used to determine the relationship between PR and cortisol concentration. There was no effect of temperament score ($P = 0.36$) on PR to ET and no relationship between PR and serum cortisol concentration (r = 0.18). Recipients that were assigned temperament scores of 4 or 5 had a higher mean serum cortisol concentration (31.1 ng/mL) than recipients assigned scores of 1 to 3 (22.9 ng/mL) but this difference was not significant. Results of this study indicate that temperament of recipient females does not have a significant effect on PR to ET nor is there a correlation between PR and stress response of the recipient at the time of ET as indicated by serum cortisol concentration immediately following ET.

Key Words: temperament, recipient females, embryo transfer

M20 Ingestive behavior and physiological parameters of crossbreed heifers under different feeding schedules. R. A. S. Pessoa*[1], F. M. Silva[1], M. A. Ferreira[1], M. Azevedo[1], L. H. S. Gomes[1], E. C. Silva[1], J. G. R. Cunha[1], A. S. S. Filho[2], D. C. Santos[2], and J. C. V. Oliveira[2], [1]*Universidade Federal Rural de Pernambuco*, *Recife, Pernambuco, Brasil*, [2]*Instituto Agronômico de Pernambuco*, *Recife, Pernambuco, Brasil*.

The objective was to evaluate the physiology variables and ingestive behavior in heifers under different feeding schedules. The maximal and minimal temperatures in the period ranged from 25.8 to 31.4°C and 21.3 to 23°C, respectively. Five crossbreed housed heifers were used, with average live weight of 250 kg and age of 24 mo, in a 5 × 5 Latin square design. Each experimental period lasted 15 d, 10 d being for the adaptation of the animals to the diet and 5 d for data collecting. The animals were fed a TMR twice daily, and the diet was composed of 70% forage (41% of cactus pear and 29% bermudagrass hay) and 30% concentrate (14% soybean meal, 13.5% of corn meal and 1.5% mineral mixture) twice a day. The first meal was provided at 7:00 for all animals. The treatments consisted by different feeding schedules of the second meal (12:00; 14:00; 16:00; 18:00 or 20:00 h). The physiology variables were record 2 h before and 2 h later of the second meal (treatment). The ingestive behavior was record in a period of 24 h, in intervals of 10 min. The data were submitted to ANOVA using the SAS. The different feeding schedules affect the respiratory frequency and the rectal temperature after the meal, which decreased with the hours (61.0 to 40.8 movements/minute and 39.0 to 38.5°C for respiratory frequency and rectal temperature, respectively). The ingestive behavior was not affected by the treatments, with average of 822, 396 and 222 min/day for total time resting, total time ruminating and total time feeding, respectively. Overall, different times of feeding changed respiratory frequency and rectal temperature, whereas it did not affect the ingestive behavior of the crossbreed heifers.

Key Words: heifers, meal, feed management

M21 Influence of exercise on feedlot performance and carcass characteristics in steers. B. J. Howell*[1], J. R. Brethour[2], and T. Noffsinger[3], [1]*Fort Hays State University*, *Hays, KS*, [2]*Agricultural Research Center, Kansas State University*, *Hays,* [3]*Production Animal Consultants*, *Benkelman, NE*.

Cattle in feed yards are not commonly exercised beyond the confines of their pen, with the exception of possibly one or 2 re-implant events. The objective of this experiment was to investigate the effect of regular exercise on animal performance and carcass characteristics. Angus crossbred steers (n = 189) were stratified by initial body weight and ultrasonically measured carcass characteristics, and assigned randomly to 2 treatment groups (control vs. exercise) with 3 replications per treatment (n = 31 hd/replication). The exercise treatment protocol consisted of daily exercise for 5 d upon arrival, followed by alternate day exercise for the next 10 d, and then exercise 2 times/week for the remainder of the feeding period. The total feeding period was 124 d for replication 1, and 166 d for replications 2 and 3. Cattle in exercise treatment pens were allowed to exit their pen into a feed alley of an area approximately 67 × 13 m for 15 min and were then returned to their pen. The control animals were not removed from their pens with the exception of ultrasonic measurement of longissimus muscle characteristics. No differences ($P > 0.05$) were observed between treatments for average daily gain, dressing percentage, backfat, calculated yield grade, marbling, proportion grading Choice, or kidney, pelvic and heart fat. Under the conditions of our study, this exercise treatment strategy did not affect feedlot average daily gain or carcass characteristics.

Key Words: exercise, beef cattle, feedlot

M22 Lack of magnetic orientation of beef cattle. M. Erikson*, E. Leduc, R. Prince, and G. Gallagher, *Berry College*, *Mount Berry, GA*.

Recently published research suggests cattle and deer orient themselves toward the magnetic poles when grazing or at rest. However, this study was based on evaluation of satellite images with stringent criterion for data inclusion. We hypothesize that if orientation of cattle was not random, it could be due to environmental influences. Therefore, the objective of this study was to determine if pastured cattle exhibited orientation preferences and if that orientation could be attributed to environmental factors. Photographs of beef cattle (n = 585) on the Berry College campus pastures, were taken twice per week from Jan 20, 2009 – Feb 21, 2009, during the day between 0700h – 1100h (n = 283) by digital camera and at night between 2000h – 2200h (n = 279) using a FLIR thermal camera. Compass readings were obtained for each photograph using visible landmarks as points of reference to verify orientation of each photograph. Temperature, wind speed, and humidity were also recorded for all photographic events. Cattle orientation was determined by placing a transparent 360° grid, divided into 8 sectors on each image. Each sector was comprised of a 45° region bisecting respective primary directions of N (Sector 1), E (Sector 3), S (Sector 5) and W (Sector 7). Remaining sectors represented NE (Sector 2), SE (Sector 4), SW (Sector 6) and NW (Sector 8). Orientation of each animal was assigned to a sector based on the direction of the head relative to the longitudinal direction of the body. Chi-squared analyses were conducted under the assumption that animal orientation within each sector would be similar (12.5%) among the 8 sectors. Results indicated a larger ($P < 0.05$) than expected (21.0%) orientation in Sector 2 (NE) and less than expected (6.6%; $P < 0.05$) in Sector 1 (N). No differences ($P > 0.05$) were found in orientation among the other sectors. These results suggest little evidence to support the concept of North – South cattle orientation as a result of the earth magnetic field or local environmental conditions.

Key Words: magnetic poles, cattle orientation

M23 Effect of cattle liner microclimate on core body temperature and shrink in market-weight heifers transported during summer months. M. Bryan*[1,2], K. Schwartzkopf-Genswein[1], T. Crowe[2], L. González[3], and J. Kastelic[1], [1]*Agriculture and Agri-Food Canada*, *Lethbridge, Alberta, Canada*, [2]*University of Saskatchewan*, *Saskatoon, Saskatchewan*, *Canada*, [3]*University of Manitoba*, *Winnipeg, Manitoba, Canada*.

Market weight heifers (n = 452; BW 619 ± 22 kg) were transported in one of 5 compartments within a cattle liner on 10 journeys (940 km) during summer months to study the effect of trailer microclimate during transit (T) and stationary (S) periods on core body temperature (baseline–journey temperature; ΔCBT) and live weight loss (loading weight–unloading weight; LWL) in market weight heifers. Microclimate measurements included temperature (Temp; °C) and temperature humidity index (THI). The trailer ceiling (TC) of all 5 compartments was fitted with a total of 45 temperature/humidity data loggers. A single data logger was also placed intravaginally in a subset of 10 heifers/liner to obtain core body temperature 2 d before transport (baseline), as well as during the entire journey until the time of off–loading. The same heifers also had a data logger affixed to their ear tag (ET) to determine the temperature at animal level. Data was analyzed with a mixed model considering the fixed effects of cattle liner, compartment and day as repeated measure, as well as the random effect of compartment x day and all possible interactions. Temp was greater during S than T (23.35 and 20.32 ± 0.44; $P < 0.0001$) and also greater for ET than TC (23.20 and 20.48 ± 0.43;$P < 0.0001$). ΔCBT was greater during S than T ($P < 0.0001$) with values of 0.36 and 0.19 ± 0.06°C, respectively. Trailer

THI did not have an impact on ΔCBT ($P > 0.10$). However, a significant positive relationship ($P < 0.03$) was observed between THI and LWL. There were no differences ($P > 0.02$) in LWL among compartments. Trailer microclimate is variable according to location (animal level vs ceiling) within a compartment and whether the truck is in transit or is stationary and can negatively impact animals during summer transport. The impact may be more severe on journeys that have long stationary periods.

Key Words: cattle, transport, microclimate

M24 Natural resistance-associated macrophage protein (Nramp1) and goat health. Y. Ahmed, M. Worku*, H. Mukhtar, and R. Noble, *North Carolina Agricultural and Technical State University*, *Greensboro*.

The objective of this study was to determine how Nramp1 expression may be associated with disease states in the goat. Natural resistance-associated macrophage protein (Nramp1) is expressed exclusively in professional phagocytes. Expression of Nramp1 affects host innate immunity to intracellular bacteria because of its ability to transport divalent cations in late endosome/lysosomes. Studying the association of the NRAMP1 gene and innate immune response to pathogens may aid in understanding and enhancement of goat genetic resistance to pathogens. Clinically healthy Boer, Spanish and Spanish-Boer cross goats (n = 60) from the NC A&T Small ruminant unit were used. Fecal samples were evaluated for levels of *Haemonchus* and *Coccidia* using McMaster slides. Blood samples were evaluated for packed cell volume and white blood cells Differential count. The FAMACHA score body condition score, body weight, body temperature, and age were recorded. Genomic DNA was extracted from blood (n = 12 goats)on FTA cards according to the manufacturer's protocol. RNA was extracted using the ZR Whole-Blood Total RNA Kit. RNA samples were reverse-transcribed and the cDNA was obtained using the Ambion-Retroscript as per the manufacturer protocol. Specific primers for Nramp1 and GAPDH as loading control were used for RT PCR. Data were analyzed using SAS ANOVA and an independent sample *t*-test. Nramp1 was expressed with variability among animals. Identification of Nramp1 in genomic DNA was not affected by breed. However, Nramp1 expression was significantly increased with increased fecal coccidia egg counts ($P < 0.05$) but was not affected by fecal *Haemonchus* egg counts ($P = 0.0677$).

Key Words: NRAMP-1, goat, pathogen

M25 Identification of serum biomarkers in poultry with leg problems. K. S. Rasaputra*[1,2], R. Liyanage[1], J. O. Lay Jr.[1], and N. C. Rath[2], [1]*University of Arkansas*, *Fayetteville,* [2]*Agricultural Research Service/ USDA*, *Fayetteville, AR*.

Disease induced changes in tissue metabolism is often reflected in the blood; therefore, serum chemistry is conventionally used for diagnosis of health problems. Being the structural and functional basis of tissues, changes in the serum protein profiles are of considerable interest as biomarkers. Tibial dyschondroplasia (TD), caused by the failure of growth plate to form bone results in lameness causing significant economic loss to the poultry industry. Serum markers could identify poultry susceptible to these problems aiding in better genetic selection. Thus, the objective of our study was to identify serum protein differences in normal and diseased birds for use as biomarkers. Similar to other applications involving serum, identification of serum protein biomarkers is hindered because of few high abundant proteins. We used combinatorial peptide ligand library based "Proteominer" beads to enrich low abundant proteins and study their differential expressions in serum. Serum was collected from 6 wk-old chickens with and without leg problems and processed through the proteominer column to deplete the high abundant and enrich the low abundant proteins. Equal amounts of proteins from both groups were subjected to 2D gel electrophoresis. The Coomassie blue stained protein spots in the gels were analyzed using Melanie software to identify differentially expressed proteins in both groups. The protein spots were subjected to in gel trypsin digestion followed by MALDI peptide mass fingerprinting for protein identification. The results showed that proteominer resulted in enrichment of several new protein spots and depletion of some of the high abundant proteins. The Coomassie stained gel showed 50 protein spots of which 21 spots were identified. Melanie analysis showed 4 differentially regulated proteins in the diseased condition. Two spots corresponding to immunoglobulin G (IgG) were upregulated while the other 2 protein spots were down-regulated. It is not known whether the pathogenesis of TD is related to immunity; however, our results show that the IgG levels are upregulated suggesting the role of immunity in TD.

Key Words: tibial dyschondroplasia, serum, proteomics

M26 The detection of bovine respiratory disease in low risk cattle using infrared thermography. A. L. Schaefer*[1], N. J. Cook[2], C. Bench[3], J. Colyn[1], B. Chabot[1], T. Liu[1], P. Lepage[1], D. Froehlich[2], L. Holt-Klimek[1], S. Marchand[1], J. Basarab[2], and E. Okine[3], [1]*Agriculture and Agri-Food Canada, Lacombe Research Centre, Lacombe, Alberta*, [2]*Alberta Agriculture, Lacombe Alberta*, [3]*Department of AFNS, University of Alberta, Edmonton, Alberta*.

Bovine respiratory disease (BRD) causes significant harm to the cattle industry. Clinical methods can identify BRD once the symptoms are advanced. However, identifying symptoms earlier in low risk cattle is more challenging yet important to avoid missing false negatives. The objective of the present study was to examine whether infrared thermography (IRT) of the eye could identify BRD in low risk calves more effectively than conventional methods. Sixty 5 crossbred calves averaging 220 kg were used. The calves were from Agriculture and Agri-Food Canada (AAFC) herds. The calves were weaned and transported approximately 1h to an auction and held over night. The animals were transported back to an AAFC feedlot facility, offloaded, weighed, blood sampled, examined for rectal temperature (RT) and placed into a feedlot pen with free access to cereal silage and water. Daily clinical scores were conducted by pen checkers and an automated, RFID triggered IRT camera (FLIR S60) was mounted at the water station to record eye temperatures. All calves were again monitored 2 weeks later. Hematology analysis included white blood cell counts (WBC) and neutrophil/lymphocyte ratios (N/L). A true positive animal (TP) for BRD needed to display 2 or more of; RT > °104 C, WBC >11 or <7 X 1000 /μL, Clinical Score values (CS) > 3 or N/L ratios >0.8 or <0.1 . No calves were identified by clinical pen checking as in need of treatment. However, hematology, CS and RT identified 11 of the 65 calves as TP with 7 of these TP at both blood sampling dates. Values for TP calves for RT, CS, WBC and N/L ratios were 103.6 ± 0.74 (SD), 4.5 ± 1.1, 11.16 ± 2.65 and 0.13 ± 0.7 respectively while for calves displaying true negative values (TN) at both sample periods were 102.1 ± 0.5, 2.11 ± 1.02, 8.97 ± 1.15 and 0.21 ± 0.1 ($P < 0.01$). Of interest was the observation that the average IRT value for the TP calves was higher throughout the 2 week period (35.44 ± 0.58 C) compared with the TN calves (34.7 ± 0.57 C, $P < 0.01$). Data from this study suggests that the use of non invasively collected eye IRT data may be useful in early identifying calves displaying BRD.

Key Words: bovine respiratory disease, infrared thermography, cattle

M27 Feeding *Lactobacillus* spp. and *Bacillus* spp. does not improve growth or survival of channel catfish experimentally challenged with *Edwardsiella ictaluri*. B. C. Peterson*[1], M. L. Wood[1], N. J. Booth[1], M. Morgan[2], N. Pumford[2], G. Tellez[2], and B. M. Hargis[2], [1]*USDA/ARS, Stoneville, MS,* [2]*University of Arkansas, Fayetteville*.

A major problem in the channel catfish industry has been high disease loss to enteric septicemia of catfish, caused by the bacterium *Edwardsiella ictaluri*. Feeding probiotics may prove beneficial in improving disease resistance. The first study examined the effects of a *Lactobacillus* probiotic (FloraMax-B11; Ivesco, LLC, Springdale, AR) (poultry origin) on growth and resistance to *E. ictaluri*. Two hundred catfish (23.5 ± 0.3 g) were assigned to 2 treatments with 5 replicates each: 1.) Control (36% CP diet) and 2.) FloraMax-B11 (11 *Lactobacillus* spp., sprayed on feed at 10^6 cfu/g of diet). The fish were fed for 6 wks and then experimentally challenged with *E. ictaluri*. The second study examined the effects of 3 spores of *Bacillus* spp. on growth and disease resistance. *Bacillus subtilis*-1 (environmental sample) and *B. subtilis* -2 (catfish origin) were previously shown to have antibacterial in vitro activity against *Escherichia coli* and *E. ictaluri*. *Bacillus pumilus* of catfish origin, which did not show in vitro antibacterial activity, was also tested in this study. Five hundred catfish (11.2 ± 0.1 g) were assigned to 4 treatments with 5 replicates each: 1) Control (36% CP diet); 2) BS-1 (*B. subtillis* at 10^7 cfu/g of diet); 3) BS-2 (*B. subtilis* at 10^7 cfu/g of diet); and 4) BP (*B. pumilus* at 10^6 cfu/g of diet). Fish were fed for 9 wks and challenged with *E. ictaluri*. Data were subjected to ANOVA with tank as the experimental unit. Addition of *Lactobacillus* spp. and *Bacillus* spp. to the diet of catfish had no effect on weight gain, FE, or survival after challenge with *E. ictaluri* ($P > 0.10$). The results of these studies suggest that neither the *Lactobacillus* based probiotic nor any of the 3 spore base probiotic candidates improved growth performance or resistance against *E. ictaluri* . Identifying other catfish specific bacteria and understanding how they may manipulate the microflora of the GI tract will be key in determining whether probiotics have a benefit in improving catfish aquaculture.

Key Words: probiotics, disease, catfish

M28 Effects of intravenous *Escherichia coli* (*E. coli*) dose on the pathophysiological response of colostrum-fed Jersey calves. M. A. Ballou*[1], J. W. Dailey[2], L. E. Hulbert1,2, C. J. Cobb[1], and J. A. Carroll[2], [1]*Texas Tech University, Department of Animal Science, Lubbock,* [2]*Livestock Issues Research Unit, USDA-ARS, Lubbock, TX*.

Objective was to determine the effects of *E. coli* dose on the pathophysiological response of dairy calves following an intravenous challenge. Eighteen 3-wk-old colostrum-fed Jersey calves were completely randomized to 1 of 6 doses of *E. coli*. The challenge doses included 0, 10^5, 10^6, 10^7, 10^8, and 10^9 colony-forming units (CFU) given as a bolus in 5 mL of sterile isotonic saline. Peripheral blood samples were collected at 0, 2, 4, 8, 12, 24, and 48h relative to the challenge for blood metabolite, total white blood cell count and differential analyses. Rectal temperatures were collected via indwelling rectal probes at 1-min intervals, and hourly averages calculated from 2d before the challenge till 2d after the challenge. All calves survived the 48h observation period following the challenge. The attitude of calves given 10^8 and 10^9 CFU was altered ($P < 0.01$) beginning 0.5h after the challenge and returned to that of the control calves by 8 and 48h for calves challenged with 10^8 and 10^9 CFU, respectively. There were treatment x time interactions ($P < 0.01$) on total white blood cell counts and plasma glucose concentrations. Calves administered 10^8 and 10^9 CFU had leucopenia and neutropenia beginning 2h after the challenge and returning to counts similar to the control calves within 24h. Additionally, those calves were hypoglycemic from 4 to 12h after the challenge with the degree of hypoglycemia inversely related to the dose of the *E. coli*. There were treatment x time interactions ($P < 0.01$) on rectal temperatures following the challenge. All calves challenged with *E. coli* developed a febrile response, but the intensity and duration of the response were dependent on the challenge dose. These data indicate that calves intravenously challenged with 10^8 and 10^9 CFU of an *E. coli* showed immediate clinical and biochemical signs indicative of septicemia. However, calves administered 10^7 or less of the *E. coli* had febrile responses, but did not develop septicemia.

Key Words: calf, *E. coli*, septicemia

M29 *Eimeria tenella* oocyst output in cecal or fecal material following challenge in restrict-fed broilers. A. Jordan*[1], D. Caldwell[1], J. Klein[1], J. Coppedge[1], S. Pohl[1], K. Jessen[1], S. Fitz-Coy[2], and J. Lee[1], [1]*Texas A&M University, College Station*, [2]*Intervet/Schering-Plough Animal Health, Summit, NJ*.

The current experiment was conducted to compare *Eimeria tenella* oocyst shedding in fecal or cecal contents in restrict-fed broilers following experimental challenge in brooder batteries. Ninety-six Cobb 500 by-product males were placed in battery pens with 8 chicks per pen. On d 14, restrict feeding was initiated and chicks were challenged with one of 3 challenge levels (1,000, 5,000, and 20,000 oocysts). Total 24 h collections of cecal and fecal material were obtained separately beginning on d 4 post-challenge through d 10 post-challenge for oocysts per gram and total output determination. Six days post-challenge, 4 broilers from each pen were removed and subjected to necropsy for lesion assessment. Data was subjected to a one-way ANOVA using the GLM procedure. Means were deemed significantly different at $P < 0.05$ and means were separated using Duncan's Multiple Range Test. Body weight gain was not affected due to challenge level throughout the experimental period. Increases ($P < 0.05$) in both gross and microscopic lesion development were observed with each increase in challenge level. Oocyst output peaked on d 8 post-challenge. Oocyst concentration was higher ($P < 0.05$) in cecal droppings as compared with fecal material throughout peak shedding. However, total output of *Eimeria tenella* oocysts was similar ($P > 0.05$) in fecal and cecal material. These data indicate that total oocyst output during an experimental challenge are similar in fecal and cecal material, however concentrations are significantly lower in fecal material compared with cecal material when compared on a output per gram basis.

Key Words: *Eimeria*, broiler, oocyst shedding

M30 Effect of aqueous iodine supplementation on growth and dental condition of newly weaned piglets. A. L. Tucker* and R. M. Friendship, *University of Guelph, Guelph, Ontario, Canada*.

Weaning is a stressful event and many pigs experience poor growth in their first weeks in the nursery. The use of antibiotics to improve growth and health has come under increasing scrutiny and alternative means of reducing bacterial load are desirable. Iodine, a broad-spectrum antiseptic, shows potential as a therapeutic agent because it has low potential for resistance and is inexpensive. It is also used to prevent oral disease, a condition that can develop in nursery age piglets. Recently, premolar eruption and the presence of poor oral conditions have been shown to affect weight gain in weaned piglets. The aim of this study was to examine the efficacy of an aqueous iodine supplement for improving piglet weight gain and oral condition. Across 3 trials, 624 piglets on a commercial farrow-wean farm were examined. An iodine-based sanitizer containing 1.75% titratable iodine was added to the water supply to a final concentration of 1 ppm. Water was supplied to via nipple drinkers

with testing confirming mean concentrations of 0.96, 0.68 and 0.91 ppm in trials 1, 2 and 3. Piglets were weighed and given oral exams within 24 h of weaning and again 3 and 6 wks later. Deciduous teeth were recorded as being erupted (vs not erupted) if any portion of the tooth crown penetrated the gingiva. Dental staining and caries (cavities) on incisors, gingivitis around any teeth and oral lesions on the gingiva, tongue, cheeks or throat were recorded. A repeated measures ANOVA (SAS Proc MIXED) was used to examine how iodine supplementation influenced growth and oral condition. Overall, the presence of staining and caries on the primary incisors increased between weaning and wk 3 ($P < 0.05$), while the incidence of both oral lesions and gingivitis increased between wks 3 and 6 ($P < 0.05$). There were no significant treatment differences in piglet growth or oral condition during the period that iodine was supplemented ($P > 0.05$). These results indicate that deleterious oral conditions do develop and increase throughout the weaning period, but, at 1 ppm, an aqueous iodine supplement does not provide an advantage for weight gain or oral condition in nursery piglets.

Key Words: growth, dentition, swine

M31 Interaction of breed and quantity of milk replacer on innate immune competence of dairy calves. M. A. Ballou* and C. J. Cobb, *Department of Animal and Food Sciences, Texas Tech University*, *Lubbock*.

Objective was to determine the influence of breed and quantity of milk replacer fed on the immune competence of dairy calves. Forty 2 bull calves (n = 20 Holstein and n = 22 Jersey, 2 ± 1 d old) were studied in a 2 × 2 factorial arrangement. Holstein and Jersey calves on the lower plane of nutrition (LPN) were fed 454 g /d of a 20/20 milk replacer. Holstein calves on the higher plan of nutrition (HPN) were fed 810 and 1,180 g / d of a 28/20 milk replacer for wk 1 and wk 2 – 6, respectively. Jersey calves on the HPN were fed 568 and 680 g / d of a 28/25 milk replacer for wk 1 and wk 2 – 6, respectively. On d 4, 42, and 77 peripheral blood was collected for ex vivo immunological analyses, and on d 7 all calves were challenged subcutaneously with LPS (4 μg/kgBW) and clinical and biochemical responses evaluated at 0, 1, 2, 3, 4, 5, 6, 9, 12, 24, and 72 h. There was a breed x plane of nutrition interaction ($P < 0.04$) on serum glucose concentrations following the LPS challenge; whereas Holsteins on the HPN had higher glucose concentrations than the other treatments. There were no breed or plane of nutrition interactions with time following the LPS challenge. Isolated mononuclear cells from Holstein calves when stimulated ex vivo with LPS on d 42 and 77 synthesized more tumor necrosis factor-α than cells from Jersey calves (2149 and 1527 pg/mL ± 149.9; $P < 0.01$). There were breed x day ($P < 0.05$) and plane of nutrition x day ($P < 0.07$) interactions on the intensity of the oxidative burst produced in response to a pathogenic *E. coli*; whereas Jersey calves fed LPN had a reduced intensity on d 77 when compared with the other treatments. Additionally, on d 77 Jerseys fed LPN had a reduced ($P < 0.04$) whole blood killing capacity when incubated with the *E. coli* for 60 min. When whole blood was incubated with the *E. coli* for 10 min, Jersey calves consistently had reduced ($P < 0.03$) killing capacities over the entire study period. These data indicate that Jersey calves had lower measures of many innate immune variables and HPN may improve aspects of the innate immune competence in a breed and immune variable specific manner.

Key Words: breed, calf, immune

M32 Effects of neomycin and oxytetracycline (N/T) fed at treatment rate for 14 days in calf milk replacer (CMR) on calf performance and health. D. Shields*[1], R. Blome[2], D. Wood[2], and J. Sowinski[2], [1]*Merrick's, Inc.*, *Middleton, WI*, [2]*Animix*, *Juneau, WI*.

New government regulations for the treatment of bacterial scours levels of the new combination (1:1) for neomycin/oxytetracycline of 10mg/lb BW for 14 d are now in effect. There is minimal calf data for feeding this new level. The objective of this study was to evaluate calf health and performance under the new federal guidelines. Auction sourced Holstein bull calves (n = 48, 3–5 d old) were stratified by weight into 2 treatment groups (24 calves/trt). Calves were weighed 1×/wk during the 8 wk trial. Calves were housed in individual hutches and fed 284 g reconstituted CMR (20% C.P., 20% fat, all milk protein) via individual nipple bottles at 0600 and 1700 h. Trt 1 received the treatment rate for bacterial scours for 14 d, and trt 2 received a non-medicated control formula. Water and a commercial textured calf starter (18% CP, 2.5% fat, Decoquinate) was offered daily for ad libitum consumption. Orts were collected and weighed daily and no hay fed. Straw-bedded hutches held a consistent nesting score ≥ 3. Subjective fecal scores (FS) were recorded 1×/d using 1–4 scale with 1 being normal and 4 severe scours. FS ≥ 3 were given electrolyte therapy. Weaning occurred at 42 d if starter intake (SI) was ≥ 454 g for 3 d and non-weaned calves were reduced to 1×/d CMR to promote SI. During the first 3 wks, ADG tended ($P \leq 0.09$) to improve with N/T (0.40 vs. 0.34 kg/d) and total SI was higher (3.7 vs. 2.1 kg). From wk 3– 6 opposite trends were observed as ADG tended ($P \leq 0.09$) to be higher for control calves (0.81 vs. 0.89 kg/d) and F/E was improved 11.7% ($P \leq 0.02$) at 0.58 vs. 0.65. Overall in the 56 d study no differences noted in growth, SI or F/E. However, N/T reduced calves that scoured 38% ($P \leq 0.06$), calves that required health treatments 36% ($P \leq 0.07$) and treatment d 28.6% ($P \leq 0.07$). Under conditions of this study N/T reduced incidence of scours, treatment days of calves treated and improved early SI but did not affect ADG, total SI or FS.

Key Words: calf, medication

M33 The effect of adding the organic complex of zinc, copper, manganese and cobalt on hoof health and performance in feedlot cattle. G. R. Noori[1], H. Amanlou[1], D. Zahmatkesh[1], E. Mahjoubi*[1], and Y. Mokhtabad[2], [1]*Zanjan University*, *Zanjan, Iran*, [2]*Azad University*, *Mazandaran, Iran*.

It has been shown that Zn, Mn, Cu and Co are essential for protein synthesis, vitamin metabolism, connective tissue synthesis and immune system function. There is, however, little evidence in finishing cattle. A study was conducted to investigate the effects of micro-mineral organic complex on lameness occurrence and performance in Holstein bull calves. Ninety-three Holstein bull calves (250.21 ± 4.21) were used in a completely randomized design. Calves were group fed a similar basal diet during 42 d experimental period. Used treatments included 1) control treatment without feed additive, and 2) experimental diet that calves consumed 7 g/d micro-mineral complex (Availa 4, an amino acid mineral complex available from ZinPro Corporation, Eden Prairie, MN), that supplied 360 mg Zn, 200 mg Mn, 125 mg Cu and 12 mg Co. Results showed that the effect of experimental diet on dry matter intake was significant (7.02 vs. 7.22 kg/d, $P < 0.001$) but feed conversion ratio was not significant (7.36 vs. 7.23, $P < 0.21$). A tendency was detected for average daily gain (0.96 vs. 1.04 kg/d, $P < 0.11$) and weight gain during the trial (40.3 vs. 43.6 kg, $P < 0.11$). The consumption of micro-mineral organic complex influenced plasma concentration of globulin (2.96 vs. 3.98 g/dL, $P < 0.03$) and albumin (3.26 vs. 2.44 g/dL, $P < 0.002$) significantly. The prevalence of lameness was higher in control group than organic complex supplemented treatment (23% vs. 11%; odds ratio

= 2.5). Generally, our results show that feeding micro-mineral organic complex can have an efficient role in reducing lameness occurrence and increasing profitability in feedlot farms.

Key Words: lameness, trace mineral, Holstein bull calves

M34 The effect of early feeding on blood factors, immune system, digestive tract and intestinal morphology of broiler chicks. M. Asgari[1], S. Rahimi*[1], M. Kiaei[2], and M. A. Karimi Torshizi[1], [1]*Tarbiat Modares University*, *Tehran, Iran*, [2]*University of Tehran*, *Tehran, Iran*.

In this study 560 male broiler chicks (ROSS 308) were used to study the effect of early feeding on blood factors, immune system, digestive tract and intestinal morphology. Birds were divided into 5 treatments with 4 replicates (112 chicks per treatment) as follows: 1. Control group (were fed starter diet 48 h after hatch); 2. Vitagel group (received 5g per bird jelly feed for the first 48 h after hatch and then starter diet); 3. Chick-mix group (were administered with starter diet); 4.Wet feed (with10% moisture for first 48 h after hatch and then starter diet); 5. Saline (1mL sterile saline were injected via subcutaneous in neck of each bird in this group after hatch and they were fed starter diet 48 h later). Body weight, feed intake, feed conversion, weight of liver, Proventriculus, gizzard, small intestine, bursa of Fabricius, spleen, pancreas, yolk sac, digestive tract, and length of small intestine were measured for all groups. Newcastle disease (NDV) and SRBC antibody titer, glucose, triglyceride, and cholesterol of serum were determined. The number of villi, length and width of villi, depth of crypt and percentage of different villi (leaf, tongue, bridge and finger shape) in small intestine were measured for all groups. At end of the experiment (40 d), weight of different parts of carcass and productive index were measured. The production index, GUT weight, intestine length, villi height and crypt depth were higher in early fed groups compared with other groups ($P < 0.05$). There were no significant differences in BW, FCR, and antibody titer against NDV and SRBC between different treatments. Serum glucose, relative weight of liver, proventriculus, pancreas, intestine, bursa of Fabricius, spleen, length of small intestine were higher in early fed groups ($P < 0.05$). In conclusion, early feeding of broiler chicks can be recommended to have better performance and immune response in these birds.

Key Words: broiler chicks, early feeding, blood factors

M35 Evaluation of effect of sodium bicarbonate as a top-dress on preventing laminitis and performance in feedlot cattle. G. R. Noori[1], H. Amanlou[1], D. Zahmatkesh[1], E. Mahjoubi*[1], and Y. Mokhtabad[2], [1]*Zanjan University*, *Zanjan, Iran*, [2]*Azad University*, *Mazandaran, Iran*.

Sodium bicarbonate is known as a pH modulator in cattle. Acidosis and, subsequently, laminitis are common in feedlot cattle. The effect of sodium bicarbonate as a top-dress has not been investigated. Therefore, our objective was to investigate the effects of sodium bicarbonate on laminitis occurrence and performance. One hundred Holstein bull calves (251.75 ± 5.75) were used in a completely randomized design. Calves were group fed a similar basal diet during 42 d experimental period. Used treatments included 1) control treatment without feed additive, and 2) experimental diet that calves consumed 50 g/d sodium bicarbonate as a top-dress. Results showed that the effect of experimental diet on dry matter intake (7.02 vs. 7.36 kg/d, $P < 0.001$), average weight gain through trial (40.3 vs. 46.6 kg, $P < 0.03$) and feed conversion ratio (7.36 vs. 6.53, $P < 0.02$) were significant. A tendency was detected for average daily gain (0.96 vs. 1.11 kg/d, $P < 0.07$). Compared with control group, occurrence of laminitis in experimental group was less (22% vs. 9%; odds ratio = 2.6). Generally, results showed that feeding of sodium bicarbonate as a top-dress can have an efficient role in reducing laminitis occurrence and increasing profitability in feedlot farms.

Key Words: laminitis, feedlot, sodium bicarbonate

M36 Expression of members of the wingless gene family in goats. M. Worku*, H. Mukhtar, and N. Mikiashvili, *North Carolina Agricultural and Technical State University*, *Greensboro*.

The objectives of this study were to identify members of the wingless (Wnt) signaling pathway (Wnt gene family) in the goat genome and to evaluate expression of genes involved in Wnt signaling in blood. The Wnt gene family encodes secreted members of the wingless family of signaling molecules that control cell fate, specification, proliferation, polarity, and movement in animal development and diseases. Wnt gene expression impacts production traits in farm animals as well as meat quality and is reported to be crucial for myogenesis and adipogenesis. Blood was collected from meat (4 Boer) and milk (4 Alpine) goats on FTA elute cards (Whatman Inc.) for DNA isolation. For RNA isolation PAXgene Blood RNA tubes were used. Genomic DNA was extracted from the FTA card according to the manufacturer's protocol. RNA was extracted using the ZR Whole-Blood Total RNA Kit. RNA samples were reverse-transcribed and the cDNA was obtained using the Ambion-Retroscript as per the manufacturer protocol. Specific primers for Wnt1, Frizzeled and secreted frizzeled were used for PCR amplification. Amplified products were run on a 1% agarose gel with PCR markers. Gels were stained with ethidium bromide and visualized using a Gel documentation system. GAPDH was used as loading control and primers in the absence of DNA were used as negative controls. Variability was observed among animals in detection of Wnt-1 in genomic DNA. Genes were detected in blood. Wnt-1 and Frizzeled genes were expressed in goats. Differential gene expression and animal to animal variability were observed. Both Wnt and Frizzeled family genes appear to be conserved in goats. This simple method for detection of Wnt-1 gene expression in goat blood will aid in the deciphering of the underlying mechanisms involved in animal development and disease impacting production traits in farm animals.

Key Words: goat, Wnt family, gene expression

M37 Dynamic changes in physiological responses to heat stress in cattle of different geographic origins. P. A. Eichen*, H. L. Vellios, B. S. Scharf, J. S. Johnson, D. K. Kishore, E. A. Coate, and D. E. Spiers, *University of Missouri*, *Columbia*.

Response to heat stress may differ in *Bos taurus* cattle originating in different US regions. Hourly measurements at specific heat stress levels may enable further understanding of these regional differences. Angus steers from Oklahoma (OK; n = 6) and Missouri (MO; n = 6) were compared with heat-tolerant Romosinuano steers (RO; n = 5) from Florida in the University of Missouri Brody Environmental Center. Initially, the 3 groups were exposed to air temperature (Ta) treatments that included a constant thermoneutral temperature (TN) of 20°C for 8 d, followed by a daily heat cycle (HS1) of 28 to 38°C for 8 d, and a greater heat cycle (HS2) of 30 to 40°C for 8 d. Twenty-four hour measurements were made after stabilization at each temperature. Hourly measurements included rectal temperature (Tr), respiration rate (RR), and skin temperatures averaged at trunk and peripheral sites. Linear regression was used to determine animal and ambient relationships, with ANOVA for group differences. There was no difference in Tr between groups at TN, but Tr was lower in RO compared with Angus during HS1 and HS2 ($\alpha = 0.05$). Relationships between Tr and Ta were similar for MO and OK during

HS1 and HS2. However, there was no relationship between Tr and Ta for RO during HS1 and HS2. RO had lower RR during TN and HS1 ($\alpha = 0.05$), but were not different from Angus during HS2 to suggest an adaptive response. Interestingly, relationships between RR and Ta for RO were equal to Angus during HS1 and HS2, indicating no group difference in the RR relationship. Skin temperatures at trunk or peripheral sites were affected by hour of day during all 3 temperature treatments ($P < 0.03 - 0.0001$). There was also an hour x group effect on trunk temperature during all 3 periods ($P < 0.05$), with no effect on peripheral sites. Geographic origin of Angus did not affect the heat stress response. Romosinuano steers exhibited characteristic heat tolerance, but showed some temporal shifts in response to prolonged heat exposure.

Key Words: heat stress, cattle, diurnal

M38 Patterns of heat response and adaptation on summer pasture: A comparison of heat sensitive (Angus) and tolerant (Romosinuano) cattle. J. S. Johnson*, B. Scharf, R. L. Weaber, P. A. Eichen, and D. E. Spiers, *University of Missouri*, *Columbia.*

Heat stress in *Bos taurus* cattle is a problem that affects many regions of the world. Numerous studies have focused on heat stress in feedlots or environmental chambers; but few have looked at undisturbed cattle on pasture. The present study followed 2 cattle breeds throughout a mid-Missouri summer to determine thermoregulatory responses to fluctuating summer air temperature (Ta). Breeds included 22 Angus grouped into 10 Missouri Angus (468 ± 11 kg BW) and 12 Oklahoma Angus (490 ± 9 kg BW). These were compared with 11 heat tolerant Romosinuano (RO; 352 ± 6 kg BW) steers from Florida. Animals were monitored on 16 d from June 8 through August 9 of 2009 on endophyte free tall fescue at the University of Missouri South Farm. For analysis, the data was divided into 2 periods that consisted of the first 11 d (Period 1; 9 d; Ta range = 19.8–34.3°C) and the last 27 d (Period 2; 7 d; Ta range = 15.5–33.4°C). Periods were determined by comparing respiration rate (RR) to Ta. Periods 1 and 2 were the times at which RR response to Ta was significantly different at ($P < 0.05$). RR was measured (counting 1 min flank movement) at 0800 and 1500 h, and ruminal temperature (Trum) was monitored hourly as an indication of core body temperature using a telemetric temperature transmitter (SmartStock, Pawnee, OK). Relationships between RR, Trum, and Ta were determined using linear regression for both breeds and groups within breeds. RR and Trum showed no significant differences between Angus groups ($P = 0.05$), however breed differences were found between Angus and RO ($P < 0.05$) steers. Slopes of RR to Ta from Periods 1 to 2 decreased from 2.55 to 1.13 bpm/°C and 2.27 to 0.49 bpm/°C for Angus and RO, respectively. Slopes of Trum to Ta also decreased from Periods 1 to 2 from 0.12 to 0.01°C /°C and 0.02 to 0.01°C /°C for Angus and RO, respectively. Correlations of Trum to Ta in Period 2 were insignificant ($P > 0.05$). Although Romosinuano have a lower respiration rate and ruminal temperature than Angus, they share a similar pattern of adaptation from early to late summer periods.

Key Words: cattle, heat stress, adaptation

M39 Taguchi approach for anti-heat stress prescription compatibility in mice spleen lymphocytes in vitro. X. Zhu*[1], G. Cheng[2,3], F. Liu[2,3], J. Yu[2], Y. Wang[1], T. Yu[2], J. Xu[1], and M. Wang[1], [1]*TCVM Laboratory, CAU-BUA TCVM Teaching & Research Team, College of Veterinary Medicine, China Agricultural University, Beijing, China*, [2]*Department of Animal Science and Technology, Beijing University of Agriculture*, *Beijing, China*, [3]*Beijing Key Laboratory of TCVM, CAU-BUA TCVM Teaching & Research Team*, *Beijing, China*.

The study was to evaluate the possible immune function of Agastache rugosa, Atractylodes lancea, Cortex Phellodendri, and Gypsum Fibrosum on spleen lymphocytes under heat stress. The Taguchi Design, which allows rapid and high efficiency to select the best conditions for the composition, was used to investigate the compatibility of the herbs. The extracts from herbs in various dilutions were added to previously cultured cells with final concentrations of 10, 50, 100, 200 μg/mL to give a total volume of 100 μL/well. Then lymphocytes exposed with extracts were incubated at 37°C for 24 h, heated at 42°C for 2 h and recovered to 37°C for 22 h. As a heat shock group (HS), lymphocytes (with ConA, 10 μg/mL or LPS, 2.5 μg/mL) were treated at 37°C for 24 h, heated at 42°C for 2 h and recovered to 37°C for 22 h. As a control, lymphocytes (with ConA, 10 μg/mL or LPS, 2.5 μg/mL) were treated at 37°C for 48 h. Lymphocyte proliferation was evaluated by MTT assay. The optical density (OD, 570nm) of HS was significantly lower than the control group ($P < 0.05$). Under heat stress the OD of higher concentrations of Agastache rugosa (200 μg/ml and 100 μg/ml), Atractylodes lancea (200 μg/ml and 100 μg/ml), Cortex Phellodendri (100 μg/ml and 50 μg/ml) and Gypsum Fibrosum (200 μg/ml and 100 μg/ml) caused a significant increase on ConA/LPS-induced proliferation of lymphocytes than HS ($P < 0.05$). The Taguchi results demonstrated that Agastache rugosa (200 μg/ml), Atractylodes lancea (200 μg/ml), Cortex Phellodendri (100 μg/ml) and Gypsum Fibrosum (100 μg/ml) were the optimal conditions for the composition of herbs. The validation experiment results confirmed that our composition in optimum extraction conditions has enhancing effects on ConA or LPS-induced lymphocytes under heat stress. The 4 herbal extracts may recover from the immunosuppression induced by heat stress. Taguchi optimization approach is a suitable method for optimization of the composition of herbs.

Key Words: heat stress, spleen lymphocytes, taguchi approach

M40 Effect of heat stress on the rat small intestine: A morphological and gene expression study. A. Lu*[1], G. Cheng[1,2], W. Luan[1], B. Zhou[1], F. Liu[1,2], and J. Xu[3], [1]*Department of Animal Science and Technology, Beijing University of Agriculture, Beijing*, *China*, [2]*Beijing Key Laboratory of TCVM, CAU-BUA TCVM Teaching & Research Team*, *Beijing, PR China*, [3]*TCVM Laboratory, CAU-BUA TCVM Teaching & Research Team, College of Veterinary Medicine, China Agricultural University, Beijing, PR China.*

The aim of the current study was to investigate changes in morphology and gene expression in the rat small intestine in response to heat stress. Forty-eight male SD rats (200 ± 20 g) were randomly divided into control or heat-stressed groups. Rats in control group housed with the environment of 25°C, while rats in heat-stressed group were subjected to 40°C for 5 h each day for 10 successive days. Rats were sacrificed on 1st, 3rd, 6th, and 10th day after heat treatment and sections of the small intestine epithelial tissue were excised for morphological examination and microarray analyses. During the microarray examination, each group contain 3 chips, 3 rats' cRNA were pooled and hybridized to each chip. The rat rectal and body surface temperature and serum cortisol levels were all significantly increased after heat treatment ($P < 0.01$). The duodenum and jejunum were significant damaged after 3

d of treatment, and the damage was recovered gradually as time went on. Microarray analysis found 289 genes upregulated (log 2ratio > 1, $P < 0.01$) and 133 genes downregulated (log2ratio < −1, $P < 0.01$) in response to heat stress. Subsequent bioinformatic analysis (including gene ontology and KEGG pathway analysis) revealed the genes altered in response to heat stress mainly related to apical part of cell, oxidation reduction, response to stress, tetrapyrrole binding, rhythmic process, oxidoreductase activity, oxygen binding, transcription factor activity. The pathway mainly involve in Antigen processing and presentation, MAPK signaling pathway, Circadian rhythm-mammal, "Glycine, serine and threonine metabolism" and Retinol metabolism. Heat stress caused significant damage to the rat small intestine and altered gene expression in the rat jejunum. The results of the bioinformatic analysis from the present study will be beneficial to further investigate the mechanisms involved in heat stress-induced damage in the rat small intestine.

Key Words: heat stress, morphology, microarray

M41 Study of immune expression profile of heat stress-induced rat using gene microarray. A. Lu*[1], G. Cheng[1,2], W. Luan[1], J. Yu[1], B. Zhou[1], F. Liu[1,2], and J. Xu[3], [1]*Department of Animal Science and Technology, Beijing University of Agriculture*, *Beijing, China*, [2]*Beijing Key Laboratory of TCVM, CAU-BUA TCVM Teaching & Research Team*, *Beijing, China*, [3]*TCVM Laboratory, CAU-BUA TCVM Teaching & Research Team, College of Veterinary Medicine*, *Beijing, China*.

The aim of the current study was to investigate the changes in morphology of intestine mucosa and gene expression of mucosal immune in the rat small intestine in response to heat stress. Forty-eight male SD rats (200 ± 20 g) were randomly divided into control or heat-stressed groups. Rats in the control group were housed with the environment of 25°C and 60% humidity daily for 10days; while heat-stressed group were housed under control group conditions, but exposed to 40°C and 60% humidity for 5h each day for 10 consecutive days. Rats were sacrificed on 1st, 3rd, 6th, and 10th day after heat treatment. Hematoxylin and eosin (HE) and periodic acid-Schiff (PAS) staining method was used to observe the Morphology changes and the numbers of immune cells. The gene expression profile was analyzed using Agilent microarray. Quantitative RT-PCR (qRT-PCR) was carried out for interesting genes that upregulated and downregulated more than 2 times to validate the reliability of microarray analysis. Structural changes of the mucosa included atrophy of some villi and a reduction in the size of crypts. In contrast to control group, the numbers of lymphocyte and chalice cell were both significantly decreased ($P < 0.01$). There were approximately 3152 expressed genes ($P < 0.01$) among total 41012 genes set in the microarray plate, and 56 immune related genes including 14 upregulated and 42 downregulated genes ($P < 0.01$). Some genes were assayed by qRT-PCR and demonstrated the same alteration tendency as in microarray analysis. Subsequent bioinformatic analysis (including gene ontology and KEGG pathway analysis) revealed the immune genes altered in response to heat stress were related to Positive regulation of immune system process, regulation of immune system, immune system development, leukocyte activation and migration, and genes involved in signal transduction. Heat stress caused significant effect to the rat small intestine mucosa and altered immune related gene expression in the rat jejunum.

Key Words: heat stress, immune, microarray

M42 Study of the mechanism of heat stress-induced IEC-6 cell apoptosis. W. Luan[1], K. Guo[1], G. Cheng[1,2], J. Yu[1], F. Liu*[1,2], and J. Xu[3], [1]*Department of Animal Science and Technology, Beijing University of Agriculture*, *Beijing, China*, [2]*Beijing Key Laboratory of TCVM, CAU-BUA TCVM Teaching & Research Team*, *Beijing, China*, [3]*TCVM Laboratory, CAU-BUA TCVM Teaching & Research Team, College of Veterinary Medicine, China Agricultural University*, *Beijing, China*.

The aim of the study was to study the effects of heat stress on apoptotic of IEC-6 in rat. The IEC-6 cell were divided into control group and heat stress group, both cultured for 4 h with the condition of 37°C and 42°C respectively. The morphological changes of IEC-6 was observed by acridine orange (AO) fluorescence staining; reverse transcription-polymerase chain reaction (RT-PCR) was used to determine the mRNA expression of apoptosis-related gene, such as caspase-3, caspase-8, caspase-9, bax and bcl-2; the early and late apoptotic rate of the 2 groups was detected by flow cytometry; the activity of terminal execute enzyme caspase-3 was detected by the UV spectrophotometry. In contrast to control group, the apoptotic cells were stained by AO and showed densely green yellow or fragment in heat stress group. The percentage of early and late apoptotic cells in heat stress group was significantly higher than that of control group ($P < 0.05$). After heat stress, mRNA expression level of the bax, caspase-3, caspase-9 were significantly increased ($P < 0.01$), mRNA expression level of the bcl-2 was significantly decreased ($P < 0.01$); and activation of Caspase-3 was significantly enhanced ($P < 0.01$). In conclusion, our results revealed that heat stress could trigger IEC-6 cell apoptosis via the mitochondrial pathway of apoptosis, depending upon the activation of caspase-9.

Key Words: IEC-6 apoptosis, mitochondrion, bax, bcl-2, caspase-3, caspase-9

M43 Coagulase-negative staphylococci mastitis management. T. E. Quirk*, L. K. Fox, J. L. Capper, D. D. Hancock, and J. R. Wenz, *Washington State University*, *Pullman*.

Coagulase-negative staphylococci (CNS) are the most common pathogens associated with intramammary infections (IMI) in dairy cows. We hypothesize that post-milking teat disinfection, teat dip, would reduce the microbial colonization of the streak canal and thus reduce the prevalence of IMI caused by CNS species. The efficacy of iodine post-milking teat dip was tested against CNS colonization of the streak canal, and incidence of IMI was measured. Using an udder-half model, 43 Holstein cows at the Washington State University Dairy were enrolled in the trial; teat dip was only applied after milking to one udder-half. Streak canal swab solutions and mammary quarter milk samples were taken in duplicate once a week for 16 weeks for microbial culture. A CNS IMI was identified when 2 of 3 consecutive duplicate quarter milk samples were identified with the same CNS species containing > 120 cfu/ml. The isolates were speciated using PCR-RFLP and gel electrophoresis. Colonization of the streak canal and IMI by CNS were assessed. Twenty-five CNS IMI were diagnosed; prevalence of IMI in control quarters and treated quarters were 8.1% and 19.7%, respectively. Isolation of CNS in milk was less likely in treated than control quarters (Odds Ratio = 0.704, $P = 0.0113$, 95% CI = 0.536–0.925). The majority of CNS IMI was by *Staphylococcus chromogenes* (44%) and appeared to be linked to streak canal colonization. Conversely, the second most prevalent cause of CNS IMI was by *Staphylococcus xylosus* (36%), but did not appear to be linked to colonization of the streak canal. In conclusion, post-milking teat dip was efficacious for reducing IMI caused by CNS, but CNS IMI was not necessarily linked to streak canal colonization.

Key Words: coagulase-negative staphylococci, mastitis, teat dip

M44 Morphometric evaluation of udders in Gir cows and the prevalence of subclinical mastitis. M. A. F. Porcionato[1], M. V. Santos*[1], C. B. M. Reis[1], M. M. Stradiotto[2], C. S. Cortinhas[1], and W. V.B Soares[3], [1]*Department of Nutrition and Animal Production, FMVZ/USP, Pirassununga, Brazil*, [2]*Department of Basic Science, FZEA/USP, Pirassununga, Brazil*, [3]*Institute of Zootecny, IZ/APTA, Mococa, Brazil*.

This trial aimed to evaluate the relation between morphological teats characteristics of Gir cows evaluated by ultrasound and the prevalence of subclinical mastitis. Eighty lactating Gir cows with 90 to 200 d of the 2nd or 3rd lactation were grouped according with their milk flow: fast or slow and milked twice a day with mechanical milker. The teats characteristics were measured by ultrasound and external morphometrical measurements. Somatic cell count (SCC) was determined by the fluoro-opto-electronic method (Somacount 300, Bentley Instrument Inc., Chaska, MN, USA). Samples were considered positive for subclinical mastitis with SCC > 200,000 cells/mL and the pathogens identified in microbiological culture. Data were analyzed using GLM procedure (SAS, version 8.2) and differences were considered significant at $P < 0.05$. Ultrasonography images showed higher ($P < 0.05$) teat channel in slow flow (25.68 mm) than in fast flow (22.31 mm) groups. No significant correlation ($P > 0.05$) was observed between Log(SCC) and morphological teats characteristics. The infrared thermography technique was used to the evaluate udder temperature variation in cows with subclinical mastitis, but no differences ($P > 0.05$) were observed for type of microorganism or Log(SCC). The channel length and the distance for the teat to floor had influence on the prevalence of subclinical mastitis, as well as the mastitis-causing pathogens in Gir cows.

Key Words: mastitis, morphology, thermography

M45 Comparison of 16S rRNA gene sequencing and aerobic culture results performed on milk samples from cows with clinical mastitis. J. R. Wenz*, T. E. Besser, and L. K. Fox, *Washington State University*, *Pullman*

The hypothesis tested in this study was that 16S rRNA gene sequencing (16S) performed on DNA from quarter milk samples of cows with clinical mastitis (CM) would identify the same bacteria found by aerobic milk culture. To test this hypothesis duplicate milk samples were collected from cows with CM. Aerobic milk culture was performed on 100 μL of milk for presumptive bacterial identification and cfu/ml determination. Cows with the same milk culture result on duplicate milk samples (n = 31) were included. Common mastitis pathogens were cultured from 24 samples and 7 were bacteriologically negative (BN). DNA was harvested from each 2 mL milk sample and quantitated. A variable region of the small ribosomal subunit gene was amplified using PCR primers complementary to flanking regions shared among eubacteria and cloned. Sequences of 12 clones from each sample were determined and GenBank searches used to identify bacterial species with the most similar sequences (>99% identity). For 18 of 24 (75%) of the samples, 16S results agreed with culture results. These samples all had >250 cfu/mL (median 13,650; range 290 to > 30,000 cfu/mL) bacteria on culture and >40ng/mL of DNA (median 444; range 45.4 to 1730 ng/mL). In contrast, the remaining 6 samples had lower bacterial counts (median 40 cfu/mL; range 10 to 520) and lower DNA yields (median 44 ng/mL; range 0.70 to 756). In 4/6 samples where culture and 16S results differed, culture identified low numbers of coagulase negative staphylococci and no consistent clone was revealed by 16S. Similarly, BN samples had low DNA yields and no consistent clone identification (and no clone consistent with common mastitis pathogens) was revealed by 16S. The results of this study suggest 16S and culture results are consistent when bacterial numbers are ≥ 300 cfu/mL. Furthermore, these results do not support the hypothesis that BN milk samples result from infection with unculturable bacterial agents.

Key Words: 16S r RNA gene sequence, clinical mastitis, aerobic culture

M46 Hyphenated mass spectrometry investigations applied to the characterization of organic chelates. A. Yiannikouris*[1], C. Connolly[2], R. Power[1], and R. Lobinski[3], [1]*Alltech Inc.*, *Nicholasville, KY,* [2]*Alltech Ireland*, *Dunboyne, County Meath, Ireland*, [3]*CNRS UMR 5254*, *Pau, France*.

This work focused on the development of a method to screen for the presence of metal-complexes in organic chelates using hyphenated techniques of inductively coupled plasma-mass spectrometry (ICP-MS). Identification and characterization of metal-peptide interactions was achieved using hyphenated techniques of mass spectrometry (ESI-MS). The ICP-MS detection in HPLC formed the basis of the methods developed because of its sensitivity regardless of the matrix, which allowed the optimization of the analyte purification before ESI-MS/MS. Analyses indicate that using size-exclusion chromatography (SEC) 5 peaks were characterized for the organic mineral. Chromatogram intensity was a linear function of the total area under the curve indicating the reproducibility of extraction (R2 = 0.999 and RSD ≤3.25%). Application to batch-to-batch reproducibility on 6 samples injected in triplicate showed that the morphology of the Cu elution pattern was identical and reproducible with significant overlapping of the chromatograms ($P \leq 0.05$). Coefficient of variation of the area under the curves ranked between 0.007 and 0.012. SEC ICP-MS detection is thus a valid technique to monitor the molecular mass distribution of metal-binding molecules to assess product quality and the unique fingerprinting per proteinate investigated, with a detection limit below 1 μg/g. This procedure offers a novel application to the detection of the complexes in premixes and feed samples. The fine characterization of the metal-peptides complexes formed through parallel ICP MS and ESI MS/MS detection enabled the identification of the ones stable enough to survive the ionization process. The precursor proteins were identified by means of the ExPASy Proteomics Server of the Swiss Institute of bioinformatics data on soybean genome. In silico molecular modeling using a force-field adapted to the protein and ligand interactions studies (CVFF) clarified the coordination of the amino acids surrounding the mineral by the evaluation of a potential energy according to environmental settings.

Key Words: organic minerals, chelates, speciation

M47 Methods to predict true disease prevalence in beef cattle. C. M. McAllister*[1], B. W. Brigham[1], R. K. Peel[1], H. Van Campen[1], G. H. Loneragan[2], R. L. Weaber[3], J. L. Salak-Johnson[4], and C. C. L. Chase[5], [1]*Colorado State University*, *Fort Collins*, [2]*West Texas A&M University*, *Canyon*, [3]*University of Missouri*, *Columbia*, [4]*University of Illinois*, *Urbana*, [5]*South Dakota State University*, *Brookings*.

Inherent complications arise during the evaluation of disease data for the genetic improvement of disease susceptibility and immune response including the imperfect diagnosis of infection, time of infection, severity of disease challenge, level of disease challenge of clinically normal individuals, and variation in prevalence across years. The objective of this study was to identify alternative methods for classifying diseased versus healthy individuals to improve the accuracy of which bovine respiratory disease (BRD) prevalence (Pr) is estimated. Data for this study included feedlot treatment records (TR), lung lesion scores (LS), early (eADG) (80 d.) and overall average daily gain (ADG) on 2,434 crossbred steers. Disease prevalence was 24.9 and 58.6% for TR and

LS, respectively. Cluster analysis was performed to group animals with similar performance based on TR, mean lung score (MLS), and eADG or ADG to estimate prevalence. A k-means method was implemented in R which utilizes an Euclidean distance matrix to form cluster groups. Principal components (PC) of the individual cluster components were used to determine the point variation explained by TR, LS, and clustered groups. Cluster 1 (C1) grouped animals on TR, MLS, and ADG. The Pr for C1 was 39.2%, recategorizing 725 animals between TRT and C1 and 477 animals between LS and C1. The first 2 PC were able to explain 72.94% of the point variation associated with TR, LS, and C1. Cluster 2 (C2) was formed by replacing ADG with eADG. The Pr of C2 was estimated to be 58.6%, recategorizing 1,202 animals between TR and C2, and no animals between LS and C2. The first 2 PC from the C2 analysis were able to explain 74.8% of the point variation of TRT, LS, BRD, and C2. The amount of point variation explained by the first 2 PC suggest that eADG is more accurate than ADG in predicting true BRD prevalence. The increased predictive power of eADG can be attributed to the majority of animals being diagnosed with BRD occurring early in the feeding period. Comparison of categorical groups indicates that LS is most sufficient at estimating true BRD prevalence during the postweaning phase.

Key Words: beef cattle, bovine respiratory disease, health

M48 A research model for inducing leg problems in broilers. R. F. Wideman*[1], F. Khajali[2], K. R. Hamal[1], A. F. Wideman[1], and H. Lester[1], [1]*University of Arkansas Division of Agriculture*, *Fayetteville,* [2]*Shahrekord University, Faculty of Agriculture*, *Shahrekord, Iran*.

Leg problems increasingly affect fast growing broiler chickens worldwide. Studies investigating practical methods for reducing lameness have been hampered by the sporadic onset and variable incidence of leg problems within experimental flocks. Our objective was to develop a model for inducing a reliably high incidence of lameness in fast growing broilers. To accomplish this we constructed wire floors to create sporadic unstable footing in broiler pens. Rectangular frameworks were constructed from 5 cm x 5 cm lumber. Each frame was 3.05 m long and 1.52 m wide, with 5 cm x 5 cm cross members added for support. Hardware cloth (1.3 cm x 2.54 cm mesh) was fastened to the frame and cross-members. Ten pens (3.05 m x 3.05 m) were set up with floor litter only and 10 pens were set up with half litter and half wire-frame floors. Initially the wire frame was placed flat on the pen floor. Tube feeders were positioned on one side of the pen and the nipples were positioned above the wire frame on the opposite side of the pen. When the chicks reached 2 weeks of age the wire floor was elevated to a 20% slope (Experiment 1) or a 30% slope (Experiment 2), forcing the chicks to walk up and down the sloping wire to drink. Chicks were placed at densities of 50 or 100 per pen in Experiments 1 and 2, respectively. Cumulative incidences of lameness were compared for 2 to 8 wk old broilers using a z-test, with significance declared at $P \leq 0.05$. The incidence of lameness induced in Experiment 1 by the 20% sloping wire floor (6.8%; 34/500 birds) did not differ from the spontaneous occurrence of lameness on litter alone (5.8%; 29/500 birds). The incidence of lameness induced in Experiment 2 by the 30% sloping wire floor (26.7%; 111/416 birds) was significantly higher ($P = 0.01$) than the spontaneous occurrence of lameness on litter alone (10.7%; 43/400 birds). Sloping wire floors can be used to reliably induce reasonably high incidences of lameness, thereby permitting future assessments of practical strategies for reducing leg problems during broiler production.

Key Words: lameness, model, broilers

M49 Microbial diversity in the ileal and cecal contents of broilers using pyrosequencing. S. J. Eom*[1], H. J. Kim[1], C. J. Cha[2], and G. B. Kim[1], [1]*Department of Animal Science and Technology, Chung-Ang University*, *Anseong 456-756, South Korea*, [2]*Department of Biotechnology (BK21 Program), Chung-Ang University*, *Anseong 456-756, South Korea*.

The microbiota in the gastrointestinal (GI) tract of animal plays a pivotal role in the animal′s overall health. However, there is a scarcity of information on the microbial diversity in the gut of livestock animals including broilers and layer hens. Recent developments in microbial ecology have utilized rapid sequencing technologies such as pyrosequencing to investigate the microbial diversity of the human and animal gut. The present study was designed to evaluate differences in the ileal and cecal microbial communities of adult broilers (5 wks old, n = 6) using a bacterial barcoded pyrosequencing strategy. The V1-V3 region of the 16S rRNA gene was amplified by PCR using bar-coded universal primers of 27F and 518R. The amplicons were combined in a single region of the picotiter plate such that approximately 5,000 sequences were obtained from each animal. Taxonomic assignment was performed using the EzTaxon database (http://www.eztaxon.org) and the quantitative analyses was carried out based on the number of sequence reads of each bacterial taxon. Lactobacilli were found to be predominant in the upper gastrointestinal tract and the most abundant *Lactobacillus* species in the ileum were *L. salivarius, L. crispatus*, and *L. aviarius*. Another 12 *Lactobacillus* species were also detected at different levels. In addition, *Enterococcus cecorum* were also abundant in the ileum of adult broilers. In the ceca, the microbial community was highly diverse and *Lactobacillus* species were not found. Clostridia were the most abundant, representing 79% of the total reads. The most common genus detected in the ceca was *Clostridium* and other genera found in the ceca were *Dorea, Alistipes, Bacteriodes*, and *Roseburia*. Pyrosequencing used in this study was proven to be a useful tool for the evaluation of the microbial diversity in the GI tract. Further studies using this tool should be done to better understand the normal microbiome associated with efficient productivity, as well as the impact of changes made in the diet including probiotics supplementation for hens or broilers.

Key Words: broilers, microbiota, pyrosequencing

M50 Use of infrared thermography to monitor risk factors in newborn piglets. J. Morales[1], A. Manso[1], M. Aparicio[1,2], and C. Pineiro*[1], [1]*PigCHAMP Pro Europa*, *Segovia, Spain*, [2]*Centro de Experimentación y Formación en Porcino*, *Segovia, Spain*.

Hypothermia is one of the most important factors affecting perinatal mortality. In this study, infrared thermography was used as a new tool to determine hypothermia and its evolution in newborn piglets. Thermography might provide high advantages in swine clinical practice, revealing lesions and risk factors that would remain hidden with other diagnostic systems. Twenty-two piglets from 2 different litters entered the study at birth time. In each litter, half of the piglets were immediately dried with an absorbent material (cut paper). The other half was not manipulated at birth. Skin temperature on the back was recorded from each piglet at birth and every 10 min time during 1.5 h using a thermographic camera (Fluke Ti45). Piglets were weighed at birth and at 2, 4 and 9 d of life. Data were analyzed using the MIXED procedure of SAS (v 9.00). The statistical model for the temperature analysis included the fixed effects of treatment (control vs drying), time (10 min intervals) and their interaction and the block effect of litter within treatment. Drying piglets immediately after birth increased the skin temperature in the first 90 min of life (39.3°C vs 37.8°C in dried and control piglets, respectively; $P < 0.05$). Evolution of the skin temperature was also different

between treatment (P treatment x time = 0.0001). Initial temperature was 39.3 ± 0.79°C and was kept almost constant in the dried-piglets in the 90 min-interval, while in the control group immediately decreased after birth and then increased progressively until 90 min after farrowing, when skin temperature did not differ between groups (P = 0.27). Body weight evolution did not differ between treatments (2.71 kg at 9 d of life). Drying piglets immediately after birth was effective to keep the body temperature, confirming it as a good management practice to prevent perinatal hypothermia. Infrared thermography demonstrated enough accuracy to be considered as a new tool to complement other diagnostic tools.

Key Words: infrared thermography, newborn piglet, hypothermia

M51 Relationship between lying patterns, feeding management, and incidence of intramammary infection in dairy cows milked in an automated system. T. J. DeVries*[1], K. E. Leslie[2], H. W. Barkema[3], J. Rodenburg[4], and G. Seguin[5], [1]*University of Guelph, Kemptville Campus*, *Kemptville, ON, Canada*, [2]*University of Guelph*, *Guelph, ON, Canada*, [3]*University of Calgary*, *Calgary, AB, Canada*, [4]*DairyLogix Consulting*, *Woodstock, ON, Canada*, [5]*Dairy Farmers of Ontario*, *Casselman, ON, Canada*.

The objectives of this study were to investigate whether feed manipulation affects post-milking standing time in cows milked in an automated milking system (AMS) and to determine if this time relates to the incidence of coagulase-negative staphylococci (CNS) intramammary infection (IMI). Over a 4-mo period, 111 lactating Holstein dairy cows, kept in a sand-bedded freestall barn with 2 pens, each with a free traffic AMS, were monitored. Feed was delivered once daily, and pushed up 2–3 times per day. Quarter milk samples were collected for bacteriological culture from each cow, once every 4 wks. A new IMI was defined as a positive culture sample following a negative culture. For 7 d before each of the last 3 milk samplings, lying behavior, and times of milking and feed manipulation (feed delivery and push up) were recorded. A logistic regression model was used to assess the relationship between post-milking standing time and occurrence of a new CNS IMI. Feed manipulation around the time cows were milked (1 h before 2 h after) resulted in the longest post-milking standing times (86.9 ± 4.3 min; P < 0.001). The shortest post-milking standing times (50.9 ± 4.6 min) were seen in those cows that were milked >4 h before feed manipulation. Over the study period, 58 new CNS IMI were detected, resulting in a herd incidence rate of 0.94 CNS IMI/quarter-year at risk. A non-linear relationship between post-milking standing time and CNS IMI incidence was found (P < 0.04). Compared with those cows that lie down <120 min after milking, those cows that lie down for the first time 120–150 min after milking had lower risk (OR = 0.26, 95% CI = 0.04, 1.98), while those cows that lie down for the first time >150 min after milking had higher risk (OR = 2.70, 95% CI = 1.08, 6.78) of a new CNS IMI. These results suggest that despite being able to manage post-milking standing time of cows milked in an AMS by providing fresh feed, as well as by pushing up feed, frequently throughout the day, the use of such a feeding management strategy in AMS will not necessarily prevent new CNS IMI.

Key Words: intramammary infection, automated milking, lying behavior

M52 Proteomics analysis of plasma and milk protein between healthy dairy cows and *Staphylococcus aureus* infected-subclinical cows. Y. X. Yang*, G. L. Cheng, H. L. Zhao, X. C. Jiang, and S. Chen, *Anhui Academy of Agricultural sciences*, *Hefei Anhui, China*.

Mastitis caused by *Staphylococcus aureus* that are most often the contagious type remains the largest problem on dairy farms. The purpose of our study was to investigate the dynamic changes of plasma and milk protein from healthy and *S. aureus* infected cows. Plasma and milk was collected from dairy cows on d 8 ± 2 and d 50 ± 2 with following diagnosis of acute subclinical mastitis (n = 6) and negative control cows (n = 10) according to the bacteriological culture of milk from all 4 quarters and somatic cell count. Plasma and milk proteins were separated by 2-dimensional electrophoresis; differentially expressed proteins were analyzed by PDQuest 8.0 software, and identified by HPLC equipped with ion trap mass spectrometer. Expression of haptoglobin was abruptly upregulated on d 8 ± 2, and similarly on d 50 ± 2, while α 1 acid glycoprotein was upregulated on d 50 ± 2 in plasma of cows subclinically infected with *S. aureus* mastitis. Expression of albumin and β-casein variant was increased on d 8 ± 2 and continuously on d 50 ± 2 in milk protein of *S. aureus* infected cows, in addition, albumin and β-casein fragments were more variation on d 50 ± 2 than control milk and on d 8 ± 2 in milk protein. The results indicated that expression abundance of plasma and milk proteins were altered and participated in the principal effects of the inflammatory response during dairy cows infected with *S. aureus* subclinical mastitis. Moreover, milk proteins from *S. aureus* infected cows had much larger variation as time goes on. The findings may be useful to provide evidence for treatment the *S. aureus* subclinical mastitis in the early stage of infection to minimize production losses.

Research was supported by the Natural Science Fund of Anhui Province (090411024).

Key Words: dairy cow, *Staphylococcus aureus* mastitis, proteome

M53 Developmental changes in plasma proteins during the transition period in dairy cows. Y. X. Yang[1,2], S. S. Li[1], J. Q. Wang*[1], D. P. Bu[1], L. Y. Zhang[1], and L. Y. Zhou[1], [1]*State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences*, *Beijing, China*, [2]*Institute of Animal Science and Veterinary Medicine, Anhui Academy of Agricultural Sciences*, *Hefei, China*.

Plasma proteins undergo programmed changes in response to parturition-induced immunosuppression during the transition period. In this study blood samples were collected at 21 d before calving, 1 d and 21 d after calving from healthy Chinese Holstein heifers (n = 6) considered free of mastitis, milk fever, and endometriosis based on the somatic cell count and clinical diagnosis. Developmental changes of plasma were examined using integrated proteomic approaches consisting of minor abundance protein enrichment by ProteoMiner, protein separation by 2-dimensional gel electrophoresis, and protein identification by HPLC equipped with ion trap mass spectrometer. Of the 4 proteins identified, expression of serum amyloid A isoform was altered at parturition, while apolipoprotein E and clusterin were upregulated in minor abundance plasma on d 1 and d 21 after calving compared with d 21 before calving. In addition, IgG, which exerts antimicrobial function, was downregulated on d 1 after calving when compared with other time points during the transition period. Quantitative determination of IgG in plasma was performed using a sandwich ELISA method. Levels of plasma IgG on d 1 after calving were 2.04 ± 0.64 mg/mL, slightly less than IgG concentrations of 2.56 ± 0.87 mg/mL and 3.45 ± 0.96 on d 21 before and after calving, respectively. The IgG concentrations detected

by ELISA were not in complete agreement with the 2-dimensional gel electrophoresis and mass spectrometer expression data. This discrepancy possibly related to IgG polymorphisms. These results may be useful in guiding future studies to investigate mechanisms of the plasma protein secretion during the transition period and to elucidate immune system response at the protein level.

Key Words: periparturient, dairy cow, plasma proteome

M54 Effects of single and combined *Mycoplasma gallisepticums* vaccination on blood electrolytes and acid–base balance in commercial egg-laying hens. H. A. Olanrewaju*, S. D. Collier, and S. L. Branton, *USDA–ARS*, *Starkville, MS*.

Previous study on F-strain *Mycoplasma gallisepticum* (FMG) inoculated layers from our laboratory showed a significant increase in arterial partial pressure of oxygen (pO_2), which is generally associated with an oxygen-dependent improvement in tissue oxygenation to improve the layer chicken's ability to withstand the harmful effects of stressors on their performance and well–being. The aim of this study was to determine whether Bacterin (killed vaccine) and TS-11 (Live vaccine) treatment combination could enhance the arterial (pO_2) levels in layer chickens. The experiment was conducted in 2 trials and arranged in a completely randomized experimental design with 4 treatments. The treatments consisted of Control (MG-Clean), Bacterin, TS-11, and Bacterin + TS-11 combined. In each of the 2 trials, 160 1-day-old *Mycoplasma gallisepticum* (MG) free pullets were raised to 10 week of age (WOA) and were transported to a poultry disease isolation facility. Sixteen isolation units were divided in 4 treatments and each of the 4 treatments had 4 replications with 10 birds/unit (40 birds/treatment). Venous blood samples were collected at the termination of the study. TS-11 vaccinated chickens had significantly ($P \leq 0.05$) higher blood (pO_2) and significantly ($P \leq 0.05$) lower partial pressure of CO_2 (pCO_2) when compared with control and combined MG vaccinated groups. However, no significant differences were observed between Bacterin and TS-11 treatment groups. Hematocrit and blood concentrations of hemoglobin were not statistically affected among treatments, but were slightly higher in TS-11 treatment group. There was a significant ($P \leq 0.05$) effect on blood concentrations of Na^+, Ca^{2+}, and anion, but no significant effect on glucose, cholesterone, triglyceride, and osmolality. These data suggest that inoculation of layers with TS-11 was more effective in elevating (pO_2), than inoculation with Bacterin or TS-11 + Bacterin combined.

Key Words: *Mycoplasma gallisepticum*, vaccine, acid–base balance

M55 Continuously growing chicken liver cell lines for the vaccine production against poultry viruses. J. Y. Lee* and B.-W. Kong, *University of Arkansas*, *Fayetteville*.

A continuously growing, immortal cell line can serve as a stable substrate to produce a cell culture based viral vaccine. The objective of this study is to develop an immortal chicken cell line that can efficiently propagate avian infectious viruses, such as infectious laryngotracheitis virus (ILTV), which causes acute upper respiratory disease in chickens. Primary chicken embryo liver (CEL) cells, which were permissive to ILTV, were transfected with various ectopic expression constructs and/or small interfering RNAs (siRNAs) for cell cycle regulatory genes. As results, 3 immortal chicken embryonic liver (CELi) cell lines were established. The CELi-si-p53 was transfected with the expression construct for siRNA against p53, the CELi-Vector was transfected with the expression vector control, and CELi-im was immortalized spontaneously without transfection. All 3 CELi lines are permissive to ILTV, but the titers produced were low levels (~10 plaque forming units/ml). To further characterize epigenetic states for CELi cells, alterations of mRNA expression for cell cycle regulatory genes were determined at passages of 30, 50, 70, and 90 for all 3 CELi cell lines by quantitative reverse transcription PCR. Throughout all passages in 3 CELi cell lines, the mRNA expression of both p53, (function for cell cycle arrest) and its transcriptional target gene, p21WAF1, were down-regulated showing 10 to 20% expression levels compared with those in primary CEL counterpart. The mRNA expression of E2F1 (function for cell cycle progression), was increased 5.3 - 7.1 fold in all 3 CELi cell lines compared with primary CEL cell counterpart. These results are correlated with mRNA expressions shown in previously established immortal chicken embryo fibroblast cell lines, that efficiently propagate Marek's disease virus (MDV). Though newly established CELi cell lines produced only low ILTV titers, those can be utilized for cell culture based vaccine production against other avian viruses, such as MDV or avian metapneumovirus.

This work was supported by US Poultry and Egg Association.

Key Words: immortal chicken liver cell lines, cell cycle regulation, virus propagation

M56 Effect of rabbit sacculus rotundus antimicrobial peptides on serum antibody titers of AIV and NDV in chicken. R. P. She*[1], K. Z. Wang[2], W. M. Ma[1], Y. Ding[1], and J. Tang[1], [1]*College of Veterinary Medicine, China Agricultural University*, *Beijing,100193,China*, [2]*Research Center of Laboratory Animal*, *Jinan, 250002, Shandong, China*.

Multicellular organisms express numerous antimicrobial peptides (AMP), which have received increased attention over the past decade; over 400 AMP have been identified to date in insects, plants, and animals. AMP have the capacity to kill or inactivate a particular spectrum of bacteria, fungi, and some enveloped viruses in vitro. Our previous research demonstrated that Rabbits Sacculus Rotundus (RSRP) AMP have been shown to improve the structure of intestine and promote intestinal mucosal immunity during the chicken growth period. The purpose of this study was to evaluate the effect of RSRP on serum antibody titers against Avian Influenza virus (AIV) and Newcastle disease (NDV) in chickens and to investigate the potential use of AMP in modulation of the immune response for animal health. Ninety one-day-old healthy Xinza chicks were randomly divided into 2 groups: 40 chickens in the control group, and 50 chickens in the experimental group and control group. AMP from RSRP was injected (I.M.) at doses of 0.1, 0.2, 0.3, 0.4, 0.5, 0.5, 0.5 mg, at the ages of 7, 14, 21, 28, 35, 42, and 49d. Chickens in control groups were given the same doses of sterile saline, respectively. Blood was drawn from chickens at the ages of 7, 14, 21, 28, 35, 42, and 56d, and serum separated. The hemagglutination inhibition titers of NDV and AIV serum antibody were detected in the serum samples of 10 chickens, which were selected randomly from each group. Results: The results were as follows, serum antibody titers of NDV and AIV in the chickens of experimental group were significantly higher than that of the control group ($P < 0.01$) at ages of 21, 28, 35, 42 and 56d. The present observation investigated that AMP of the RSRP could enhance significantly the serum antibody titers of ND live vaccine and AI inactivate vaccine.

Key Words: antibacterial peptide, Newcastle disease, avian influenza, serum antibody titers

M57 Results from the US National Johne's Disease Demonstration Herd Project: Most important areas from the Johne's risk assessment. C. Fossler* and J. Lombard, *USDA:APHIS:VS*, *Fort Collins, CO*.

The National Johne's Demonstration Herd Project (NJDDHP) in the United States was initiated to evaluate the long-term feasibility and effectiveness of management-related practices designed to control Johne's disease on dairy and beef cattle operations. The NJDDHP began in 2003 and includes 62 dairy herds and 20 beef herds in 17 states. All herds began with culture-confirmed Mycobacterium avium subspecies paratuberculosis (MAP) on the operation, and all herd owners agreed to make efforts to control Johne's disease on the operation. Risk assessments, management plans, and testing of herds were completed on an annual basis. Results to date indicate that, for both beef and dairy herds, prevalence of *Mycobacterium avium* subspecies *paratuberculosis* (MAP) in the third, fourth, and fifth years of participation was significantly lower than prevalence during the first year of participation. An analysis using Poisson regression was undertaken to identify areas from the risk assessment most important with regard to MAP prevalence. Among the main areas from the risk assessment (which included calving area, preweaned heifers, postweaned heifers, bred heifers, cows and bulls, and additions/replacements), preliminary results indicate that for dairy and beef herds, the calving and preweaned heifer areas appeared to be most important with regard to risk of cattle being MAP-positive. Specific factors related to the calving and preweaned heifer areas will be further assessed to identify practices associated with a greater risk for cattle to be MAP-positive. For dairy herds, preliminary results indicate that making sure udders and legs of cows in the calving area are clean, using individual animal calving areas (or allowing fewer animals in the calving area), and preventing Johne's disease clinical or suspect animals from entering the calving area were most important with regard to control of Johne's disease on dairy operations.

Key Words: Johne's, control, demonstration herds

M58 Evaluation of the next-generation Parachek ELISA for high-throughput detection of Johne's disease in milk and serum samples. P. Schacher[1], A. Zurfluh[1], D. Zwald[1], T. Byrem[2], and A. J. Raeber*[1], [1]*Prionics AG*, *Schlieren, Switzerland*, [2]*AntelBioSystems Inc*, *Lansing, MI*.

Frequent testing of milk samples for antibodies to *Mycobacterium avium* ssp. *paratuberculosis* (MAP) by ELISA has become an important tool in managing control of Johne's disease in dairy cattle operations. Originally developed for serum samples, Parachek ELISA (also marketed as AntelBio Johne's Milk ELISA) has been validated with bovine milk samples for which it received approval from the USDA in 2006 and is currently marketed in the US by AntelBio. In the last 10 years, Parachek, also known as the AntelBio Johne's Milk ELISA, has been used successfully on more than 750,000 samples within the laboratory network of the Dairy Herd Improvement Association (DHIA). To simplify the use and increase throughput, we have further improved Parachek to make it more user-friendly and allow full automation. The performance of the improved Parachek2 was evaluated on a set of 368 bovine milk samples of which 16 were fecal culture positive, 351 were fecal culture negative or derived from free herds and from 1 sample no culture result was available. Fecal culture for *M. paratuberculosis* was performed by the TREK ESP para-JEM Culture System II. Parachek2 has a sensitivity of 56% (95% CI of 32% - 81%) and a specificity of 98% (95% CI of 92% - 100%). A comparison of the improved Parachek 2 with the currently used Parachek2 showed an almost perfect agreement with a Cohen′s kappa value of 0.93. To enhance throughput Parachek2 was automated on a Beckman Coulter Biomek FXP. The Laboratory Automation Workstation was equipped with a 96-well plate washer and a plate reader which allows for a throughput of up to 16 plates in one working day (8.5 h) starting from serum or milk samples. Comparison of the fully automated system with manual processing showed almost perfect agreement with a kappa value of 0.96. These results demonstrate that Parachek2 can be easily run on an automated system with the same excellent performance as with manual processing of the samples using the Parachek and thus enabling laboratories to save time and freeing staff for other work.

Key Words: Johne's disease, ELISA, milk

M59 Analysis of the immune response to a major membrane protein of *Mycobacterium avium* ssp. *paratuberculosis* in experimentally and naturally infected cattle. G. S. Abdellrazeq*[1], H. M. Rihan[2], M. J. Hamilton[3], A. J. Allen[3], K. T. Park[3], J. P. Bannantine[4], J. R. Stabel[4], and W. C. Davis[3], [1]*Faculty of Vet Med, Alexandria Univ*, *Edfina, Rosetta-line, Behera Province, Alexandria University, Egypt,* [2]*Faculty of Vet Med, Mansoura Univ*, *El Mansoura, Egypt,* [3]*Wash State Univ*, *Pullman*, [4]*USDA-ARS National Animal Disease Center*, *Ames IA*.

The 35 kDa major membrane protein (MMP) of *Mycobacterium avium* ssp. *paratuberculosis* was studied to determine the potential of using MMP to develop a subunit vaccine. A flow cytometric (FC) assay was developed to conduct the study. Comparison of the immune responses to MMP, purified protein derivative (PPD) and soluble antigen (SAg) in experimentally (n = 5) infected calves revealed the CD4 response was stronger than the CD8 response to MMP at 3 mo ($P < 0.05$). No significant differences were observed in the CD4 response to MMP compared with PPD and SAg. A significant difference was observed between CD8 response to MMP compared with PPD and SAg ($P < 0.05$). At 12 mo the CD4 response to MMP was still stronger than the CD8 response. The CD4 response to PPD and SAg was significantly stronger than the response to MMP ($P < 0.05$). No significant difference was observed in the CD8 response to MMP compared with PPD and SAg. The CD4 and CD8 response to MMP, PPD, and SAg was significantly higher in naturally infected cows compared with the response in experimentally infected calves, at the preclinical (n = 3) and clinical (n = 5) stage of disease ($P < 0.05$). The findings show the cell-mediated immune response to MMP develops slowly, as detected by FC, and is not diminished at any stage of infection. These findings indicate that MMP does not elicit a protective immune response in its native form. A strategy is needed to modify MMP so that it elicits a strong early response, essential for blocking the capacity of Map to dysregulate the immune response and cause disease.

Key Words: *Mycobacterium avium* ssp. *paratuberculosis*, MMP, immune response

M60 Flow cytometric and in-house ELISA methods of milk testing for Johne's disease diagnosis. A. Wadhwa*[1], J. P. Bannantine[2], B. A. Elliot[1], M. C. Scott[1], and S. Eda[1], [1]*University of Tennessee, Knoxville*, [2]*United States Department of Agriculture*, *Ames, IA*.

Use of enzyme-linked immunosorbent assay (ELISA) in dairy herds is recommended as a Johne's disease (JD) control measure; however, current ELISA tests suffer low sensitivity. The long-term goal of this project is to develop a sensitive ELISA method of testing milk samples for JD diagnosis. By using a flow cytometric method (FCM), we demonstrated previously that *Mycobacterium avium* ssp. *paratuberculosis* (MAP)-infected cattle produced serum antibodies against surface antigens of MAP. Also, an in-house ELISA test developed using surface antigens of MAP showed a higher level of sensitivity in detecting MAP infections than that of current ELISA tests. The objective of this study is to demonstrate a "proof-of-concept" that surface antigens of MAP can be used for detection of anti-MAP antibodies in milk as well as serum samples. FCM-Intact MAP bacilli were incubated with 48 bovine serum and milk samples and subsequently with fluorescein-labeled anti-bovine IgG secondary antibody. Antibody binding to the surface of MAP was detected by using a flow cytometer. In-house ELISA-Surface antigens of MAP were extracted by a brief treatment of the bacteria with 80% ethanol, coated on a microtiter plate, and reacted with bovine milk samples. Antibody binding to the immobilized MAP surface antigens was detected in an ELISA format by using a horseradish peroxidase–labeled secondary antibody and its substrate. The following conditions were optimized: concentrations of antigen, milk, and secondary antibody for better differentiation of milk samples obtained from JD-positive and JD-negative herds and 6 different mycobacteria were tested as absorbent of cross reactive antibodies. In FCM, a high level of correlation (r^2 = 0.79) between antibody binding levels of serum and milk was observed. In the optimized in-house ELISA test, 9 out of 10 JD-positive milk samples showed positive antibody reactions. These results suggest that MAP-infected cattle produce milk antibodies against surface antigens of MAP. Further study may reveal whether a sensitive ELISA test can be developed based on the surface antigens of MAP.

Key Words: *Mycobacterium paratuberculosis*, antigen, diagnosis

M61 Induction of B cell responses upon experimental infection of neonatal calves with *Mycobacterium avium* ssp. *paratuberculosis*. J. R. Stabel*[1], J. P. Bannantine[1], S. Eda[2], and S. Robbe-Austerman[3], [1]*USDA-ARS-NADC*, *Ames, IA,* [2]*University of Tennessee*, *Knoxville,* [3]*USDA-APHIS-NVSL*, *Ames, IA*.

Animal models are useful for studying host responses to infection and aid in the development of diagnostic tools and vaccines. The current study was designed to compare the effects of different methods of experimental infection: Oral (*Mycobacterium avium* ssp. *parauberculosis* (MAP) strain K-10; Oral/DXM (pretreatment with dexamethasone before oral inoculation with strain K-10); IP (intraperitoneal inoculation with strain K-10); and Oral/M (oral inoculation with mucosal scrapings from a clinical cow) in neonatal calves. The objective of this study was to determine if infection with MAP over 12-mo period would invoke changes in the percentages of total B cells in the peripheral blood mononuclear cell population and in subpopulations of B cells as determined by CD5, CD25, and CD45RO markers. Over the course of the study, the percentage of total B cells in nonstimulated and antigen-stimulated cell cultures increased ($P < 0.01$) for orally and intraperitoneally infected calves, with the highest percentages noted at 3 and 6 mo post-infection. Oral infection of calves with a clinical strain of MAP (Oral/M) resulted in increased ($P < 0.05$) percentages of $CD5^{dim}$ and $CD5^{bright}$ B cells, regardless of in vitro stimulation, by 9 and 12 mo post-infection. Experimental infection by all methods resulted in increased ($P < 0.05$) expression of CD25+B cells and CD45RO+ B cells early in the study but the most significant results were observed at 12 mo for calves pre-treated with dexamethasone before oral inoculation with strain K-10 (Oral/DXM) and Oral/M calves. Immunoblot analyses demonstrated the greatest reactivity to a whole-cell sonicate of MAP in sera from IP calves and the lowest was observed in calves orally inoculated with strain K-10. Further evidence of strong MAP-specific antibody responses in the IP calves was demonstrated using the EvELISA method. In summary, the method of experimental inoculation with MAP did affect the induction of B cell subpopulations and the appearance of MAP-specific antibody during the 12-mo study period.

Key Words: *Mycobacterium avium* ssp. *paratuberculosis*, cattle, B cells

M62 Deletion of *relA* attenuates in vivo survival of *Mycobacterium avium* ssp. *paratuberculosis*. K. T. Park*[1], A. J. Allen[2], M. J. Hamilton[1], A. Grimm[1], H. M. Rihan[3], G. S. Abdellrazeq[4], and W. C. Davis[1], [1]*Department of Veterinary Microbiology and Pathology, Washington State University*, *Pullman,* [2]*Department of Veterinary Clinical Sciences, Washington State University*, *Pullman,* [3]*Department of Bacteriology, Mycology and Immunology, Mansoura University*, *Egypt*, [4]*Department of Microbiology, Alexandria University*, *Egypt*.

Extensive effort is underway to develop a mutant *Mycobacterium avium* ssp. *paratuberculosis* that can be used as a vaccine to control paratuberculosis in cattle. Studies in mice have shown that deletion of *relA* in *M. tuberculosis* attenuates survival in vivo. Mice infected with the *relA* mutant survived longer with a reduction in bacterial burden and pathology. The objective of the present study was to test the hypothesis that deletion of *relA* also attenuates survival of *Map in vitro* and in vivo. To test the hypothesis we generated a deletion mutant (*relA*) in the K10 strain of *Map*, tagged with the green fluorescent protein gene (*gfp*) and infected calves (n = 5). Wild type K10-*gfp* was used as a control (n = 3). Analysis in an in vitro assay revealed deletion of *relA* reduced survival in monocyte derived macrophages compared with survival of wild type K10 at 6 d post infection (12.5% ± 6.3 SD vs. 29.4% ± 3.6 SD) ($P < 0.05$ by Kruskal-Wallis test). Analysis in vivo using a calf cannulated ileum model showed that deletion attenuated survival without altering the immune response to *Map* 3 mo PI. At necropsy, 9 different tissue sites were processed for *Map* culture. No bacteria were detected in any tissue sample (n = 45) from calves infected with the mutant at 3 mo PI. In contrast, bacteria were detected in 13 of 27 tissue sites obtained from calves infected with wild type K10 (all 3 animals had at least 4 positive tissues) ($P < 0.05$ by chi-squared test). The findings show that further studies are warranted to determine if a *relA* deletion mutant can be used as a vaccine.

Key Words: live vaccine, paratuberculosis

M63 Microfluidic system for serodiagnosis of Johne's disease. S. Eda*[1], A. Wadhwa[1], J. P. Bannantine[2], M. C. Scott[1], R. W. Shaw[3], and R. S. Foote[3], [1]*University of Tennessee, Knoxville*, [2]*United States Department of Agriculture*, *Ames, IA,* [3]*Oak Ridge National Laboratory*, *Oak Ridge, TN.*

Microfluidics (Lab-on-a-chip) technology has been used in various analytical processes, including electrophoresis, single-cell analysis, biochemical assays, and immune assays. The technology offers opportunities for the development of point-of-care diagnostic devices for various infectious diseases. Diagnosis of Johne's disease (JD) is currently conducted in diagnostic laboratories, creating dairy farmers costly expenses

for veterinary service, sample handling, and shipping. An automated point-of-care diagnostic device for JD would reduce diagnosis-related costs and also may improve the accuracy of testing because it would require a minimum of examiner intervention. The long-term goal of this project is to develop a point-of-care serological diagnostic device for JD. For this report, we tested serum antibodies against *Mycobacterium avium* ssp. *paratuberculosis*, the causative agent of JD, using a microfluidic system. In this project, magnetic micro-beads were used as the solid phase for antibody binding reactions. Magnetic micro-beads were treated with ethanol-extracted antigens of *M. paratuberculosis*, serum sample, and then a fluorescently labeled secondary antibody. Antibody binding was subsequently detected by using a flow cytometer. Assay conditions were optimized for higher analytical sensitivity and specificity of the bead-based flow cytometric test. Using the optimized conditions, we then tested JD-negative and JD-positive serum samples in a microfluidic system. Using a well-classified set of 155 serum samples, diagnostic sensitivity and specificity of the flow cytometric test were estimated to be 60.0% and 98.0%, respectively. Five serum samples were tested using a microfluidic system we designed and the results were compared with those of the flow cytometric test on the same set of samples. As a result, a high level of correlation (linear regression, $r^2 = 0.994$) between the results of flow cytometric and microfluidic tests was observed. Our data demonstrated a 'proof-of-the-concept' that JD can be diagnosed by employing a test based on microfluidics technology.

Key Words: paratuberculosis, diagnosis, microfluidics

M64 Evaluation of *Mycobacterium avium* ssp. *paratuberculosis* strains and a locus associated with tissue infection. H. L. Neibergs*[1], Y. Schukken[2], R. H. Whitlock[3], A. Pradhan[2], J. M. Smith[4], and E. Hovingh[5], [1]*Washington State University*, *Pullman*, [2]*Cornell University*, *Ithaca, NY*, [3]*University of Pennsylvania*, *Kennett Square*, [4]*Unversity of Vermont*, *Burlington*, [5]*Pennsylvania State University*, *University Park*.

Mycobacterium avium ssp. *paratuberculosis* (*Map*) strains vary by the presence of multiple copies of fatty acid metabolism genes which are thought to increase the virulence of the mycobacterium and potentially increase the incidence of Johne's disease. We previously identified a locus on chromosome 3 (*ss86341066*) that showed that animals with an A allele were 3 times less likely to be tissue infected with *Map* than those with a C allele (Settles et al. 2009, Animal Genetics, 40, 655–662). The objective of this study was to determine if there was an interaction between *Map* strains and the genotypes of hosts with *Map*-infected tissue. *Map* strain types were identified by multilocus short sequence repeat analysis from ileo-cecal lymph nodes, ileo-cecal valve, or ileum and fecal samples from19 Holstein cows representing 3 herds. *Map* strain types coded as 2, 3, 4, 6, 9, 11 and 12 were identified in 10, 1, 4, 4, 1, 1, and 1 sample, respectively. Three animals had 2 different strains isolated from their tissue and feces (2 animals-type 2 and 4; 1 animal-type 3 and 6). *Map* strains 3, 4, 6, 9, 11 and 12 were combined into one group for analysis due to the small number of observations. A Fishers exact test compared the *ss86341066* allele frequencies with the *Map* strain that infected each animal. For animals infected with *Map* strain types 3, 4, 6, 9, 11 and 12 the frequency of the minor protective allele (A) was 0.0 and the frequency was 1.0 for the major allele (C). For animals with *Map* strain type 2, the frequency of the minor allele (A) was 0.25 and the frequency was 0.75 for the major allele (C). The frequency of the *ss86341066* alleles differed ($P < 0.05$) between animals with *Map* strain type 2 and *Map* strains type 3, 4, 6, 9, 11 and 12. These data suggest that *Map* strain type 2 may be more virulent in the Holstein animals tested than *Map* strain types 3, 4, 6, 9, 11 and 12 and that there is an interaction between *Map* strains and *ss86341066* associated with tissue infection. Further studies with larger sample sizes will be needed to confirm and further characterize this interaction.

Key Words: Johne's, strains, locus

M65 Genome sequence of a *Mycobacterium avium* subspecies *paratuberculosis* isolate from a patient with Crohn's Disease. L. Li*[1], A. Amonsin[2], S. Sreevatsan[3], and V. Kapur[1], [1]*Penn State University*, *University Park,* [2]*Chulalongkorn University*, *Bangkok, Thailand*, [3]*University of Minnesota*, *St. Paul.*

Mycobacterium avium subspecies *paratuberculosis* (Map) has been associated with human Crohn's disease, a chronic inflammatory bowel disease. To identify polymorphic sequences with potential relevance to host specificity and evolution, an isolate recovered from a Crohn's disease patient, MAP4 has been sequenced. Second-generation sequencing approaches were used to generate a total of 88.5 million base pairs of finished sequence, representing an 18-fold coverage of the genome. Currently, the genome has been assembled into ~60 contiguous pieces accounting for ~98% of the K10 genome. Whole-genome comparison of MAP4 with K10 revealed a lack of major large-sequence polymorphisms. A total 171 single-nucleotide polymorphisms (SNPs) were identified, with 152 in coding regions, which is ~6-fold lower than SNPs found in genome comparison of 2 Mycobacterium tuberculosis strains. Two-thirds of the SNPs in coding regions were non-synonymous and were primarily found in genes encoding metabolic pathways, cell envelope, and virulence genes involved in invading mammalian cells. Fifty-eight synonymous SNPs were identified and the pattern of synonymous nucleotide substitution between 2 genomes at 4,350 putatively orthologous loci showed a synonymous substitution rate of 3.7×10^{-5}, suggesting a relatively recent divergence between MAP4 and K10. Many of the SNPs identified in MAP4 were verified in 10 isolates from human and cattle and the results indicate that these were not specific in isolates from human hosts. Overall, the comparison of 2 genome sequences confirmed restricted allelic variation in Map, and clearly showed the considerable similarity in sequences between Map isolates recovered from cattle and humans.

Key Words: *Mycobacterium avium* ssp. *paratuberculosis*, genome sequence, single-nucleotide polymorphism

M66 Impact of vaccination against Johne's disease on lactation performance of dairy cows: Milk production, reproduction and overall culling. J. R. Lima*[1], E. Patton[2], B. Knust[1], J. Bohn[3], and S. J. Wells[1], [1]*University of Minnesota*, *St. Paul*, [2]*Wisconsin Department of Agriculture*, *Madison*, [3]*Veterinary Clinic*, *Amery, WI*.

Our objective was to evaluate the impact of vaccination against Johne's disease on lactation performance measured by milk production, reproductive outcomes and overall culling rate. Three dairy herds in the state of Wisconsin previously identified with *Mycobacterium avium* ssp. *paratuberculosis* (MAP) infection, by a combination of diagnostic tests (serum ELISA and TREK fecal culture) and presence of clinical disease were enrolled in this study. Within each herd, heifer calves at birth were systematically allocated to a vaccination or control group, until 2 cohorts of 50 animals or 10% of the adult cow herd was formed, establishing an overall sample size across herds of 307 animals (vaccinated = 162 vs. control = 145). Vaccination was performed up to 35 d of age. From each of the study cows a fecal sample was collected at first freshening, at 90 d of pregnancy in the first lactation, at 90 d of pregnancy for all following lactations and at time of culling to assess MAP infection. Milk production, reproductive performance and culling

data, from the year 2005 until 2009, were obtained from the dairy herd records and fecal culture results were collected from the laboratory. Animals were classified positive for MAP if the TREK fecal culture score was ≥ 1. Mixed modeling was used to analyze differences in total milk production per lactation between the 2 groups. Logistic regression was used to evaluate conception at first breeding and Cox regression was used to estimate days in milk (DIM) to conception and days from birth until culling. Vaccination against Johne's disease had no effect on total milk production across lactations, conception at first breeding and DIM to conception. Time to test positive for Johne's disease was statistically significantly longer among vaccinates but no difference was observed in overall culling rate between groups. In this study, vaccination against Johne's disease had no improvement on overall lactation performance.

Key Words: *Mycobacterium avium* ssp. *paratuberculosis*, Johne's disease, lactation performance

M67 Effect of Tri-Lution (T), a synbiotic, on milk production and shedding of *Mycobacterium avium* ssp. *paratuberculosis* (MAP) in a commercial dairy herd. D. M. Albin*, C. Jones-Anding, D. P. Casper, D. A. Spangler, and G. A. Ayangbile, *Agri-King, Inc.*, *Fulton, IL*.

The effects of feeding T (synbiotic) in a dairy herd with Johne's disease on milk production and shedding of MAP (causative agent of Johne's) was evaluated for 10 mos. Thirty-six lactating Holsteins on a commercial dairy farm were divided into 2 groups, T (n = 19) and control (C, n = 17), based on days in milk and fecal shedding of MAP. Tri-Lution was added to a corn silage, haylage, and high-moisture corn diet. Tri-Lution was included at 56.7 g/cow/d for 22 weeks, and then 113.4 g until the end. Milk production and composition data were obtained monthly via Dairy Herd Improvement Association sampling. Fecal samples were collected every other week. Samples were used to assess MAP shedding via polymerase chain reaction. Fat-corrected milk (3.5%, FCM) production was increased for cows fed 56.7 g T within 5 mos compared with cows fed C (33.2 ± 4.3 vs 26.8 ± 2.4 kg/d for T and C, respectively). Cows fed 113.4 g T within 3 mos (8 mos total) had greater FCM production than cows fed C (33.0 ± 3.9 and 25.1 ± 4.5 kg/d). In addition, when cows were fed 56.7 g T, the decline in milk production was slower than C (−0.6 vs −1.2 kg FCM/cow/mo) and less linear (r^2 = 0.56 for T, 0.81 for C). For cows fed T, milk shedding of MAP was reduced by 39%, and incidence of shedding (number of positive samples) was reduced 16%, with 56.7 g T vs C. When cows were fed 113.4 g T, following 56.7, MAP shedding in milk was further reduced 9%, while incidence was further reduced 1%. For cows fed 56.7 g/d T fecal shedding of MAP was reduced by 18%, while incidence was reduced 5%. With 113.4 g T, fecal shedding was further reduced 3%, while incidence was further reduced 8% vs C. Relative standard error of shedding data ranged from 8.7 to 30%. Tri-Lution improved milk production, and reduced milk and fecal shedding of MAP (Johne's), over a 10-mo period. Tri-Lution can be a beneficial management practice on commercial dairy farms with Johne's disease.

Key Words: synbiotic, Johne's disease, milk production

M68 Survivability of *Mycobacterium avium* subsp paratuberculosis in grass silage after fermentation and exposure to low pH and high organic acids. S. A. Flis*[1], K. L. Cook[2], and C. S. Ballard[3], [1]*Bourdeau Bros.*, *Middlebury, VT*, [2]*USDA–ARS*, *Bowling Green, KY*, [3]*W. H. Miner Agricultural Research Institute*, *Chazy, NY*.

Mycobacterium avium ssp. *paratuberculosis* (Map) is a pathogen of concern in dairy production due to its ability to withstand harsh conditions and cause new infections. Infection is a result of ingesting Map from contaminated feed, water, or manure. The study objective was to evaluate the ability of Map to survive low pH and high organic acid concentrations encountered as part of ensiling. Three experiments were conducted to evaluate survivability and the ability to differentiate live and dead bacteria. Study 1 evaluated survivability in grass silage fermented in vacuum bags. Forage was inoculated with live Map, dead Map, or no Map (control) and incubated for 25, 50, 75, or 100d. Fermented forage averaged 4.7 ± 0.11 pH, 8.3 ± 2.1 lactic acid (% DM), 3.5 ± 0.9 acetic acid (% DM), and 0.05 ± 0.03 propionic acid (% DM). Study 2 evaluated survivability in buffered citric acid solutions of pH 4, 5, 6, and 7. Live Map bacteria were added to solutions and bacterial concentrations were measured at 0, 5, 15, 20, 30, and 35 d. Study 3 evaluated survivability in exudates from control silage in study 1. Exudates were filter sterilized to eliminate background population interference and pure live Map was exposed to exudates for 0, 5, 10, 15, 20, 25, or 30 d. Study 1 found no changes in concentration of Map regardless of number of fermentation days or viability/presence of MAP inoculated. After exposure to citric acid in study 2, samples were analyzed for Map concentration by PCR (total bacteria) and propidium monoazide (PMA; live bacteria). Study 2 found that live MAP concentration decreased as pH decreased and exposure time increased with a 2-fold log reduction for pH 4 at 37d. In study 3, no change in Map concentration was found when bacteria were exposed to exudates. These results indicate that while Map is sensitive to low pH, this only occurs with concentrations of acid higher than experienced with proper forage fermentation. Map present in manure and applied to forage grasses may survive ensilaging process and silage may therefore be a potential route of infection.

Key Words: *Mycobacterium avium* ssp. *paratuberculosis*, silage, quantitative PCR

M69 A membrane associated serine protease of *Mycobacterium avium* subspecies *paratuberculosis* plays a role in resistance to phagosomal acid stress. A. Kugadas*[1], H. K. Janagama[1], E. A. Lamont[1], and S. Sreevatsan[1,2], [1]*Department of Veterinary Population Medicine, University of Minnesota*, *Saint Paul*, [2]*Department of Veterinary Biomedical Sciences, University of Minnesota*, *Saint Paul*.

Pathogenic mycobacteria successfully survive in the acidic micro-environment of the phagosome. We hypothesize that *Mycobacterium avium* ssp. *paratuberculosis* (MAP) expresses a membrane associated serine protease encoded by MAP0403, in response to phagosomal acidification and is vital for the intracellular survival. Expression of serine protease by MAP K-10 was studied at 10, 30, and 120-min. post infection of bovine monocyte derived macrophages treated with or without bafilomycin to block phagosomal acidification. MAP serine protease was significantly upregulated exclusively in the acidified phagosomes. Highest level of MAP0403 expression coincided with the timing of peak phagosome acidification in the macrophages. Inasmuch as *Mycobacterium smegmatis mc^2 155* cannot resist and persist in the acidified phagosome, we cloned the open reading frame of MAP0403 via a pSM417 vector into *M. smegmatis mc^2 155*. Compared with controls, *M. smegmatis mc^2 155* transformants carrying the MAP serine protease show a temporal survival advantage during the in vitro acid stress for 30 and 120min. Our studies suggest that MAP serine protease is critical in resisting the phagosomal acid stress by MAP. Further establishment of this mechanism will lead to better understanding of a proximal step in the pathogenesis of mycobacterial infections to establish an intracellular niche.

M70 Quantifying Johne's disease infectivity in Indiana dairy herds. C. C. Wu*, T. L. Lin, A. Storm, C. A. Alinovi, and M. P. Ward, *Purdue University*, *West Lafayette, IN*.

Analysis of fecal culture and ELISA serology for Johne's disease (JD) was conducted on 5 dairy herds to quantify infectivity of JD from 2004 to 2009. Various positive management practices and risk assessment have been employed in these herds. Spearman′s coefficient was calculated for the relationship between fecal shedding level and ELISA score. In a large open Holstein herd (900 milking) prevalence of JD by semiquantitative fecal culture was 36.1% in 2004, 18.5% in 2005, and 18.7% in 2006. In a small closed herd (50 milking) none of the tested cows were positive for JD by fecal culture in 2004. This herd did have one cow that was fecal culture positive in 2005 (0.9%), though all cows were negative for JD when tested in 2006. Two small open herds were studied. In one herd (80 milking) 19% of cows were positive for JD by fecal culture in 2004, 9.4% in 2005, and only 3.3% of cows were positive in 2006. The herd prevalence for JD went up to 24.6% in 2007 with new unvaccinated cows added to the herd, but reduced to 4.2% in 2008. In the other small herd (60 milking), 4.2% of the cows were positive for JD by fecal culture in 2005, 4.5% in 2006, and all tested animals were negative for JD in 2007 (0.0%). The fifth herd is a medium-sized (300 milking) open dairy herd where 10% of cows were fecal positive for JD in 2003 and herd prevalence had risen to 31.7% when tested in 2005. In subsequent years, the herd prevalence of JD decreased to 14.8% in 2006 and 9.8% in 2007. Vaccination against JD was practiced in all herds except the small closed herd (50 milking). Between 2003 and 2007, mean ELISA values increased in herds practicing vaccination with little change in the non-vaccinated herds. In conclusion, ELISA testing alone cannot be used to identify positive and shedding animals for culling program. ELISA is best used to screen the status of JD in herd and fecal culture remains the most accurate ante-mortem method to identify animals that are mycobacterial shedders.

Key Words: Johne's disease, infectivity, culture

M71 Preliminary observation of an indigenous Johne's disease vaccine study in infected cattle herd in India. S. V. Singh*, A. Srivastva, B. Singh, A. Kumar, and A. V. Singh, and P. K. Singh, *Central Institute for Research on Goats*, *Makhdoom, Farah, Mathura (UP), India*.

Ineffective control strategies of Johne's disease (JD) by 'test and cull' method, banned on culling of cows due to social issue, high presence of Mycobacterium avium ssp. paratuberculosis (MAP) in livestock, humans and in environment, difficulties in early diagnosis etc. were major challenges to successful JD control program in India. An indigenous JD vaccine has been developed using a native MAP strain of 'Indian Bison type' of goat origin and found very effective in preventing and also curing of JD in goats and sheep. In present study the status of MAP infection and the efficacy of indigenous vaccine for the control of JD in a naturally infected cattle herd (based on preliminary data) were described. Fecal, blood and serum samples from 135 cows (100 adult and 35 calves), showing moderate to advanced symptoms of JD were processed for assessing the status of MAP infection before vaccination by microscopy, PCR and ELISA test, respectively. A total of 60 and 31.85% cows were positive by ELISA and blood PCR. Positive samples by PCR were further genotyped as MAP Bison type by IS 1311 PCR-REA. Out of 32 calves and 51 adult cows, 65.6 and 84.3% were positive in microscopy of fecal smear, respectively. Necropsy of few died cows showed advanced gross lesions of JD. All the cows were vaccinated, sampled (20%) and monitored for improvement in physical condition, reduction in MAP shedding, morbidity, mortality and immune response. Sample results and other data recorded before and 2 mo post vaccination showed reduction in number of MAP shedder/positive cows as well as shedding level, reduced morbidity and mortality despite of extreme winter condition, accelerated sero-conversion, checked diarrhea, increased appetite, no untoward reaction etc. were recorded. Conclusively, developed indigenous vaccine may perform equally (as in previous study on goat and sheep) in controlling the clinical cases of JD in cattle.

Key Words: indigenous vaccine, Johne's disease, *Mycobacterium avium* ssp. *paratuberculosis*

M72 Association of a single nucleotide polymorphism of calpain 1 gene with meat tenderness of the yak. X. J. Wu[1], L. Yang[1], H. L. Wang[1], L. P. Zhang[1], J. H. Wang[1], M. A. Brown*[2], and J. P. Wu[1], [1]*Gansu Agricultural University*, *Lanzhou, Gansu, China*, [2]*USDA-ARS, Grazinglands Research Laboratory*, *El Reno, OK*.

The association of a single nucleotide polymorphism (SNP) of calpain 1 (CAPN1) gene with shear force of 2.54 cm steaks from *M. longissimus dorsi* from Gannan yaks (*Bos grunniens*, n = 181) was studied. The experimental design was a repeated measures with the main unit in a completely randomized design with a factorial arrangement of treatments (age at harvest x SNP) and the repeated subunit was aging days. Individual animal was used as the experimental unit. Yaks were harvested at 2, 3, and 4 yr of age (n = 51, 59, and 71, respectively), and samples of each yak carcass were aged at 4°C for 0, 1, 3, 7, 14 or 21d. Shear force for each sample was determined at each of 6 postmortem aging times using Warner-Bratzler shear force methodology. Fragments of the yak CAPN1 gene including exon 9 and intron 9 were amplified and subjected to single strand conformation polymorphism analysis. A SNP was found within intron 9 of the CAPN1 gene G5837A, and there were 2 genotypes of GG and GA identified, respectively. The genotypic frequency of GG was 82.87% compared with 17.13% for GA. Statistical analysis was done using SAS PROC MIXED. Interaction of SNP × age at harvest × aging days was demonstrated ($P < 0.10$) for shear force. In 2-yr-old yak, genotype GG had lesser shear force than that of GA at the aging times of 0, 3, and 7 d (0.78, 0.92, and 0.65 kg, respectively; $P < 0.05$); however, in 3-yr- and 4-yr-old yak, genotype GG had lesser shear force than GA at aging time of 14 d (0.71 and 0.58 kg, respectively; $P < 0.05$). Genotype had little effect ($P > 0.05$) on shear force for 3- and 4-yr-old yaks averaged over aging time. In 2-yr-old yak, genotype GG had 0.57 kg lesser shear force than yaks with genotype GA ($P < 0.05$) averaged over aging time. Therefore, results from this research suggest that the CAPN1 SNP affected shear force of *M. longissimus dorsi* but the effect differed depending on age of yak and aging time of the meat.

Key Words: yak, calpain, genotype

M73 The effects of single nucleotide polymorphisms of calpastatin gene on meat tenderness of the yak. J. H. Wang[1], J. P. Wu*[1], H. L. Wan[1], L. Yang[1], X. J. Wu[1], M. A. Brown[2], and L. P. Zhang[1], [1]*Gansu Agricultural University*, *Lanzhou, Gansu, China*, [2]*USDA-ARS, Grazinglands Research Laboratory*, *El Reno, OK*.

The association of single nucleotide polymorphisms (SNPs) of calpastatin (CAST) gene with shear force of 2.54 cm steaks from *M. longissimus dorsi* from Gannan yaks (*Bos grunniens*, n = 181) was studied. Yaks were harvested at 2, 3, and 4 yr of age (n = 51, 59, and 71, respectively), and samples of each yak carcass were aged at 4°C for 0, 1, 3, 7, 14 or 21d. Shear force for each sample was determined at each of the 6 postmortem aging-day using Warner-Bratzler shear force methodology. Fragments of the yak CAST gene including exon 3 were amplified and subjected to single strand conformation polymorphism analysis. Two linkage SNPs were found within exon 3 of the CAST gene: G40455A and G40463A, and there were 2 genotypes of GG/AA and GA/GA demonstrated respectively. The genotypic frequency of GG/AA was 72.93% compared with 27.07% for GA/GA. Statistical analysis was done using SAS PROC MIXED. Interaction of genotype × age at harvest × aging time was demonstrated ($P < 0.05$) for shear force. In 2-yr-old yak, GG/AA had lesser shear force than GA/GA at the aging times of 1 and 7 d (1.15 and 0.57 kg, respectively; $P < 0.05$); 4-yr-old yak GG/AA had lesser shear force than GA/GA at aging times of 7 and 14 d (0.64 and 0.49 kg, respectively; $P < 0.05$). Genotype had little effect ($P > 0.05$) on shear force in 2-yr- and 3-yr-old yak averaged over aging time. In 4-yr-old yak, GG/AA had 0.40 kg lesser shear force than GA/GA ($P < 0.05$) averaged over aging time. Therefore, it was concluded that the CAST SNPs affect ($P < 0.10$) shear force of *M. longissimus dorsi* depending on age of yak and aging time of the meat. Further study should focus on the ontogeny of CAST gene mRNA expression.

Key Words: yak, calpastatin, tenderness

M74 Estimation of inbreeding and effective population size of fullblood Wagyu cattle registered with the American Wagyu Association. H. L. Neibergs*[1], R. Zanella[1], J. F. Taylor[2], C. T. Gaskins[1], J. J. Reeves[1], and J. M. de Avila[1], [1]*Washington State University*, *Pullman*, [2]*University of Missouri*, *Columbia*.

The founders of the American Wagyu herds were imported from Japan during a period when inbreeding was high and the effective population size of the Japanese Wagyu was low. The effective population size represents the number of breeding animals in an ideal population where each male and female has an equal chance of contributing to the next generation. The objectives of this research were to estimate the inbreeding and effective population size of the Wagyu breed using pedigree information from 2504 fullblood animals registered with the American Wagyu Association and from genotypes of 50 fullblood Wagyu animals representing 8 prominent sire lines. The Illumina BovineSNP50 BeadArray was used to genotype the Wagyu samples. Excess homozygosity was used to estimate inbreeding by genotype using PLINK (Purcell et al. 2007) while inbreeding based on pedigree was estimated with FSpeed Pro (http://www.tenset.co.uk/fspeed/fspeed.html). The effective population size was estimated for the period of 1990 to 2007 as described by Nomura et al. (2001) where the annual rate of inbreeding ($\Delta F_{ST,y}$) was used to estimate the annual effective population size (N_e). The estimated level of inbreeding for American Wagyu based on pedigrees was 5.8% which reflects that inbreeding is underestimated for foundation animals with shallow pedigrees. The estimated inbreeding based on pedigrees and genotypes in the 8 sire lines are shown in Table 1. The effective population size averaged 8.8 between 1990 and 2007, with a low of 1.5 in 1991 and a high of 16 in 2007. Wagyu in America are the result of a small number of cattle imported from Japan between 1976 and 1999 and additional importations in the near future are not expected. Strategies to increase genetic diversity and limit inbreeding should be considered to maintain this unique breed of cattle.

Table 1. The percent inbreeding for each of 8 sires based on their 5 generation pedigree and genotypes from the SNP50 BeadArray

Sires	%Inbreeding: Pedigree	%Inbreeding: Genotype
TF Itomichi 1/2	0	25
Kitaguni Junior	0	18.4
TF Kikuhana	18.7	39.1
Kitateruyasudoi	9.4	27.3
Michifuku	6.2	28.1
Sanjirou	12.9	33.1
Takazakura	12.5	31.2
JVP Fukutsuru 068	9.4	21.9

Key Words: Wagyu, inbreeding, population

M75 Genetic network update for economically important traits in a Wagyu x Limousin reference population. Z. Jiang*[1], J. J. Michal[1], T. F. Daniels[1], J. Chen[1], Z. X. Pan[1], T. Kunej[1], M. D. Garcia[2], C. T. Gaskins[1], J. R. Busboom[1], L. J. Alexander[3], R. W. Wright Jr.[1], and M. D. MacNeil[3], [1]*Washington State University*, *Pullman,* [2]*Louisiana State University*, *Baton Rouge,* [3]*USDA-ARS, Fort Keogh Livestock and Range Research Laboratory*, *Miles City, MT*.

In the present study, 84 genes representing 6 different biological pathways were investigated for their associations with 5 carcass, 6 eating quality and 8 fatty acid composition traits in a Wagyu × Limousin reference population, including 6 F1 bulls, 113 F1 dams, and 246 F2 progeny. A total of 157 mutations, mainly single nucleotide polymorphisms were genotyped using a Sequenom assay, but only 135 tagged mutations were selected by the HAPLOVIEW analysis for the association study. Single marker-trait association runs revealed 153 significant associations ($P < 0.05$), which were then placed into 3 groups of quantitative trait modes (QTMs) with additive, dominant and overdominant effects if a marker had 3 genotypes with at least 9 animals for each group of genotypes. All significant markers and their QTMs associated with each of these 19 traits were involved in a linear regression model analysis, which confirmed single-gene associations for 4 traits, but revealed 2-gene networks for 9 traits and 3-gene networks for 4 traits. Such genetic networks involving both genotypes and QTMs resulted in high correlations between predicted and actual values of performance, thus providing evidence that the classical Mendelian principles of inheritance can be applied in understanding the genetic complexity of complex phenotypes. Our present study also indicated that carcass, eating quality and fatty acid composition traits rarely share genetic networks. Therefore, marker-assisted selection for improvement of one category of these traits would not interfere with improvement of another.

Key Words: quantitative traits, genetic networks, beef cattle

M76 Genetic trends for image analysis traits in Japanese Black cattle. Y. Nakahashi*, S. Ido, and K. Kuchida, *Obihiro University of A & VM*, *Obihiro-shi, Hokkaido, Japan*.

Intramuscular fat has been a concern in genetic improvement of Japanese Black cattle. Beef Marbling Standard (BMS) has been used as an indicator of the amount of marbling. However, there are factors other than marbling that are known to affect BMS, such as the coarseness or fineness of marbling flecks. In the present study, we investigated genetic trends and the relationships between traits related to BMS. A total of 10,556 of Japanese Black cattle that were shipped to a meat processing plant in Hokkaido, Japan, were used in the study. High quality digital images were collected and analyzed to calculate the marbling percent (MP) and coarseness index of marbling (CIM). The AIREMLF90 program was used for estimation of genetic parameters. Genetic trends were calculated as the average of standardized breeding values (BV) of the dams by birth year for every trait. Regression coefficients (β) were used to compare the genetic trends. The estimated heritabilities of BMS, MP, and CIM were 0.63 ± 0.04, 0.74 ± 0.04, and 0.51 ± 0.04, respectively. The genetic correlation coefficients of BMS with MP and CIM were 0.58 and 0.96, respectively. The trend in average BMS BV was flat from 1937 to 1970 ($\beta = -0.01$), increasing from 1970 to 1990 ($\beta = 0.04$), and accelerating after 1990 ($\beta = 0.18$). Similarly, the genetic trends for MP and CIM also increased. These results indicated that the genetic improvement of BMS is occurring, but at the same time genetic merit for the undesirable trait of marbling coarseness is also increasing. To achieve improvement of BMS without increasing coarseness of marbling, it is suggested to utilize image analysis in genetic evaluation, as this technology can indicate detailed characteristics of marbling.

Key Words: genetic trend, image analysis, Japanese Black cattle

M77 Multivariate analyses of weight traits fitting reduced rank and factor analytic models in Nellore cattle. A. A. Boligon*[1], A. B. Bignardi[1], M. E. Z. Mercadante[2], and L. G. Albuquerque[1], [1]*FCAV/UNESP*, *Jaboticabal, São Paulo, Brazil*, [2]*Instituto de Zootecnia*, *Sertãozinho, São Paulo, Brazil*.

A total of 61.528 records from 12,246 animals from the Nellore Cattle Breeding Program were used to estimate genetic parameters using multivariate analysis (MV). Reduced rank analyses fitting the first m = 2, 3, 4 and 5 genetic principal components (RR) and analyses that fitted a factor analytic structure considering m = 2, 3, 4 and 5 factors (FA), were carried out. The traits evaluated were: birth weight (BW), weaning weight (WW), weight at 365 (W365) and 550 d of age (W550), and weight at 2, 3, 4, 5 and 6 year of age (W2Y, W3Y, W4Y, W5Y and W6Y, respectively). Genetic additive direct effects and residual effects were considered as random. For BW and WW, the genetic maternal and maternal permanent environment effects were included as random effect. Contemporary group (farm, sex, year, and month of birth) was included as a fixed effect. Linear and quadratic effects of animal age at recording (except BW), and dam age at calving (for BW, WW, W365 and W550) were included as covariables. The residual, genetic maternal and permanent environment covariance matrix was assumed to have full rank throughout. Models were compared by Akaike's Information Criterion (AIC) and Schwarz's Bayesian Information Criterion (BIC). The model containing the largest number of parameters - MV (96 parameters) showed the worst fit. For models with the factor number equal to the principal component number, the value of log L was very similar. In general, the results indicate that RR models with 3 principal components (RR-PC3) are sufficient to model the genetic covariance structure among the weight traits. The 3 principal components explained more than 90% of the genetic variation. Genetic correlation estimates between weights traits ranged from 0.42 to 0.96. Results from RR-PC3 agreed closely with estimates from MV analyses and literature results. The RR estimation decreased computational requirements relative to MV analyses.

Key Words: growth traits, genetic parameters, principal component analysis

M78 Genetic parameters for weight traits from birth to 630 days of age in Guzera cattle by random regression models. I. S. Silva*[1], I. U. Packer[2], L. O. C. Silva[3], C. M. R. Melo[4], and R. A. A. Torres Junior[3], [1]*University of Brasília - UnB*, *Brasília /DF, Brazil*, [2]*University of São Paulo - USP/ESALQ*, *Piracicaba/SP, Brazil*, [3]*Embrapa Gado de Corte*, *Campo Grande/MS, Brazil*, [4]*Federal University of Santa Catarina - UFSC*, *Florianópolis/SC, Brazil.*

A total of 60,782 body weight records belonging to Guzera breed from birth to 630 d of age were analyzed to estimate the variance components and the genetic parameters by random regression models and the REML methodology. Ten regression models were analyzed with contemporary group as fixed effect and age of dam as a covariate. Covariance functions of different order were analyzed for direct additive genetic random (kA), animal permanent environmental (kC), maternal permanent environmental (kQ) and residual effects with homogeneous (r1) and heterogeneous variance structures, with 5 (r5) or 10 (r10) residual variance classes. Models were compared by the Likelihood Ratio Test, the Akaike Information Criterion (AIC) and the Schwarz's Bayesian Information Criterion (BIC). The variance estimates in the analyses by the regression models were relatively similar. AIC values showed that the adjustment of the model with order of covariance functions of 6 for kA, kC, kQ (Reg666) and r10, was superior in relation to the other models. BIC values showed that the most parsimonious model

had order of covariance functions of 6 for kA, 5 for kC and 3 for kQ (Reg653), and r10, was optimal among the models with 10 residual variance classes. The heritability estimates for weights at birth (WB), 205 (W205), 365 (W365) and 550 (W550) days of age were 0.13, 0.43, 0.46, 0.48 for the model Reg666-r10, and 0.13, 0.46, 0.54, 0.56, for the model Reg653–10. The phenotypic, genetic, animal and maternal permanent environmental correlations were all positive and were similar for all models. Considering the most parsimonious model, Reg653 and r10, the genetic correlations between WB/W205, WB/W365, WB/W550, W205/W365, W205/W550 and W365/W550 were 0.40, 0.40, 0.42, 0.68, 0.74 and 0.81, respectively. Models with variance homogeneity were inadequate. It was observed that division of the residual variance into 10 distinct classes was the most suitable model for describing variation in the weights studied herein.

Key Words: beef cattle, variance components, random regression

M79 Principal component analysis of traits contributing to genetic evaluation of Brahman bulls in Brazil. J. C. Souza*[1], L. O. C. Silva[2], A. Gondo[2], P. B. Ferraz Filho[3], J. A. Freitas[4], C. H. M. Malhado[5,7], R. L. Weaber[6], and W. L. Lamberson[6], [1]*Mato Grosso do Sul Federal University - UFMS*, *Aquidauana, MS, Brazil*, [2]*Empresa Brasileira de Pesquisa Agropecuaria - EMBRAPA*, *Campo Grande, MS, Brazil*, [3]*Mato Grosso do Sul Federal University - UFMS*, *Tres Lagoas, MS, Brazil*, [4]*Parana Federal University - UFPR*, *Palotina, PR, Brazil*, [5]*UESB*, *Jequie, BA, Brazil*, [6]*Animal Sciences, MU - USA*, *Columbia, MO,* [7]*Scholarship of CNPq*, *Brazilia, DF - Brazil*.

The objective of this study was to evaluate the contribution of each trait contributing to genetic evaluation of Brahman sires. The data were from the 2006 summary of Brahman bulls published by EMBRAPA/CNPGC. Estimates of EPD were obtained using a multiple trait animal model including: weight to maternal phase – 120 d (PM); weight total maternal phase (TMMP); weaning weight (WW); total maternal weaning weight (TMW); yearling weight (YW); pre-weaning gain (GNW) (g/day); total maternal pre-weaning gain (TMPG); post-weaning gain (YGP); age (days) at first calving (IPP); interval between the 1st and 2nd calving (I2P); interval and other calving (IOP); scrotal circumference measurements (SC); and genetic qualification index (IQG = 10% * PM + 15% * WW + 20%*TMW + 30% * YW + 10% * IPP + 10% * I2P + 5% * SC)) of 542 bulls. The characteristics were evaluated by using the PRINCOMP procedure of SAS. The eigenvalues and proportions of the first 5 principal components were 6.72, 0.52; 1.78, 0.14; 1.49, 011; 1.18, 0.09; 0.61, 0.05, respectively; the first eigenvalue totaled 0.52; first 2 0.65; the first 3 0.77, the first 4 0.86, and a total of 5 0.91. The estimated contribution of the first principal component for each trait was WW (0.3757); IQG (0.3749); YGP (0.3724), YW (0.3573); TMW (0.3569); TMPG (0.3526); TMMP (0.3161); YGP (0.2316), SC (0.1515), IOP (0.1347), IPP (0.0527), PM (−0.0060); and I2P (−0.0528). The traits that most contributed were weaning weight, genetic qualification index and post-weaning gain. The traits which contributed least were weight to maternal phase and interval between 1st and 2nd calving. The largest genetic correlations were between weaning weight and post-weaning gain (0.96); yearling weight (0.97); and IQG (0.9556).

Key Words: gain, principal components, Zebu

M80 Allelic frequencies of polymorphisms associated with feed efficiency in Aberdeen Angus cattle in Uruguay. A. I. Trujillo, P. Grignola, I. Pandulli, P. Nicolini, A. Casal, A. Espasandin, F. Peñagaricano, and M. Carriquiry*, *Universidad de la Republica*, *Montevideo, Montevideo, Uruguay*.

We are interested in selecting cattle with improved feed efficiency by searching for residual feed intake (RFI) candidate genes. In confinement systems, neuropeptide Y (NPY), leptin (LEP) and insulin growth factor-1 (IGF-1) have shown association with feed efficiency. Since frequencies of single nucleotide polymorphisms (SNP) of NPY, LEP and IGF-1 are unknown in beef cattle population in Uruguay, our objective was to study the distribution of these SNP in the Aberdeen Angus breed. This is a first step in evaluating the associations of these SNP with RFI and investigating their use as molecular markers for assisted selection in pasture-based system. A totally of 130 genetically unrelated calves from 5 Aberdeen Angus herds (the major contributors to the national genetic pool) were sampled. DNA was extracted from fresh blood using the "salting out" procedure. High resolution melting (HRM) of PCR small amplicons in presence of SYBR Green dye was used to genotype. An A/G SNP located in intron 2 of the NPY gene, a C/T SNP located in exon 2 of the LEP gene and a C/T SNP located in the promoter region of IGF-1 gene, were the markers genotyped. The allelic frequencies of SNP were 0.76 and 0.24 (A and G) for NPY, 0.46 and 0.54 (C and T) for LEP, and 0.61 and 0.39 (C and T) for IGF-1. The SNP frequencies distributions were similar across different herds ($P \geq 0.05$, Chi-squared test). This data shows that the frequency of "favorable" alleles is lower than the "unfavorable" alleles in Aberdeen Angus cattle in Uruguay. These results support our proposal that it is possible to improve feed efficiency by using marker-assisted selection in the context of a national program.

Key Words: SNP NPY LEP IGF-1, feed efficiency, Aberdeen Angus breed

M81 Techniques for sifting inconsistent data points from repeatedly weighed beef cattle. S. E. Speidel*, C. M. McAllister, D. H. Crews Jr., and R. M. Enns, *Colorado State University*, *Fort Collins*.

Prior to their inclusion in genetic evaluations, phenotypic records are typically sifted following Beef Improvement Federation guidelines to exclude erroneous data points. Random regression techniques allow the use of data points regardless of age at measurement. Given the range of ages typically seen in field data sets, it can be challenging to identify problematic observations. The objective of this study was to compare data sifting procedures that can be implemented on a large scale for the purpose of identifying individual data points inconsistent within an individual animal's growth curve. The data set consisted of 1372 animals with an average of 10.98 weight observations per animal ranging from 0 to 519 d of age. Three methods were used to identify inconsistent data within a given animal. First individual animals with R^2 values less than 0.90 for the linear regression of weight on age were examined. Second, residuals from this regression were compared with residuals on all animals, to identify observations with residuals greater than 4, 5, and 6 standard deviations (SD) from 0. Finally, each weight was compared with the overall variability of weight within age window across years, to identify those greater than 4, 5, and 6 SD from the mean. This last method was the least robust of all 3 failing to identify any erroneous data points. The R^2 method was not sensitive enough in this data set given that only 5 animals possessed an R^2 less than 0.90, although one individual animal was identified with a data point not consistent with his remaining values. The most sensitive method compared each individual residual value to the overall residual variability. Here, a total of 10, 2

and 0 animals were identified with residuals greater than 4, 5, and 6 SD from the mean, respectively. For this data set, the inclusion of birth and weaning weights along with the test weights gave better predictions of average daily gain by more precisely estimating the intercept for each regression line. Since the R^2 values were so high the residual method easily found those observations inconsistent with the remaining records on the individuals.

Key Words: beef cattle, data sifting, longitudinal data

M82 Use of principal component approach to predict direct genomic breeding values for meat traits in Italian Simmental Bulls. M. A. Pintus[1], G. Gaspa[1], N. P. P. Macciotta*[1], P. Carnier[2], E. L. Nicolazzi[3], C. Dimauro[1], D. Vicario[4], P. Ajmone-Marsan[3], A. Nardone[5], and A. Valentini[5], [1]*Università di Sassari*, *Sassari, Italia*, [2]*Università di Padova*, *Padova, Italia*, [3]*Università di Piacenza*, *Piacenza Italia*, [4]*ANAPRI*, *Udine, Italia*, [5]*Università della Tuscia*, *Viterbo, Italia*.

In the current study, principal component (PC) analysis was used to reduce the number of predictors in the estimation of direct genomic breeding values (DGV) for meat traits in a sample of 457 Italian Simmental bulls. SNP marker genotypes were determined with the 54K Illumina beadchip. After edits, 40,179 SNPs were retained. PC extraction was carried out separately for each chromosome and 2,466 new variables able to explain 70% of total variance were obtained. Bulls were divided into reference and validation population. Three scenarios of the ratio reference/validation were tested: 70:30, 80:20, 90:10. Effect of PC scores on polygenic EBVs was estimated in the reference population with a BLUP model. Traits analyzed were daily live weight gain, size score, muscularity score, feet and legs score, beef index (economic index), calving ease direct effect, and cow muscularity. Accuracy was calculated as correlation between DGV and polygenic EBV in the validation bulls. Muscularity, feet and legs, and the beef index show the highest accuracies (Table 1), calving ease the lowest. In general, accuracies are slightly higher (Table 1) when reference animals are selected at random and the best scenario is 90:10.

Table 1. Accuracy of GEBV for 7 meat traits

	Scenarios					
	Sorted by birth year			Random		
Trait	70:30	80:20	90:10	70:30	80:20	90:10
Daily live weight gain	0.38	0.35	0.53	0.47	0.37	0.63
Size score	0.44	0.47	0.54	0.49	0.47	0.47
Muscularity score	0.71	0.67	0.80	0.71	0.70	0.79
Feet and leg score	0.72	0.74	0.85	0.76	0.77	0.83
Beef index	0.63	0.57	0.74	0.63	0.60	0.77
Calving ease direct effect	0.23	0.23	0.24	0.34	0.26	0.29
Cow muscularity	0.80	0.85	0.83	0.82	0.84	0.82

Key Words: principal component analysis, genomic selection, meat trait

M83 Genetic analysis of visual score data with different distributions and genetic parameters using linear and nonlinear models. F. Barichello*[1], M. M. Alencar[2], and R. A. A. Torres Júnior[3], [1]*Unesp*, *Jaboticabal, SP, Brazil*, [2]*Embrapa Southeast Livestock*, *São Carlos, SP, Brazil*, [3]*Embrapa Beef Cattle*, *Campo Grande, MS, Brazil*.

The aim of this study was to evaluate the effect of the way (Y) of assigning discrete visual scores (VS, 6 levels) for the values of a continuous underlying scale (USC) on the estimated breeding values (BV) for 2 heritability values (h^2: 0.25 and 0.49) and 2 magnitudes of contemporary group variance (CG: 0.25 and 1.00). Three different models (M) (linear, threshold, and linear with transformed data) were used for the analysis. Herds with 40 sires and 1,200 dams, mated at random, were simulated for 20 years. Direct and maternal BV, maternal permanent environmental, CG, and age of dam effects were generated and combined with an independent error term to form the phenotype in the USC. The USC were assigned, as a function of CG, according to normal relative (Y_1) and normal fixed (Y_2) distributions. The BVs were estimated using the GIBBS2F90 and THRGIBBS1F90 programs with previously estimated variance components. The procedure was repeated 10 times for each combination. Correlations (R) between estimated and true BV were obtained for each animal class (sires, dams and offspring). Significant effects of Y on R for all animal classes were found. The Y_1 distribution presented better estimates than Y_2 distribution for all animal classes (sires: 0.92 vs 0.91; dams: 0.61 vs 0.60; offspring: 0.69 vs 0.68). For dams and offspring, significant effect of h^2 on R was found, where high level of h^2 provided greater correlation between true and estimated BV (dams: 0.67 vs 0.55; offspring: 0.74 vs 0.63). For sires, significant effects of h^2 x CG interaction on R were found (at $h^2 = 0.49$ no differences were found between levels of CG, but at $h^2 = 0.25$ greater R values were found with a low level of CG). M had no effect on R. The results indicate slightly better performance of the Y_1 way of assigning VS to US values, and all M yielded consistent results for VS evaluation.

Key Words: breeding value, threshold model, transformed data

M84 Multibreed genetic evaluation of calving ease and birth weight using a threshold-linear model in Gelbvieh cattle. S. Tsuruta*, A. H. Nelson, J. K. Bertrand, and I. Misztal, *University of Georgia*, *Athens*.

Multibreed genetic evaluation (MBE) was implemented for calving ease (CE) and birth weight (BW) using a threshold-linear model applied to data from the American Gelbvieh Association. Data included 138,072 CE records (3 categories) and 941,811 BW records from 1972 to 2008. The pedigree file contained 1,204,867 animals. Heterosis priors of CE were not available from the literature, so they were constructed by making them proportional (0.02) to the BW priors. Priors of unknown parent group within breeds (breed effects) for CE were also constructed in proportion to those for BW. Priors of external BW and CE EPD for Angus sires in the Gelbvieh data set were provided by the American Angus Association. The computer program used a preconditioned conjugate gradient and iteration on data method. The MBE converged when priors for heterosis and breed effects were used without considering prior external EPD information; however, analyses did not converge when the external EPD priors were included. Correlations between EPD with and without heterosis and breed effect priors were 0.95 and 0.99 for CE and BW, respectively. Correlations of the Angus sire EPD computed in the Gelbvieh MBE with the external EPD of the same Angus sires were 0.23 and 0.33 for CE and BW, respectively, indicating that the external EPD for Angus sires were not good priors in the Gelbvieh data. When low accuracies were assumed for the external Angus EPD for CE and BW, the program converged. This indicates that CE provided from an Angus sire mated to a Gelbvieh female may not be representative of the Angus sire's performance based on external EPD, which were the result of mating Angus sires to Angus dams. This result may suggest that the external EPD priors for BW only should be used in the MBE because informative external EPD priors may not be available for CE.

Key Words: multibreed evaluation, calving ease, threshold-linear model

M85 Comparison of a feed efficiency measure for steer progeny produced from divergently mated sires and dams phenotyped for residual feed intake. N. O. Minton*, R. L. Weaber, R. L. Kallenbach, and M. S. Kerley, *University of Missouri*, *Columbia*.

Objectives of this research were to determine feed efficiency of progeny produced from mating RFI phenotyped sires and dams and the effect of test duration (0 to 70 d, 0 to 120 d, and 70 to 120 d) on RFI values of calves. We hypothesized that parent RFI would influence progeny feed efficiency. We further hypothesized that an increase in test duration for RFI is necessary to accommodate for pre-test effects that could alter RFI values of calves. Simmental crossbred heifers (n = 12 RFI- and n = 12 RFI+) were mated with RFI- (n = 2) and RFI+ (n = 2) bulls. Sire was used as an independent variable to measure the effect of sire on progeny performance. Three dam groups were formed by assigning one SD greater than (INEFF) and one SD less than (EFF) average (AVG) RFI. Steer progeny were placed on feed post weaning where intake and BW were measured over 120 d. Intake and weight data were used to calculate ADG, intake, FCR and RFI. Progeny performance differed among sire groups. Progeny from RFI- sires were more efficient than progeny from RFI+ sires on test durations 0 to 70 d (−0.50 v −0.06; $P < 0.12$) and 0 to 120 d (−0.51 v −0.05; $P < 0.15$). Unexpectedly, one RFI+ sire's progeny performed similar to progeny of 2 RFI- sires. Progeny from INEFF dams had greater RFI's (0.5 v −0.63; $P < 0.03$) from 0 to 70 d and from 0 to 120 d (0.55 v −0.72; $P < 0.03$) than progeny of EFF dams. Progeny RFI values were not significantly different from 70 to 120 d between sire and dam groups. Correlations for RFI were high between test durations of 0 to 70 d and 0 to 120 d (0.87) and 0 to 120 d and 70 to 120 d (0.88). Correlations were low for RFI between 0 to 70 d and 70 to 120 d (0.54). We concluded selecting against the lower third of INEFF dams within a population will improve progeny feed efficiency. Furthermore, extending the test duration is required for progeny that are not acclimated to the test facility or ration before intake collection.

Key Words: residual feed intake, feed efficiency, beef

M86 The relationship of bovine respiratory disease and carcass ultrasound measures. B. W. Brigham*[1], C. M. McAllister[1], R. K. Peel[1], H. Van Campen[2], R. L. Weaber[3], G. H. Loneragan[4], J. L. Salak-Johnson[5], C. C. L. Chase[6], E. J. Pollak[7], and R. M. Enns[1], [1]*Department of Animal Science, Colorado State University*, *Fort Collins,* [2]*Department of Microbiology, Immunology and Pathology, Colorado State University*, *Fort Collins,* [3]*Department of Animal Science, University of Missouri*, *Columbia,* [4]*Department of Agricultural Sciences, West Texas A&M University*, *Canyon,* [5]*Department of Animal Sciences, University of Illinois*, *Urbana,* [6]*Department of Biology and Microbiology, South Dakota State University*, *Brookings,* [7]*Department of Animal Science, Cornell University*, *Ithaca, NY*, [8]*Department of Agricultural Sciences, West Texas A&M University*.

Bovine respiratory disease (BRD) has been identified as an economically relevant trait which lacks selection tools to reduce post-weaning incidence. The lack of sufficient field morbidity data has been a major obstruction to development of tools for genetic improvement. The objective of this study was to investigate the genetic associations among real time carcass ultrasound (US) measures and probability of treatment for BRD. Phenotypes of 2,870 crossbred steers were collected over 2 years (1,551 yr 1; 1,319 yr 2). The US measurements were collected at 3 times during the feeding period; receiving (0d), processing 2 (80d) and processing 3 (150d). US measurements included ribeye area (UREA, cm^2), backfat thickness (UFAT, cm) and percent intramuscular fat (UIMF, %). Morbidity data were collected over the entire 240d feeding period and classified as a binary observation, 1 for treated and 0 for non-treated, respectively. Data included 796 morbidity records; 2,848 first; 2,682 s; and 2,444 third US measurements with a sire pedigree (n = 3,255). (Co)Variance components were estimated for each individual processing period using a multivariate sire model and average information REML procedures to obtain estimates of heritability and genetic correlations. Model fixed effects included contemporary group for all traits and processing weight as a linear covariate for US traits. Contemporary groups were comprised of year, ranch of origin and feedlot pen. An additional factor of US date was added to the definition for each respective processing period. Heritability estimates of morbidity, UREA, UFAT and UIMF at first, second and third processing were 0.15, 0.10, 0.06, 0.20; 0.16, 0.11, 0.09, 0.12; and 0.15, 0.14, 0.11, 0.06 respectively. Morbidity had a negative genetic correlation with all US measurements. The genetic correlations with the greatest magnitude were between morbidity and UREA, UFAT, and UIMF taken at receiving of −0.15, −0.58, and −0.11 respectively. These results imply those individuals with smaller ribeye area and less backfat upon arrival to the feedlot have the highest probability of suffering from a BRD incidence.

Key Words: beef cattle, health, carcass ultrasound

M87 Performance and live-ultrasound traits of beef cattle breeds associated with DNA commercial markers. F. Loya-Olguín*[1], M. Encinias[2], R. E. Kirksey[2], L. Lauriault[2], and L. Avendaño-Reyes[1], [1]*Universidad Autonoma d Baja California*, *Ejido Nuevo Leon, Valle de Mexicali, Baja California, Mexico*, [2]*New Mexico State University*, *Las Cruces*.

The commercially available DNA markers, such as GeneSTAR Markers, provide prediction of phenotypic performance of tested animals. The objective of the present study was to evaluate performance and live-ultrasound traits of 4 beef cattle breeds using commercial DNA markers. Seventy 2 bulls from breeds Angus (n = 30), Charolais (n = 20), Hereford (n = 8), and Maine-Anjou (n = 15) were utilized. Initial BW for Angus, Charolais, Hereford, Maine-Anjou were 326.31, 360.66, 306.94, and 330.48 kg, respectively. The performance test lasted 112 d. All bulls were live-ultrasound for rumpfat (RF), ribfat (RBF), rib-eye (RE), and intramuscular fat (IMF). Also, were recorded average daily gain (ADG), weight per day of age (WDA); and genetic progeny difference on feed efficiency (GPDFE), tenderness (GPDT) and quality grade (GPDQG). The Charolais bulls had higher average number of stars, RE, WDA and GPDFE (11.32 ± 0.41, 14.73 ± 0.28 cm2, 1.50 ± 0.03 kg, - 3.44 ± 0.11 kg, respectively) than ($P < 0.05$) Angus, Maine-Anjou and Hereford bulls. Average of stars, RE and WDA of Angus and Maine-Anjou (10.30 ± 0.35, 13.37 ± 0.24 cm2, 1.42 ± 0.02 kg and 10.13 ± 0.47, 13.25 ± 0.32 cm2, 1.39 ± 0.03 kg, respectively) bulls were similar. Meanwhile, Angus bulls had higher ($P < 0.05$) RF, RBF, IMF, ADG, and GPDT (0.36 ± 0.01 cm, 0.28 ± 0.009 cm, 4.56 ± 0.12%, 1.97 ± 0.03 kg, and −1.42 ± 0.08 kg, respectively) than the Charolais, Maine-Anjou and Hereford bulls. The use of ultrasound technology in live animals and commercial markers data can be useful tools to select a potential genetically superior breed, and within the breed, can sort and predict a potential bull.

Key Words: molecular value predictions, rib-eye area, Charolais

M88 No evidence for association between leptin polymorphism C.73 C>T and bovine viral diarrhea virus (BVDV) vaccine response. X. Fang*[1], L. A. Hoff[1], J. A. Walker[1], K. C. Olson[1], G. A. Perry[1], J. X. Wu[1], C. Maltecca[2], and M. G. Gonda[1], [1]*South Dakota State University*, *Brookings*, [2]*North Carolina State University*, *Raleigh*.

We have previously reported that sire affected humoral Bovine Viral Diarrhea Virus (BVDV) vaccine response in beef calves, suggesting that genetics may contribute to BVDV vaccine variation. In this study, we hypothesized that a single nucleotide polymorphism (SNP) within the leptin gene (LEP C.73 C > T) may be associated with BVDV vaccine response. To test this hypothesis, humoral BVDV vaccine response was measured in 209 Angus and Angus-cross calves. Calves were born between February and May 2009 at the South Dakota State University Antelope, Cottonwood and Cow-calf research herds. All individuals were vaccinated with Bovi-Shield GOLD-10 or −5, which includes modified-live BVDV strains type 1 and 2 (Pfizer, Inc., Exton, PA). Blood samples were collected at time of vaccination (d = 0) and post-vaccination (d = 21). Samples collected on d 0 were used to measure maternal BVDV antibody and to test for persistently infected (PI) BVDV calves, while samples collected on d 21 were used to measure humoral BVDV response to the vaccine. Real-time RT-PCR for BVDV on RNA isolated from plasma samples (Qiagen, Valencia, CA) revealed that none of the calves were PI with BVDV. A BVDV antibody ELISA (Idexx, Inc., Westbrook, ME) was used to measure total BVDV-specific antibody present on d 0 and 21. Antibody concentrations were converted to sample-to-positive (S/P) ratios, and maternal antibody S/P ratios (d = 0) were subtracted from d = 21 S/P ratios to calculate vaccine response. A PCR-RFLP assay was used to genotype the leptin polymorphism. To investigate a possible effect of the leptin polymorphism on BVDV vaccine response, an ANOVA model including effects of leptin genotype, month of birth, gender, and herd was fitted. Herd was significantly associated with vaccine response ($P < 0.05$) and gender approached significance ($P < 0.10$). Leptin genotype and month of birth were not significantly associated with BVDV vaccine response. Our results suggest that selection on the leptin genotype to improve beef cattle carcass quality will not have a pleiotropic effect on BVDV vaccine response.

Key Words: BVDV, leptin, vaccine response

M89 A genotype combination approach using μ-calpain as a candidate gene for growth, carcass, and meat quality in bulls of Senepol and Charolais inheritance. P. Rivera*, J. Bosques, A. Casas, D. Cianzio, and M. Pagan, *University of Puerto Rico at Mayaguez*, *Mayaguez, PR*.

A cytosine/guanine transversion in the μ-calpain regulatory subunit (CAPN1–316) and cytosine/ thymine transition in catalytic subunit (CAPN1–4751) were organized as combined genotypes to investigate its potential associations with growth, carcass, and meat quality traits. Senepol, Charolais, and Senepol × Charolais bulls grown under grazing conditions were genotyped (n = 94) for each individual single nucleotide polymorphisms and organized in a total of 9 combinations (CC/CC, CC/TT, CC/CT, GG/CC, GG/TT, GG/CT, CG/CC, CG/TT, and CG/CT). For growth traits, a subset of 36 animals were used for the correspondent statistical analyses using the more representative CG/CT (n = 16), GG/CT (n = 10), and GG/TT (n = 10) bulls. CAPN1 was associated with heavier body weights: at birth, 205 d, 240 d, and daily weight gain at 205 and 240 d. At birth, animals with the GG/CT combination were heavier ($P < 0.05$) than those with CG/CT. However, CG/CT bulls were heavier ($P < 0.05$) at 205 d, and gain at both 205 and 240 d than the GG/TT. Moreover, at 240 d, CG/CT animals were heavier than GG/CT and GG/TT, and at slaughter CG/CT weighed more ($P < 0.05$) than GG/CT only. For carcass and meat quality traits (CG/CT, n = 9; GG/CT, n = 6; GG/TT, n = 5), CG/CT bulls presented greater tenderness ($P < 0.05$) at 0 d (24 h aging period) than GG/CT, as determined by sensory evaluation of the loin. After 14 d of aging, beef from CG/CT was classified as moderately tender while GG/CT improved from moderately tough to slightly tender (hedonic scale; 1 = extremely tough/8 = extremely tender). In addition, in that same period, differences in sensory tenderness between CG/CT and GG/TT (less tender) were significant ($P < 0.01$). However, the longissimus dorsi and bicep femoris muscle weights were lower ($P < 0.05$) in the double heterozygous. The results of this study suggest that the double heterozygous for CAPN1 (316 = CG, 4751 = CT) presented more desirable growth, carcass, and meat quality traits. Therefore, the usefulness of these markers seems to be beyond its exclusive association with meat tenderness.

Key Words: CAPN1, growth, heterozygous

M90 An insertion/deletion polymorphism at the bovine Calpastatin locus is associated with economically important traits. N. Vega*[1], D. Velez[1], A. Casas[1], D. Cianzio[1], C. W. Ernst[2], and M. Pagan[1], [1]*University of Puerto Rico*, *Mayaguez, PR*, [2]*Michigan State University*, *East Lansing*.

A total of 126 bulls (50% to purebred Senepol and Charolais) were genotyped for a cytosine insertion/deletion identified at intron 2 of the bovine Calpastatin locus to determine its segregation and potential associations with growth and meat quality traits. Overall, the frequency of the allele labeled as A (cytosine deletion) was higher (0.84) than the B (cytosine insertion) allele (0.16). In bulls of Senepol descent, allele frequencies were 0.90A/0.10B, whereas in those with Charolais blood, frequencies were 0.68A/0.32B. Genotypic frequencies were 0.82AA, 0.17AB, 0.01BB and 0.45AA, 0.47AB, 0.08BB for Senepol and Charolais bulls, respectively. Because the BB genotype was only observed in one Senepol bull and 3 Charolais bulls, it was excluded for corresponding statistical analyses (n = 55 for growth; n = 24 for meat quality traits). At birth, AB genotype bulls were heavier than AA bulls ($P < 0.05$). However, the AA bulls presented higher body weights and weight gain at 205 and 240 d ($P < 0.05$). After a 24 h aging period, lower Warner Bratzler shear force (WBS) was found in AA bulls (4.48 kg) than AB bulls (6.05 kg) in the longissimus dorsi muscle for a difference between genotypes of 1.57 kg ($P < 0.01$). The difference in WBS after 14 d of aging was 0.60 kg (AA = 3.13 kg, AB = 3.73 kg; $P > 0.05$). These results indicate that the Senepol breed has a higher AA genotype frequency than the Charolais breed, and may imply a tendency for Senepol animals to gain weight efficiently and produce tender beef. Therefore, this study suggests that this calpastatin polymorphism might be useful in animal selection due to its significant relationship with important beef traits.

Key Words: Calpastatin, Senepol, polymorphism

M91 Partial characterization of bovine complement receptor-2 (CR2) in Angus cattle. S. A. Olenich*, X. Fang, L. A. Hoff, J. A. Walker, K. C. Olson, G. A. Perry, and M. G. Gonda, *South Dakota State University*, *Brookings*.

Complement receptor-2 (CR2, or CD21), found on T-helper cells, assists in antigen recognition of B cells by reducing the threshold for antigen receptor stimulation. Antigen receptor stimulation is important for developing an effective vaccine response; therefore, CR2 is a candidate gene that could be associated with vaccine response in

cattle. Thus, our objective was to characterize genetic variation in CR2 among beef cattle using a DNA-pooling sequencing approach. Blood samples were collected from 300 Angus and Angus-cross calves from 3 research herds in South Dakota: the SDSU Cow-Calf Unit, Cottonwood Research Station, and Antelope Research Station. The DNA was extracted from white blood cells by phenol and chloroform extraction. Pools of equal amounts of DNA (n = 50) were formed (6 pools total) and CR2 exon sequences were amplified using pooled DNA. Forward and reverse primers were designed in CR2 introns to ensure that the entire exon coding region would be amplified. Amplicons were sequenced in both the forward and reverse direction with the same primers used for amplification. Polymorphisms were identified by visually inspecting sequence traces. To date, we have characterized exons 1–4 and partial intron sequences flanking these exons. We have putatively identified a SNP in intron 1 (CR2 c.58+36 *t* > G) and an SSR within intron 2 (CR2 c.181–34T[12_13]). We have not found any polymorphisms within exons 1–4. This study reports the identification of 2 novel, putative intronic CR2 polymorphisms in Angus influenced beef cattle. The polymorphisms discovered in this study will be used to test for association between CR2 polymorphisms and vaccine response in cattle.

Key Words: CR2, CD21, polymorphisms

M92 Evaluation of insertion/deletion and single nucleotide polymorphisms identified at the bovine insulin like growth factor binding protein-2 locus. D. Velez*[1], C. W. Ernst[2], and M. Pagan[1], [1]*University of Puerto Rico at Mayaguez*, *Mayaguez, Puerto Rico, Puerto Rico*, [2]*Michigan State University*, *East Lansing*.

A total of 54 bulls of Senepol and Charolais inheritance were genotyped for 9 single nucleotide polymorphisms (SNPs) previously identified in a 1,180 bp sequence tagged site of the insulin-like growth factor binding protein-2 (IGFBP-2) gene locus (GenBank Accession Number: BV680048). These SNPs have been identified as C/G (nt 162), G/A (nt 254), G/C (nt 259, 822) C/T (nt 345, 433, 448), A/G (nt 719), and T/C (nt 1109) substitutions. In addition, an insertion/deletion polymorphism creates an alternative allele that lacks the base at position 443 and has a GG insertion between bases 449 and 450. Additional genotyping was performed for a recently identified SNP located at position 245 (A/T) and a trinucleotide insertion/deletion (TGT) at nt 1103–1105. The presence of C at nt 443 was linked to the insertion of TGT at nt 1103 in these animals. The majority of animals genotyped exhibited deletions at both nt 443 and nt 1103–1105 (frequency 0.78), which were in linkage disequilibrium with homozygous SNP genotypes at nt 448 (TT/0.77), 433 (CC/0.85), 345 (TT/0.61), 259 (CC/0.83), 254 (AA/0.77), 245 (AA/0.62) and 162 (GG/0.73). A limited number of animals were heterozygous for the insertion/deletions (frequency 0.17 and 0.13 for nt 443 and nt 1103–1105, respectively). For these animals, because of different allele lengths, genotypes for SNP's at nt 822 and 719 could not be determined. Most of the IGFBP2 polymorphisms were segregating at very low frequencies in the purebred Senepol, purebred Charolais and crossbred Charolais animals. With the exception of SNPs at nt 245 (AT frequency 0.54) and 345 (CT frequency 0.62), most markers were also not segregating in the Senepol crossbred cattle. The SNPs at these 2 positions were associated with ribeye area (AA > AT for nt 245; TT > CT for nt 345; $P < 0.05$). Therefore, further evaluation of these IGFBP2 polymorphisms and polymorphism combinations in additional animals is needed.

Key Words: IGFBP-2, SNP, bovine

M93 Residue of melamine and cyanuric acid in milk and tissues of dairy cows fed with different doses of melamine. J. S. Shen, J. Q. Wang*, H. Y. Wei, D. P. Bu, P. Sun, G. C. Luan, and Z. F. Zhou, *State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences*, *Beijing, China*.

Melamine (MEL) may be degraded into cyanuric acid (CYA) and some other analogs by rumen microorganism. This study was conducted to investigate the residue of MEL and CYA in milk and tissues of dairy cows fed with different doses of MEL. Forty mid-lactation dairy cows (157 ± 43 DIM, 20.8 ± 1.4 kg of milk/d) were divided into 4 groups (n = 10/group) in a completely randomized design. The cows of the 4 groups were dosed with MEL (purity ≥99.5%) at 0 (Control), 300 (TRT 1), 500 (TRT 2) and 1000 (TRT 3) mg/d per cow, respectively. The whole trial lasted for 18 d (12 d feeding period, followed by 6 d clearance period). Milk samples were collected at d 1, 2, 3, 4, 8, 12, 13, 14, 15 and 18. On d 13, 3 cows of TRT 2 and TRT 3 were chosen randomly to slaughter, and tissue samples (kidney, liver, mammary, bladder, gluteus medius and longissimus dorsi) were collected. Milk and tissue samples were analyzed for MEL and CYA simultaneously by liquid chromatography tandem mass spectrometry (LS-MS/MS). Minor MEL was detected in concentrated feed background (6.23 ± 1.26 mg/kg), however, no CYA was detected. In MEL treated groups, milk MEL concentration increased quickly and reached a stable concentration at d 4, 8 and 12 after the first administration of MEL. Milk MEL concentration of treated groups in steady-state condition (0.18, 0.27 and 0.50 mg/L for TRT1, TRT2, TRT3, respectively) was significantly affected by MEL feeding dose ($P < 0.05$), with a linearly relationship between MEL intake and milk MEL concentration ($R^2 = 0.91$). No CYA was detected in milk of all groups. MEL residue in tissues of TRT 4 was about 2-fold higher than TRT 3, with the highest concentration in the kidney. The difference of CYA residue in tissues of TRT 4 and TRT 3 was not very obvious. Liver, kidney and bladder has higher CYA residue than other tissue. The CYA may come from the degradation of MEL in rumen.

Key Words: melamine, cyanuric acid, dairy cow

M94 Factors affecting microbiological and physicochemical characteristics of milk produced in dairies located in central Mexico (Altos de Jalisco). A. S. Aguilar, M. A. Lopez-Carlos, C. F. Arechiga*, J. I. Aguilera, F. Mendez-Llorente, H. Rodriguez, M. Rincon, and C. Diaz-Mora, *University of Zacatecas*, *Zacatecas, Mexico*.

Factors affecting physicochemical and microbiological characteristics of milk from 54 dairies located in 2 regions of central Mexico were evaluated. Effects of region, month, season, farm sanitary conditions; farm size and water hardness were evaluated. Variables measured were: protein, lactose, total solids (TS), non-fat solids (NFS), reductase, temperature, acidity, cryoscopy, and density; and the microbiological characteristics: CFU and SCC. Data was analyzed by SAS (proc- mixed). Fat, protein and lactose decreased in January and February. Northeast region scored higher values of milk quality compared with West region. Moreover, microbiological and physicochemical characteristics showed a quadratic trend with farm sanitary conditions. Whereas, physicochemical conditions showed a linear trend for volume, fat, protein, and lactose. A quadratic effect was observed for SCC in herds over 101 cows. Herd size showed a positive linear trend for milk volume, protein, TS, NFS and cryoscopy. Water hardness influenced microbiological characteristics, resulting in higher CFU and SCC by using medium-hard water compared with soft-water (196×10^6 vs. 126×10^6 for CFU and 748×10^6 vs. 631×10^6 SCC, respectively). Furthermore, soft-water hardness significantly affected fat, lactose TS, and NFS in milk. Finally, season of the year affected SCC (summer: 877×10^6 vs. autumn: 709×10^6; $P > 0.05$), and had no effect on CFU. In conclusion, factors evaluated confirmed the need to improved sanitary conditions and to monitor water hardness. It became evident the need to implement preventive medicine programs and stricter health controls for milking during periods with elevated incidence of subclinical mastitis especially in big herds.

Key Words: milk, microbiologic, physicochemical

M95 Determination of Cd and Pb content on tissues of beef cattle raised in a tropical pasture based system in Brazil. J. R. Lima*[1], M. B. M. Teixeira[2], J. L. B. Silva[2], E. F. Silva[2], R. G. Reis[2], L. R. D. A. Neto[1], H. M. Queiroz[2], and L. G. Nussio[1], [1]*University of São Paulo/ESALQ*, *Piracicaba, Brazil*, [2]*Ministry of Agriculture, Livestock and Food Supply*, *Campinas, São Paulo, Brazil*.

To satisfy the requirements of the international market it is necessary to monitor several quality traits in meat products such as heavy metals. The purpose of this study was to determine Cd and Pb in liver and Pb in kidney tissues of 27 beef steers pasture raised in a tropical grazing system to compare the accumulation of Cd and Pb at the same tissue and Pb in 2 different tissues. The animals were fed at *Brachiaria brizantha* (palisade grass) pastures stocked under a rotational grazing system for 8 mo receiving energy and mineral supplementation sources. They were allocated in 3 treatments with 3 replications up to the finishing period which was taken at feedlot in a random block design. The supplements supplied on pasture were: 1) mineral supplementation (MS) *ad libitum*; 2) MS + ground corn (0.3% of BW); 3) MS + ground corn (0.6% of BW). There was no intentional contamination with Cd and Pb of animal feed, soil or water to provide a positive control and the analyzed heavy metals were checked for all of them. Livers and kidneys samples were taken at slaughter and immediately frozen. The analysis method utilized was previously validated according to Commission Decision 2002/657/EC and Regulation 2007/333/EC and accredited, in accordance with ISO/IEC 17025/2005. Duplicates samples of about 10 g of each tissue were weighted and twice burned at 500°C in a muffle furnace and ashes were washed with HNO_3. The concentration was determined with a graphite furnace atomic absorption spectrometry (GF AAS) technique with quantification limits for Cd and Pb of 22µg/kg and 75µg/kg, respectively. Mean levels for Cd and Pb content in all samples of the liver and Pb in the kidney were bellow acceptable levels (Cd - 500µg/kg and Pb - 500µg/kg on wet basis) established by European Community (Regulation 2006/1881/EC) and bellow the quantification limits too. The lack of contamination of beef livers and kidneys with Cd and Pb suggests the meat from a typical grazing system in Brazil is considered safe based on the European Community regulations.

Support: FAPESP, CNPq

Key Words: heavy metals, beef cattle, graphite furnace atomic absorption spectrometry

M96 Effects of iodine intake and teat dipping practices on milk iodine concentrations. S. I. Borucki Castro*[1], R. Berthiaume[1], A. Fouquet[2], A. Robichaud[2], F. Beraldin[2], and P. Lacasse[1], [1]*Dairy and Swine Research and Development Centre, Agriculture and Agri-Food Canada*, *Sherbrooke, Québec.*, [2]*Food Directorate, Health Products and Food Branch, Health Canada*, *Montréal, Québec.*

A study was conducted to determine the effects of different iodine levels in lactating cow diets and different post dip practices on the concentration of milk iodine. Sixty 3 cows in mid-lactation were assigned to a 3 × 3 factorial with: 0.25, 0.5 and 1.0 mg dietary iodine / kg DM and 3 different post dip managements: chlorhexidine with dip cup, 1% iodine dip cup and 1% iodine spray, for a total of 9 treatments. During the 13-d pre-experimental and the 17-d experimental period, non-iodized sanitizers were used in premilking management or flushing of the milking units. At the end of the pre-experimental period, where all cows were fed 0.5 mg iodine/ kg DM and chlorhexidine was used as post dip, the levels of milk iodine averaged 299.5 (±11.55) µg/kg and no relationship was found with lactation number, days of lactation or milk production. Dietary iodine and milking management both affected milk iodine concentrations ($P < 0.001$). Although teat dipping with 1% iodine had no effect on milk iodine concentration, the same solution applied by spraying greatly increased milk iodine levels ($P < 0.05$). The results from this study confirm that iodine should not be overfed to preserve the safety of milk. Spraying iodine-based teat dipping solutions result in large increases of milk iodine contents and should be avoided.

Table 1. Least square means (LSM) of milk iodine concentrations at the end of 17-d treatment (µg/kg)

	Post milking management		(SEM=42.6)	
Dietary iodine (mg/kg DM; SEM 42.5)	Chlorhexidine - dip	1% Iodine - dip	1% Iodine - spray	Diet (SEM = 24.3)[1]
Low (0.28)	143	201	593	312_a
Recommended (0.53)	261	289	700	417_b
High (0.99)	325	386	665	459_b
Post dip (SEM=24.3)[2]	243_a	292_a	653_b	

[1]LSM in the column with different subscripts differ ($P < 0.05$).
[2]LSM in the row with different subscripts differ ($P < 0.001$).

Key Words: iodine intake, milk iodine, teat dip

M97 Iodine concentrations in feeds in farms with contrasting levels of iodine in milk. S. I. Borucki Castro*[1], P. Lacasse[1], A. Fouquet[2], A. Robichaud[2], F. Beraldin[2], and R. Berthiaume[1], [1]*Dairy and Swine Research and Development Centre, Agriculture and Agri-Food Canada*, *Sherbrooke, Québec, Canada,* [2]*Food Directorate. Health Products and Food Branch, Health Canada*, *Montréal, Québec, Canada.*

In a previous study, iodine concentration of bulk-tank milk in Canada (n = 501 farms) was found to vary considerably and appeared to be influenced by feeding practices. A subset of 200 participating farms was used to determine the relationship between milk iodine concentrations and concentration of this mineral in different feeds and diets of lactating dairy cows. The 30 farms with the lowest (Low) and the 30 farms with the highest (High) levels of iodine in milk were selected. Each of them completed a questionnaire providing information about the feeding management and samples of all feed ingredients, water and bulk tank milk were collected. The iodine offered on each of the farms was estimated using the amount recommended by the software Ration′L and the iodine concentration in the feed sampled and analyzed using inductively coupled plasma mass spectrometry. Milk iodine concentrations averaged 146 (±13.9) µg/kg (Low) and 487 (±44.6) µg/kg (High). Dietary concentrations of iodine offered daily were 33% lower ($P < 0.01$) for the group Low compared with the group High, 1.20 (±0.099) vs. 1.81 (±0.195) mg/ kg DM, respectively. A linear relationship ($P < 0.01$) was found between dietary iodine concentration and milk iodine levels: (y) Milk iodine (µg/kg) = 145 (±66.9) + 113 (±39.4) x (dietary iodine concentration, mg/kg DM). However, the low R^2 (0.15) indicates that other factors such as milking management and the presence of goitrogens, must have affected the concentrations of iodine in milk. Forages supplied approximately 17% of iodine requirements in the average lactating cow diet. Therefore, variation in the iodine content of forages are unlikely to cause iodine overfeeding. Conversely, 27% of mineral mix samples presented iodine concentrations above 100,000 µg/kg DM (and up to 322,000 µg/kg DM). More than 80% of the farms tested fed higher iodine levels than dietary iodine recommendations (0.50 mg iodine/kg DM; NRC, 2001). Our results suggest that iodine supplements should be used with caution in lactating cow diets.

Key Words: iodine, milk iodine, feed ingredients

M98 European Union principles for the risk assessment of feed additives. M. Anguita*, J. Galobart, and C. Roncancio-Peña, *European Food Safety Authority*, *Parma I43121, Italy*.

In the European Union (EU), all feed additives before being placed on the market undergo an authorization procedure as established in the Regulation (EC) No 1831/2003. In this procedure the European Food Safety Authority (EFSA), and in particular the Panel on additives and products or substances used in animal feed (FEEDAP), is the responsible of assessing the safety and the efficacy of the additive. Feed additives are substances, microorganisms or preparations, other than feed material and premixtures, which are intentionally added to feed or water to perform one or more of the following functions: favorably affect the characteristics of feed or animal products, favorably affect the color of ornamental fish and birds, satisfy the nutritional needs of animals, favorably affect the environmental consequences of animal production, favorably affect animal production, performance or welfare or have a coccidiostatic or histomonostatic effect. To be authorized, feed additives should be safe, and therefore should not have (i) an adverse effect on the animal health, human health or the environment, and (ii) should not be presented in a manner which may mislead the user; the additives should also be efficacious. Any person seeking the authorization of an additive should submit an application to the European Commission and a technical dossier to EFSA. The dossier should be compiled following Commission Regulation (EC) No 429/2008 and the guidance documents that EFSA has prepared to help the applicants. The data provided in the technical dossier should allow a complete assessment of (i) the identity of the additive, (ii) the safety for the target animals, for the consumers of food products derived from animals fed diets containing the additive, for those persons handling the additive and for the environment and (iii) the efficacy of the additive, according to the claim made. The scientific assessment carried out by the FEEDAP Panel finishes with the adoption of a scientific opinion which will be the basis for the Commission to grant or deny the authorization of the product for its use in the EU market.

Key Words: additives, assessment, European Union

M99 Development an on-farm technique using lactic acid bacteria as a biomarker to detect of toxins in milk. M. H. Hathurusinghe*[1], A. AbuGhazaleh[2], M. R. Reddy[1], S. A. Ibrahim[1], M. Tajkarimi[1], and D. Song[1], [1]*North Carolina Agricultural and Technical State University*, *Greensboro, NC*, [2]*Southern Illinois University*, *Carbondale*.

Because many dairy farms lack adequate biosecurity there is a risk of intentional contamination of milk with harmful chemicals. Such contamination has potential health risk to the human consumers as well as major economic losses to the country. Most of the existing methods to detect toxins are expensive and time consuming. Thus, there is an urgent need for developing simple on-farm techniques that can detect toxins in raw milk. The objective of this study was to determine the effect of brodifacoum, bromadiolon, strychnine, and sodium cyanide on the growth of selected strains of lactic acid bacteria (LAB) and to test the potential of LAB as a biomarker for early detection of toxins in milk. Three strains of bifidobacteria, one strain of *Lactobacillus rhamnosus* GG and a commercially available yogurt culture were used to detect their sensitivity to selected toxins. Toxins at different concentrations were added into separate tubes containing different strains of bacteria. Samples were incubated at 37°C for 24 h. Milk samples without toxins were used as the control. The turbidity of the sample was recorded at 3, 9 and 24 h intervals. Results showed that *B. longum* was not sensitive to the tested toxins. *B. adolescentis* and *B. breve* were sensitive to the toxins and the inhibition was observed after 24 h. The yogurt culture and *L. rhamnosus* GG were the most sensitive to all the toxins at levels of 1µg/ml and 2µg/ml respectively, except for sodium cyanide which was 0.1µg/ml for both yogurt culture and *L. rhamnosus* GG after 3 h of incubation. These findings suggest that a highly sensitive, environmentally safe, fast and accurate test kit could be developed using selected LAB as a universal biomarker.

Key Words: toxin, lactic acid bacteria, biomarker

M100 Food safety in developing countries using no technology: The Wagashi study case. F. La Terra[1], G. Belvedere[1], M. Manenti[1], C. Pediliggieri[1], S. Mirabella[1], J. C. Codjia[2], S. Doko[3], and G. Licitra*[1,4], [1]*CoRFiLaC, Regione Siciliana*, *Ragusa, Italy*, [2]*University of Abomey-Calavi*, *Benin*, [3]*University of Parakou*, *Benin*, [4]*DACPA, Catania University*, *Catania, Italy*.

The Wagashi cheese, produced in Benin from Peuhl communities, is a cheese that has a homogeneous structure and can be found usually in round shaped 300 to 800 g pieces. To produce Wagashi cheese, milk coagulation occurs at temperatures higher than 70°C. This allows a first thermic treatment of milk extremely important when production hygiene conditions cannot be controlled. Fresh milk is first heated at 60°C for 5 min. After, a vegetal coagulant extracted from the latex of *Calotropis procera* leaves is added and temperature is raised and maintained at 95°C for 3 to 5 min until curd separates from whey. The latex of *Calotropis procera* is used to produce the Wagashi cheese with very low proteolytic activity that allows boiling the cheese over and over again, every 2 d, for about 20–30 d since it has been produced. This simple practice makes the cheese safe. Alternatively, cheese can be sun-dried to extend shelf life. The aim of this study was to assess variations of chemical, biochemical, and microbiological properties of Wagashi cheese, to evaluate the food security conditions. Production conditions and processes were reproduced and monitored in a laboratory trial. Eleven 500-g cheeses were produced using cow raw milk. Cheeses were sampled after cheese making process and, after 24h and 48h, before and after boiling for 10, 20, and 40 min. Cheese samples were analyzed for pH, soluble proteins (TCA 12%), soluble proteins pH 4.6, fat, total nitrogen, urea PAGE, total bacteria count (TBC), total and fecal coliform count, and *S. aureus* count. After 24h, 10-min boiling were sufficient to reduce TBC in the center of the cheese from 3.5×10^3 to 10^2 cfu/g. After 48h, 10-min boiling reduced TBC from 1.10×10^6 to 6.30×10^4 cfu/g, whereas 20 min were necessary to reduce TBC to 10^1 cfu/g. The proteolytic profiles of Wagashi cheese obtained before and after boiling treatment were in overlapping, confirming the low proteolytic activity. The results showed how the temperature during cheese making is an important factor for the microbiological food safety and in addition the re-boiling process for 20 min each 48h guarantee its shelf-life for several days.

Key Words: food safety, proteolysis, Wagashi cheese

M101 Stress-induced adaptive tolerance response influences virulence in *Campylobacter jejuni*. G. S. Kumar*, I. Hanning, Y. Ma, and M. Slavik, *University of Arkansas*, *Fayetteville*.

Campylobacter jejuni, the major cause of human gastroenteritis, is a fragile bacterium requiring special conditions in the laboratory for its growth. In nature, however, this organism is able to survive in very diverse and hostile environments and produce disease in humans. The mechanisms that the organism has evolved for its survival in stressful conditions are not fully understood. To determine the effect of acid stress on *C. jejuni*, 4 different strains of *C. jejuni* were exposed to an acid pH of 5.5 and then re-challenged with a pH of 4.5. Acid-adapted cells were found to have higher viability to survive further acid stress, but adaptation and survival were time-dependent. The effects of starvation stress also were studied. Expression of virulence gene *cadF* was upregulated by starvation stress, while virulence genes *cdtB* and *ciaB* were downregulated. Adhesion and invasion are thought to be important factors for the colonization of *C. jejuni* in the intestinal tract of host. In vitro studies with INT 407 tissue culture model (mammalian intestinal cells) were conducted with different times of exposure to acid (2h and 3h), to determine the effects of stress on adhesion and invasion of *C. jejuni*. All the tissue culture experiments were performed in replicates of 3. Results indicated that acid-adapted bacteria had increased adhesion and invasiveness, but varied with the strains and the time of exposure to the acid. Exposure of acid-adapted *C. jejuni* to further stress of starvation for 24 h did not have any significant difference in the adhesion and invasion abilities as compared with cells exposed to starvation stress only. These results indicate that *C.jejuni* surviving stress may be more resistant to further stress such as passage through the human gastrointestinal tract and that stress may be a significant factor in inducing some virulence genes.

Key Words: *C. jejuni*, stress, acid-adapted

M102 *Salmonella* Enteritidis challenge in chicks of different genotypes. P. E. N. Givisiez*[1], E. G. Santos[1], F. G. P. Costa[1], J. H. V. Silva[1], and A. Berchieri Jr.[2], [1]*Universidade Federal da Paraiba*, *Areia, PB, Brazil*, [2]*Universidade Estadual Paulista*, *Jaboticabal, SP, Brazil*.

Alternative poultry production is a promising business for small farmers, who should choose breeds based on robustness, consumer concerns and health issues. This study evaluated the resistance of Cobb and Naked Neck birds fed 2 threonine levels and challenged with *Salmonella* Enteritidis at 2 d of age. Twenty Cobb chicks (CC) and 20 naked neck chicks (NN) were distributed into a completely randomized design according to a 2 × 2 factorial (2 genotypes and 2 threonine levels) and 8 repetitions. Antibiotic-free corn-soybean diets with 0.821 and 0.917% digestible threonine were used. The birds were inoculated with *Salmonella* Enteritidis $^{Nal++}$ (1.2×10^8 CFU.mL^{-1}) and killed at 10 d of age for performance evaluation and bacterial counts (CFU.g^{-1}), which were

transformed into Log10. Data were subjected to ANOVA and means were compared using Tukey's multiple comparison test ($P < 0.05$). There was no interaction between genotype and threonine level ($P > 0.05$). Lower *Salmonella* counts ($P > 0.01$) were seen for NN compared with CC (1.37 vs 6.91). Furthermore, 94% of CC (15/16) and 25% (4/16) of NN were positive for salmonella counts. Body weight and weight gain were higher ($P < 0.01$) for CC (250.13 vs 120.19 g and 206 vs 77.75 g, respectively). Although threonine has been suggested to help diminishing enteric pathogen infection, higher threonine levels had no effect on salmonella counts or performance. The results corroborate the need of *Salmonella* control during the first week of rearing, since birds contaminated during this period may be infected until slaughter and there is potential risk for consumers. NN was best fitted for alternative production, considering the higher resistance to infection by *Salmonella* and slower growth rate. In conclusion, naked neck chicks were more resistant to *Salmonella* Enteritidis than Cobb independent of threonine dietary levels.

Key Words: alternative poultry, salmonellosis, nutrition

M103 Effect of feeding distillers dried grains to lactating cows on farms in the southern dairy region of Chile. R. Shaver*[1], R. Ehrenfeld[2], M. Olivares[2], J. Cuellar[3], and F. Inostroza[1], [1]*University of Wisconsin*, *Madison,* [2]*Cooprinsem*, *Osorno, Chile*, [3]*US Grains Council*, *Bogota, Columbia*.

A field trial was conducted on 5 farms to determine the effect of feeding distillers dried grains (DDGS) on milk production in the southern dairy region of Chile. The trial was repeated on each farm during winter (July and August; primarily silage-based rations) and spring (November and December; pasture-based rations). Only for one farm could the treatments be applied concurrently by feeding different isonitrogenous concentrate mixes to randomly assigned cows in the milking parlor with data analyzed as a randomized complete block design. Milk yield tended ($P < 0.07$) to be greater for cows fed DDGS (2.0 kg/cow per d) by 1.9 kg/d in winter and 1.8 kg/d in spring. In winter, milk protein yield was ($P < 0.02$) greater for cows fed DDGS by 73 g/d. Milk fat content was ($P < 0.01$) lower for cows fed DDGS by 0.26%-units in the spring, however, milk fat yield was unaffected by treatment. The 4 farms that could not apply the treatments concurrently were randomly assigned to either a control to DDGS or a DDGS to control isonitrogenous concentrate treatment sequence in a crossover design with monthly feeding periods during the winter and spring. Data were analyzed as a crossover design with farm as the experimental unit. Milk yield was ($P < 0.05$) greater for farms fed DDGS (2.5 kg/cow per d) by 0.9 kg/d in winter. We conclude that DDGS was an effective dairy concentrate ingredient in the southern dairy region of Chile.

Key Words: pasture, dairy cows, distillers grains

M104 Yield and quality of grasses and legumes for dairy cattle feeding. E. E. Corea Guillén*[1], J. M. Flores Tensos[1], F. M. Salinas Munguia[1], E. A. Crespin Payés[1], and J. A. Elizondo-Salazar[2], [1]*Departamento de Zootecnia, Facultad de Ciencias Agronómicas, Universidad de El Salvador, El Salvador,* [2]*Estación Experimental Alfredo Volio Mata, Facultad de Ciencias Agroalimentarias, Universidad de Costa Rica, Costa Rica.*

Forages used in a cut-and-carry system are a very important feed resource for dairy cattle in El Salvador and many areas of Central America. However, forages are extremely variable in terms of yield and quality and they are usually low in CP content. Planting legumes mixed with grasses is a management practice to take advantage of their unique ability to bind atmospheric N and to improve the quality of the forage when harvested. This study was conducted to determine yield and quality of 2 forages, 2 legumes and a 1:1 sward mixture between them. Two varieties of Sorghum (*Sorghum bicolor* var. CENTA S-2 and *Sorghum bicolor* var. RCV) and the legumes Canavalia (*Canavalia ensiformis*) and Vigna (*Vigna sinensis*) were used in the study. Forages were established in 12 × 12-m plots with 3 replications in a randomized block design. Seeding rate was 250000, 250000, 50000, and 75000 plants/ha for S-2, RCV, Canavalia and Vigna, respectively. They were planted in different days so that they would be harvested at maturity age (75, 70, 80, and 60 d for S-2, RCV, Canavalia and Vigna, respectively). Samples were taken at maturity age to estimate yield and for determination of DM yield, DM, CP, NDF, and ADF concentration. Variables were analyzed using GLM procedure of SAS 9.1. Separation of means was done using the Duncan's multiple comparison procedure. There were differences ($P < 0.01$) between treatments for all variables studied. Grasses produced more available DM (kg/ha) than legumes. Legumes had higher CP content than grasses as expected. The findings of the study corroborate that grasses (S-2 and RCV) produced more biomass than legumes and that a mixture of both is a way to improve the yield of the legume alone and the quality of the grass alone.

Table 1. Yield and quality of grasses and legumes

Forage	Available DM, kg/ha	DM, %	CP, %	NDF, %	ADF, %
Sorghum					
S-2	15970.8[a]	17.9[a]	10.2[d]	67.3[c]	44.0[bc]
RCV	8941.1[c]	16.3[ab]	11.5[cd]	71.5[a]	42.4[e]
Legume					
Canavalia	6133.5[d]	16.2[ab]	17.4[a]	56.3[f]	45.2[a]
Vigna	3146.8[e]	10.0[c]	16.9[a]	52.7[g]	39.3[f]
Mixture					
S2_Canavalia	12938.9[b]	18.1[a]	11.7[cd]	67.8[c]	42.9[de]
S2_Vigna	12102.6[b]	15.4[b]	14.6[b]	68.7[b]	44.6[ab]
RCV_Canavalia	9500.8[c]	17.0[ab]	14.6[b]	66.0[d]	43.5[cd]
RCV_Vigna	8978.2[c]	15.1[b]	13.7[bc]	63.4[e]	39.4[f]

[a-g] $P < 0.01$, comparing least squares means within column.

Key Words: grasses, legumes, forages

M105 Quality of ensiled grasses and legumes for dairy cattle feeding. E. E. Corea Guillén*[1], J. M. Flores Tensos[1], F. M. Salinas Munguia[1], E. A. Crespin Payés[1], and J. A. Elizondo-Salazar[2], [1]*Departamento de Zootecnia. Facultad de Ciencias Agronómicas*, *Universidad de El Salvador, El Salvador*, [2]*Estación Experimental Alfredo Volio Mata. Facultad de Ciencias Agroalimentarias*, *Universidad de Costa Rica, Costa Rica*.

Silage is an excellent way to preserve forages at the optimum stage of growth for use during a time when it is unavailable. This is very important in all Central American countries in which there is a very marked dry season. However, it is well known that nutritional quality of grasses is not high and studies have demonstrated the superiority of grass-legume silages in comparison with grass silages. There is also a growing interest in organic and low-input production systems. A study was conducted to assess the nutritional value and quality of microsilages prepared from different combinations of grasses and legumes. A completely randomized design was used with 2 varieties of Sorghum (*Sorghum bicolor* var. CENTA S-2 and *Sorghum bicolor* var. RCV) and 2 legumes Canavalia (*Canavalia ensiformis*) and Vigna (*Vigna sinensis*). Forages were harvested at maturity age (75, 70, 80, and 60 d for S-2, RCV, Canavalia and Vigna, respectively). Seven kg of fresh-chopped forages in the proportions of 100:0, 70:30, and 50:50% w/w for grass and legume respectively, were placed in plastic bags in triplicate. Air was extracted by compacting the forage mass and bags were tightly sealed. Microsilages were open after a 21 d period and a sample was taken to determine pH, and for DM, CP, NDF, and ADF concentration. Variables were analyzed using GLM procedure of SAS 9.1. Separation of means was done using the Duncan's multiple comparison procedure. There were significant differences ($P < 0.01$) for the variables studied among the different mixtures. pH was among accepted values. Dry matter content was highest when grasses were ensiled alone. CP values were higher when a 50:50 proportion was used. Differences in the chemical composition of these silages reflect variations in the proportion of each forage type.

Table 1. pH and quality of ensiled forages

Proportion	pH	DM, %	CP, %	NDF, %	ADF, %
100:0					
S2_Canavalia	3.7[a]	23.1[a]	8.4[a]	61.7[a]	38.6[a]
RCV_Canavalia	3.6[b]	24.0[a]	8.0[a]	52.1[b]	33.5[b]
70:30					
S2_Canavalia	3.8[ab]	23.1[ab]	10.9[a]	57.1[b]	37.8[b]
S2_Vigna	3.9[a]	21.0[b]	9.7[b]	61.1[a]	40.4[a]
RCV_Canavalia	3.8[ab]	23.4[a]	10.8[a]	56.1[bc]	37.6[b]
RCV_Vigna	3.7[b]	21.7[ab]	9.9[b]	55.9[c]	35.3[c]
50:50					
S2_Canavalia	4.1[a]	21.5[a]	12.7[ab]	62.6[a]	42.3[a]
S2_Vigna	4.0[b]	18.5[b]	11.6[b]	60.9[b]	42.4[a]
RCV_Canavalia	4.0[b]	21.3[a]	13.3[a]	57.9[c]	40.3[b]
RCV_Vigna	4.1[a]	19.0[b]	13.8[a]	54.3[d]	34.7[c]

[a-c]$P < 0.01$, comparing LSM.

Key Words: microsilage, grasses, legumes

M106 Chewing and ruminating with various forage qualities in non-lactating dairy cows. M. Fustini*[1], A. Palmonari[1], A. J. Heinrichs[2], and A. Formigoni[1], [1]*Università di Bologna*, *Bologna, Italy*, [2]*Department of Dairy and Animal Science*, *The Pennsylvania State University, University Park*.

In Parmigiano Reggiano cheese area use of silages is not allowed. Thus, hay is the sole source of fiber in these diets. Forage quality strongly affects eating behavior, in particular if hay is represented by alfalfa. This study investigated typical dry forage diets used in the Parmigiano Reggiano area. Six multiparous, non-lactating Holstein cows were used in a replicated 3 × 3 Latin square to evaluate 3 different cuts of alfalfa hay fed as the sole forage source. First diet contained a first cut forage, while a second cut (poorly digestible) and a fifth cut (highly digestible) were used in the second and third diet. Eating and ruminating behavior were studied to investigate forage properties related to chewing activity. Digestibility was evaluated in vitro using the Tilley and Terry technique. Statistical analysis was conducted using PROC MIXED of SAS. No differences were found in eating time (average value 220.5, 261.7, 235.5 min/d for 1st, 2nd and 3rd diet respectively, $P > 0.05$); however, ruminating time per kilogram of physically effective neutral detergent fiber was greater when cows were fed first cut alfalfa than second or fifth cut (average value 136.1, 111.2, 107.1 min/d for 1st, 2nd and 3rd diet respectively, $P < 0.05$), despite not different digestibility and diet particle size of first and third diet (% dNDF 24h average values 50.44, 48.38 for 1st and 3rd diet respectively, $P > 0.05$). In summary, this study found no differences in eating time for the 3 hays fed. Ruminating time was not related to overall nutrient composition or digestibility of the hay, but varied by cutting with first cutting hay promoting more rumination.

Key Words: eating behavior, ruminating, forage quality

M107 The effect of management on corn silage quality. L. O. Abdelhadi*[1], C. A. Malaspina[2], W. R. Barneix[2], P. A. Saravia[2], and C. de Elia[3], [1]*Est. El Encuentro, Research & Extension in Ruminant Nutrition*, *Cnel. Brandsen, Bs.As., Argentina*, [2]*CACF*, *Argentina*, [3]*Alltech Biotechnology*, *Argentina*.

When formulating diets, corn silage quality is usually evaluated from samples taken before feedout and exposure to air, underestimating the losses related to exposure, extraction, mixing and feeding. A completely randomized design with a 3x2 factorial arrangement of treatments was used to evaluate the effects of silo type and sample location on CS nutrient composition in 12 commercial dairy and beef farms. Corn silage was manufactured in either bunker (n = 6) or bag (n = 6) silos, was inoculated with 5g/ton of Sil-All and sealed with plastic for 45d before feed out. The feed out rate was 0.2 to 0.3m twice daily for all bags and bunkers. Composite samples for analysis were collected from 3 locations: Depth = sample taken at 1m depth from the exposed face; Face = sample taken from the surface of the exposed face; and Feed bunk (FB) = sample taken from the FB after exposure to air for 3 to 4 h. Samples from the center of the silo were collected using a forage sampler at 0.5, 1.0 and 1.5 m from the floor. Sub samples were hand-mixed, divided into equal quarters, with 2 opposite quarters selected to obtain the composite sample including the fines. Samples were analyzed for DM, OM, NDF, WSC, CP, Starch, pH and in vitro DM digestibility (IVDMD). Although no effects of sampling location were detected for most variables, IVDMD tended ($P = 0.07$) to be reduced from Depth to FB, independently of silo type. This reduction seemed to be associated with a higher pH ($P = 0.09$) from depth to FB. These results suggest that CS extraction and distribution negatively affect the nutritional quality and this change should be considered for a more accurate diet formulation.

Table 1. Corn silage quality by sampling site or type of silo

	Sampling site (n=12)				Type of silo (n=18)		
Variable	Depth	Face	FB	SE	Bunker	Bag	SE
DM, %	31.9	30.7	32.3	2.32	33.1	30.1	1.89
% on DM basis							
OM	93.5	93.1	92.5	0.66	92.7	93.4	0.54
NDF	44.2	46.6	48.2	2.21	48.4a	44.3b	1.81
WSC	6.7	5.6	5.6	0.86	5.8	6.1	0.70
CP	5.9	5.9	6.2	0.41	5.9	6.2	0.34
Starch	16.9	13.2	13.5	3.51	15.0	14.0	2.87
IVDMD	70.9a	68.4b	67.5c	1.49	69.5	68.5	1.21
pH	3.88b	3.87b	4.03a	0.08	3.98	3.88	0.06

[abc]Means within a row with unlike letters differ ($P < 0.09$). SE= standard error (diff. of 2 means).

Key Words: corn silage, management, quality

M108 Whole-plant corn quality parameters for ensiled and unensiled samples: Effects of hybrid and length of fermentation. C. M. Fish*[1,2], R. D. Shaver[1], D. C. Weakley[2], J. G. Lauer[1], and T. E. Piper[2], [1]*University of Wisconsin*, *Madison,* [2]*Land O' Lakes Inc.*, *Shoreview, MN*.

Most corn hybrid trials use unensiled samples for laboratory analysis of forage quality parameters. The purpose of this study was to determine the effect of ensiling on ranking hybrids for silage quality. Twenty-nine corn hybrids of differing genetic backgrounds from early, mid, and late relative maturity groups were planted in replicated field test plots using a randomized complete block design at Lancaster, Plymouth and West Salem, WI. During harvest at 30–35% whole-plant DM content, 3 400-g samples were obtained from each field test plot; one sample was immediately refrigerated (0 d fermentation) for no more than 48 h before drying and 2 were ensiled in 25 cm by 33 cm vacuum-sealed bags stored at room temperature at the Land O'Lakes warehouse in Vincent, IA for 30 d or 120 d fermentation times. Refrigerated and ensiled samples were dried in a forced-air oven at 43–46°C for 48 h, ground on a Wiley mill to pass a 6mm screen, and analyzed using the Perten Diode Array 7200 NIR Analyzer. Parameters analyzed were starch, NDF, ivNDFD (30 h; % of NDF), and an index of in vitro starch digestibility (GPN).

Quality data were used to calculate milk per ton (MPT; kg per US ton; MILK2006). Data were analyzed using Proc Mixed in SAS with fixed effects of fermentation, hybrid and their interaction, and random effects of location, replication, and location interactions. Maturity trial averages and P-values for quality parameters are presented in the Table. Hybrid differences were detected for most parameters. There was a significant effect of fermentation on NDF, ivNDFD, GPN and MPT. However, interactions between hybrid and fermentation were not detected. Unensiled sample data may be used in quality evaluation trials for ranking corn silage hybrids, but fermentation influences silage quality parameter results.

Table 1. Maturity trial averages and P values for main effects and interaction

	NDF%	ivNDFD%	Starch%	GPN	MPT, kg/ton
Early Trial Avg	39.5	45.6	35.9	8.13	1502
Hybrid	0.159	0.029	0.122	0.785	0.073
Ferm	0.120	<.0001	0.349	0.014	0.024
Ferm*Hybrid	0.999	0.998	0.993	0.432	0.999
Mid Trial Avg	38.6	48.4	37.0	8.01	1540
Hybrid	<.0001	<.0001	0.0002	0.070	0.006
Ferm	0.059	0.011	0.476	0.007	0.009
Ferm*Hybrid	0.701	0.582	0.926	0.010	0.641
Late Trial Avg	38.4	46.9	38.7	8.09	1537
Hybrid	0.015	0.046	0.001	0.226	0.169
Ferm	<.0001	0.032	0.157	0.052	0.011
Ferm*Hybrid	0.985	0.994	0.967	0.253	0.995

Key Words: corn silage, starch, NDF

M109 Fermentation characteristics of corn-lablab bean silage mixtures. F. E. Contreras-Govea*[1], M. A. Marsalis[2], S. V. Angadi[3], G. R. Smith[4], and L. M. Lauriault[5], [1]*New Mexico State University, Plant and Environmental Sciences Department*, *Artesia,* [2]*New Mexico State University, Extension Plant Sciences Department*, *Clovis,* [3]*New Mexico State University, Plant and Environmental Sciences Department*, *Clovis,* [4]*Texas AgriLife Research, Texas A&M University System*, *Overton,* [5]*New Mexico State University, Plant and Environmental Sciences Department*, *Tucumcari.*

The objective of this study was to assess the fermentation characteristics of corn (*Zea mays* L.) when in mixture with different proportions of lablab bean (*Lablab purpureus* (L.) Sweet) for silage. Corn and lablab bean cv Rio Verde were grown in separate fields at 2 locations in 2009. Corn was harvested between 1/3 and 1/2 milk line and lablab between 5% and 15% bloom. Corn and lablab bean were chopped to a theoretical length of 25-mm. Chopped samples of both crops were hand mixed on per cent fresh weight basis to obtain 6 corn-lablab composite mixtures, 1) 100–0, 2) 90–10, 3) 75–25, 4) 50–50, 5) 25–75, and 6) 0–100. Mixtures were ensiled in 1-L glass jars at a density of 500-g of fresh material per jar. Four replications per treatment were included at each location. Mini-silos were fermented for 60 d at room temperature (25°C). At opening 250-g of fresh silage was vacuum sealed in plastic bags, frozen, for later analysis of fiber and fermentation characteristics. Data analysis was conducted as a randomized complete design for each location. Crude protein ($P < 0.01$) increased from 8.0% to 20.0% as the proportion of lablab bean increased in the mixture at both locations. At Location 1 NDF ($P < 0.003$) decreased and at Location 2 ($P < 0.01$) increased as lablab increased in mixture. At location 2, 48 h in vitro DM digestibility decreased from 87.3% to 81.3% as lablab increased in mixture, with no differences at the Location 1 ($P > 0.634$). Silage pH ($P < 0.0001$) and lactic acid concentration ($P < 0.01$) increased as well as the proportion of lablab increased in the mixture at both locations. Mixing lablab bean with corn for silage can potentially reduce protein supplementation requirements in dairy cow rations.

Key Words: corn, lablab bean, silage fermentation

M110 Fermentation characteristics of forage sorghum-lablab bean silage mixtures. F. E. Contreras-Govea*[1], M. A. Marsalis[2], S. V. Angadi[3], G. R. Smith[4], and L. M. Lauriault[5], [1]*New Mexico State University, Plant and Environmental Sciences Department*, *Artesia,* [2]*New Mexico State University, Extension Plant Sciences Department*, *Clovis,* [3]*New Mexico State University, Plant and Environmental Sciences Department*, *Clovis,* [4]*Texas AgriLife Research, Texas A&M University System*, *Overton,* [5]*New Mexico State University, Plant and Environmental Sciences Department*, *Tucumcari.*

The objective of this study was to assess the fermentation characteristics of forage sorghum (FS) [*Sorghum bicolor* (L.) Moench] for silage when in mixture with different proportions of lablab bean (*Lablab purpureus* (L.) Sweet) cv Rio Verde. Forage sorghum and lablab were grown in separate fields at 2 locations in 2009. Forage sorghum was harvested between soft and late dough stage of the kernel and lablab bean between 5% and 15% bloom. Forage sorghum and lablab were chopped to a theoretical length of 25 mm. Chopped crops were hand mixed on per cent fresh weight to obtain 6 FS-lablab composite mixtures, 1) 100–0, 2) 90–10, 3) 75–25, 4) 50–50, 5) 25–75, and 6) 0–100. Mixtures were ensiled in 1-L glass jars at a density of 500-g of fresh material per jar. Four replications per treatment were included at each location. Mini-silos were fermented for 60 d at room temperature (25°C). At opening, 250-g of fresh silage was vacuum sealed in plastic bags, and frozen for later analysis of fiber and fermentation characteristics. Data analysis was conducted as a randomized complete design for each location. Over both locations CP ($P < 0.0001$) and IVTD ($P < 0.01$) increased from 9.0% to 20.6% and from 79% to 85% respectively, as the proportion of lablab bean increased in the mixture. However, ADF ($P < 0.0001$) also increased with the addition of lablab bean in the mixture. Lactic ($P < 0.0001$) and Acetic ($P < 0.0001$) acids, and pH ($P < 0.0001$) also increased with the addition of lablab in the mixture. Mixing lablab bean with FS for silage can potentially reduce protein supplementation in rations for dairy or beef cattle and improves digestibility of the silage.

Key Words: forage sorghum, lablab bean, silage fermentation

M111 Growing degree-days as corn silage harvest indicator. J. S. Oliveira*[1], E. J. D. de Almeida[2], F. C. F. Lopes[1], and E. C. M. de Lanes[3], [1]*Embrapa Gado de Leite*, *Juiz de Fora, MG, Brazil*, [2]*Universidade Federal de Juiz de Fora*, *Juiz de Fora, MG, Brazil*, [3]*Centro de Ensino Superior de Juiz de Fora*, *Juiz de Fora, MG, Brazil*.

Dry matter content (DM%) at harvesting is important to have high quality corn silage. Ideal DM% ranges from 31 to 35 for bunker silos. Methods used by farmers to estimate DM% of corn crop are laborious or not reliable. This research studied the relation between growing degree-days (GDD) and DM% in different corn hybrids and its use as a tool to predict DM% in a corn crop. The field work was done at National Dairy Center Research, EMBRAPA, Coronel Pacheco, MG, Brazil. Six hybrids were planted in 4 dates (12/15/2004, 01/14/2005, 10/26/2005, 11/24/2005) using a casual block design and 3 replications. The experimental unit was a line 20 m long with 90 plants. After the eightieth day, 5 plants were sequentially harvested every 3 d from each line for dry matter content determination (DM%). Starting at seedling, maximum and minimum daily temperatures were recorded and used to calculate GDD using the formula GDD = [(Tmax - Tmin) / 2] - TB,

where TB is the base temperature, considered 8 for that region. Pairs of DM% and GDD originated a linear regression equation to estimate the required GDD for plants of each experimental unit reach 33% dry matter (GDD33). From the 72 equations, only 5 presented *P* value higher than 0.01 for parameter b. The GDD33 of only one of the 6 hybrids was affected ($P < 0.05$) by planting date. Also, GDD33 average was different ($P < 0.05$) between hybrids. Considering 80% precision, the error when using GDD33 to estimate 33% of DM varied from ± 2 (one hybrid) to ± 3 (5 hybrids) DM% units. Because DM content for ensiling must be in a range and not a fixed value, GDD seems to be a reliable tool to predict the proper time for corn silage harvest. This information should be included by seed companies when recommending a corn hybrid for silage.

Funded by FAPEMIG.

Key Words: growing degree units, dry matter, hybrids

M112 Production and quality of alfalfa harvested at different stages of maturity. R. Copado[1], C. Arzola*[1], J. A. Payan[2], J. Salinas[3], O. Ruiz[1], C. Rodriguez-Muela[1], E. Rodriguez[1], J. A. Ortega[1], and O. Serna[2], [1]*Universidad Autonoma de Chihuahua*, *Chihuahua, Chih., Mexico*, [2]*INIFAP*, *Chihuahua, Chih., Mexico*, [3]*Universidad Autonoma de Tamaulipas*, *Cd. Victoria, Tams., Mexico*.

To evaluate the effect of maturity upon the nutritional quality of 2 varieties of alfalfa ("Cuff-101" and "Excellent multileaf") harvested on 2 seasons (summer and fall), the production (kg/ha) and quality of forage was characterized. There were determined the leaf/stem ratio of biomass and its content of dry matter, crude protein, neutral detergent fiber, acid detergent fiber and lignin over a range of maturity following an initial phenologic stage characterized by an average stem length of about 0.3 m, (but not visible buds, flowers, or seedpods) within the 2 seasons. Within each season, plots were clipped initially (d 0) and then additional sampling dates were scheduled at 5-d intervals for the next 20 d, resulting in a total of 5 clipping dates (0, 5, 10, 15, and 20 d). Data were analyzed as a split-plot experiment, the plots arranged factorially in a randomized complete block design, being the alfalfa varieties and season the main effects, and maturity the subplot term. Season influenced both production and forage quality, so during the fall the production of dry matter was lower ($P < 0.01$). On d 20 in summer a yield of 5.8 ton MS/ha was registered and in fall only 4.9 ton MS/ha, without differences among varieties ($P > 0.05$). Dry matter crude protein (CP) content of leaves in fall in growing stage was 35.0% on d 0, whereas stem's was 25.3% and whole plant was 31.8%. In summer, CP was 32.7% in leaves, 22.6% in stems and 29.3% in the whole plant. On the 20 d (flowering stage) of fall the leaves had 25.4% CP, stems 20.2% and whole plant 23.7%, compared with 23.5%, 19.1% y 21.6% CP in summer, respectively. Contents of FDN and FDA diminished ($P < 0.01$) in fall, due to a dilution effect or an observed diminution of fiber for a rapid accumulation of biomass. In summer, the accumulation of biomass on both varieties was larger than 4 ton/ha of DM. It was concluded that the best quality of forage is obtained during fall regardless of variety, but yield is lower. With the advancement of maturity, nutritional quality of alfalfa diminished, whereas production increased.

Key Words: alfalfa, stage of maturity, nutritional quality

M113 Gas production profiles of two varieties of alfalfa harvested on different stages of maturity. O. Serna-Beltran[1,2], C. Arzola*[1], E. Santellano-Estrada[1], J. A. Payan-Garcia[2], A. Corral-Luna3,1, O. Ruiz[1], C. Rodriguez-Muela[1], and J. Salinas[4], [1]*Universidad Autonoma de Chihuahua*, *Chihuahua, Mexico*, [2]*Instituto Nacional de Investigaciones Forestales, Agricolas y Pecuarias*, *Delicias, Chihuahua, Mexico*, [3]*Department of Animal Sciences-University of Illinois at Urbana-Champaign*, *Illinois*, [4]*Universidad Autonoma de Tamaulipas*, *Reynosa, Tams. Mexico*.

Alfalfa (*Medicago sativa*) dry matter is readily fermented in the rumen. Even though this phenomenon has been extensively studied in relation to the effects of the conservation method, there are not many studies regarding the effect of maturity upon the rumen degradability of alfalfa hay. The objective of this study was to assess the effect of maturity, expressed as time of harvest over a range of sampling periods (0, 5, 10, 15, and 20 d following Stage 2, (when stem length was > 0.40 m, but no buds, flowers, or seedpods were visible) of 2 varieties ("Excellent 9HQ and "Excelent multifoliar 9HQ ML," AgriBioTech) on 4 seasons (spring, early and late summer, and fall). An exclosure was sub-divided on 5 stripes on each of 8 locations of Delicias, Chih., Mexico, and sampled within 5 d intervals after an initial cut. Data were analyzed with a sub-plot design, with variety and period as main effects and day of cutting as sub-plot term. Statistical analysis used the GLM procedure of SAS. Gas production data were adjusted with the monophasic model of Groot, using proc NLIN of SAS. Linear, quadratic, cubic and quartic effects tests were performed for forage composition traits and gas production kinetics parameters within each maturity stage. There were not differences among varieties ($P > 0.05$) in the content of crude protein (CP), neutral detergent fiber (NDF), acid detergent fiber (ADF) and acid detergent lignin (ADL). As maturity advanced, CP decreased linearly ($P < 0.001$), yet NDF, ADF, and ADL increased ($P < 0.001$) linearly. Maturity had also a strong effect upon the ruminal degradability of alfalfa as assessed with gas production profiles. A significant linear tendency ($P < 0.01$) was found for both A (gas production asymptote) and B (time after incubation at which half of the asymptotic amount of gas has been formed) parameters increasing as maturity advanced. Parameter C (a constant determining the sharpness of the switching characteristic of the profile) declined, showing linear ($P < 0.01$) effects.

Key Words: alfalfa, degradability, maturity

M114 Can different ME estimation methods give different values for tanniferous forages? H. Khalilvandi-Behroozyar*[1,2], M. Dehghan-Banadaky[1], and K. Reza Yazdi[1], [1]*Department of Animal Science, University of Tehran*, *Karaj, Tehran, I.R. Iran*, [2]*Department of Animal Science, University of Urmia*, *Urmia, West Azerbaijan, I.R. Iran*.

Condensed tannins (CT) are antinutritional factors, reduced nutrient digestibility by binding them and probably can disrupt digestibility estimation methods. To determine any possible effects, experiments carried out with different methods for estimating metabolizable energy of sainfoin. Forages were taken from farms in Isfahan and representative dry samples were analyzed for DM, OM and CT. For gas production test, 2 mm sieved samples, were used in Triplicates and 2 separated runs. Rumen fluid was obtained from 2 maintenance level fed, rumen fistulated Taleshi cows. 24h gas production data were used for calculation of ME content by follow equations: 1) $ME = 2.2 + 0.1357GP_{24} + 0.0057CP + 0.0002859CP^2$, 2) $ME = 2.2 + 0.136GP_{24} + 0.057CP + 0.0029CF^2$ & 3)%OMD = $14.88 + 0.8893GP_{24} + 0.0448CP + 0.0651$ash. For in vitro digestion trial, samples milled through a 1 mm sieve. Two separated runs, each in triplicates and 3 jars as blank, applied. ME estimated using ME = 0.0157 × DOMD. Also, an in vivo digestibility trial (17 d, with7

d for fecal collection) was done using 3 ruminally fistulated Holstein cows. Forages were fed as sole diet at 10% above maintenance energy requirements. Total fecal collection and marker assay including AIA and Cr_2O_3 (5 gr infused from ruminal fistula, d 8 to 14) were done for determining OM digestibility. Data were analyzed by GLM procedure of SAS 9.1 with CRD design and Duncan test ($P \leq 0.05$). CT content was 21.3 g/kg DM. Estimated ME from in vitro digestion trial was 10.11 and mean estimations from gas production and in vivo trial was 7.19 and 8.75 MJ kg^{-1} DM. No significant differences were exist between different ME estimates of gas production or between in vivo methods. Also, OM digestibility in in vitro was higher than values determined by in vivo and gas production profiles. Higher OM digestibility values for filtration based methods can be explained by rapid passing of phenols throughout filter paper that take part in digestible fraction. It seems that in vitro digestibility trial overestimate OM digestibility of tanniferous forages and cannot be used efficaciously and precisely for estimation of ME in high tannin forages.

Key Words: sainfoin, tannin, ME

M115 Ruminal degradability of nutrients in Sainfoin, a tanniferous legume forage. H. Khalilvandi-Behroozyar*[1,2], K. Reza Yazdi[1], and M. Dehghan-Banadaki[1], [1]*Department of animal Science, University of Tehran*, *Karaj, Tehran, I. R. Iran*, [2]*Department of animal Science, University of Urmia*, *Urmia, West Azerbaijan, I.R. Iran*.

Sainfoin (*Onobrychis viciifolia* Scop.), a nonbloating member of the Fabaceae family. Information regarding nutritive value of sainfoin is scarce, that limit its use in balanced rations. This experiment was done using second cut, mid bloom forage samples taken from farms in Isfahan, Iran for determining degradability of sainfoin nutrients. Representative samples obtained from at least 30 bales. An In situ experiment designed for evaluating sainfoin hay for DM, OM, CP, NDF and NDF_{OM} degradability, by 3 ruminally fistulated Holstein cows (multiparous, 680 ± 20kg of BW), fed 2 equal meals (0800 and 1800) of a balanced ration with CNCPS V5 for 10% above maintenance requirements with forage:concentrate ratio of 60:40.Samples were ground to pass 2 mm screen size (Wiley mill) and then sieved to remove particles less than 50µ. Five gram samples were weighed into nylon bags (10 × 20 cm) with 50µ pore size, to create sample size: surface area of 12.5 mg/cm^2. Duplicate samples were incubated for 4, 8, 12, 24, 48, 72 and 96h in ventral rumen, just before morning meal. After incubation, bags were removed and rinsed with cold tap water, until the rinsed water remained clear. To obtain the 0 h values triplicates were rinsed by 39°C water for 20 min. bags were dried at 60°C for 48 h in a forced air oven and then weighed. Aliquots were used for ash, CP, NDF and NDFom determination. Degradation profiles were calculated by the nonlinear model. The effective degradability (ED) in the rumen with digesta passage rate of 0.05 h^{-1} was calculated using NEWAY computer package. Total tannin and Condensed tannin contents were 38.5 and 21.3 g/kg DM. Low CP degradability can be explained by formation of tannin-protein complexes that are not available for microbial degradation. Tannins extracted from sainfoin can inhibit proteolysis by rumen major proteolitic bacteria. Lower cell wall degradability can be explained by formation of unbearable tannin complexes with plant cell wall that can recovered as ADL (during digestion) and preventing microbial attachment, condensed tannins can prevent microbial cellulase activity and deactivation of β endoglucanases.

Table 1. In situ degradation parameters of sainfoin (g/g)

	a	b	c(h^{-1})	ED
DM	0.334±0	0.363±0.01	0.07±0.02	0.540±0.02
OM	0.316±0	0.387±0.01	0.09±0.02	0.548±0.02
CP	0.171±0	0.459±0.05	0.04±0.01	0.379±0.02
NDF	0.014±0	0.518±0.01	0.05±0.01	0.271±0.03
NDF_{OM}	0.042±0	0.505±0.02	0.05±0.01	0.265±0.02

Reported values are means ± standard deviations.

Key Words: sainfoin, tannin, degradability

M116 A survey of molds and yeasts in Canadian corn silage. H. V. L. N. Swamy*, A. M. A. Heeg, and A. B. Rae, *Alltech Canada*, *Guelph, ON, Canada*.

Penicillium mycotoxins from silage have been implicated in various disorders in ruminant animals, especially dairy cows. Commercial facilities to analyze silage *Penicillium* mycotoxins, except PR toxin, are currently not available in North America. Mold count and identification in silage have been used to indirectly assess the potential toxicity of *Penicillium* mycotoxins. Such information, however, is not available for Canadian silage. A survey, therefore, was conducted in the summer of 2008 wherein 34 corn silage bunks in Ontario were sampled for mold and yeast counts. Samples with mold count exceeding 1000 col/gm were further subjected to mold identification. All the samples were analyzed at Dairyland Laboratories, Inc., WI, USA. The samples were frozen immediately after collection and were shifted to USA in dry ice. The average mold count was 65,000 col/gm and the average yeast count was 3.2 million col/g. Twenty 4 samples were above 1000 col/gm and they were subsequently subjected to mold identification. *Penicillium* mold represented 50% of mold spectrum while *Mucor* and *Fusarium* were at 15 and 14%, respectively. *Penicillium* mold was the dominant species among all in contrast to the conventional thinking. Given the temperate climate in Canada, *Fusarium* molds were thought to be the primary molds in Canadian feedstuffs. This survey for the first time indicated that Canadian silages should be tested for *Penicillium* molds and/or mycotoxins along with *Fusarium* mycotoxins to assess the total animal toxicity.

Key Words: silage, *Penicillium*, mycotoxins

M117 A survey of mold count and identification in Pennsylvanian dairy feed ingredients. H. V. L. N. Swamy*[1], J. M. Lawrence[2], and N. J. Adams[2], [1]*Alltech Canada*, *Guelph, ON, Canada*, [2]*Alltech California*, *Fresno, CA*.

Penicillium mycotoxins from silage have been implicated in various disorders in ruminant animals, especially dairy cows. Commercial facilities to analyze silage *Penicillium* mycotoxins, except PR toxin, are currently not available in North America. Mold count and identification in feed ingredients have been used to indirectly assess the potential toxicity of *Penicillium* mycotoxins. Such information, however, is not published specific to Pennsylvania region in USA. A survey, therefore, was conducted in 2009 wherein 278 feed ingredients, collected from commercial dairy farms in PA, were sampled for mold and yeast counts. Samples with mold count exceeding 1000 col/gm were further subjected to mold identification. The major ingredients tested included corn silage (n = 107), haylage (n = 45), high moisture corn (n = 40), TMR (n = 30) and hay (n = 8). All the samples were analyzed at Dairyland Laboratories, Inc., WI, USA. The samples were frozen immediately after collection and were shifted to lab in dry ice. The samples with mold count more

than 1000 col/gm were considered positive and this was amounted to 74.5%. Among these 39.6, 40.6, 11.1, and 8.7% samples had mold counts between 1001 and 10,000, 10,001 and 100,000, 100,001 and 1 million, and more than 1 million col/gm, respectively. Mold count more than 10,000 col/gm has potential to cause production losses and this was amounted to 60.4% of positive samples. Mold identification revealed that *Penicillium* mold represented 62.3% of mold spectrum while *Mucor*, *Aspergillus*, *Fusarium* and *Cladosporium* were at 46.4, 7.7, 7.7 and 6.3%, respectively. It is important to note that mold identification percentages need not have to add up to 100% as some samples can be contaminated with more than one mold type. *Penicillium* mold was the dominant species among all in contrast to the conventional thinking. Given the temperate climate in Pennsylvania, *Fusarium* molds were thought to be the primary molds in dairy feedstuffs. This survey indicated that silages should be tested for *Penicillium* molds and/or mycotoxins along with *Fusarium* mycotoxins to assess the total animal toxicity.

Key Words: silage, *Penicillium*, mycotoxins

M118 Summer annuals for fall grazing in the high elevation Intermountain West. J. B. Hall*, B. R. Johnson, R. H. Stokes, and R. Ambrosek, *University of Idaho*, *Moscow*.

The objective of this study was to compare summer annuals for fall and winter grazing on irrigated pastures in the Intermountain West. The cool desert areas of this region have short growing seasons (≤120 d) with high daytime temperatures and cool nights resulting in sufficent growing degree days, but impaired production on cool season forages during late summer. Five species were planted in Carmen, ID (45°17′N, 113°53′W; 1155 m elevation) in 0.10 ha plots with 3 plot replicates per species. Four species were planted in yr 1 and 2: CORN (*Zea mays*), sorghum x sudangrass (*Sorghum* spp; SUDEX), TEFF (*Eragrostis tef*), and GERMAN foxtail (*Setaria italica*). PEARL millet (*Pennisetum glaucum*) planted in yr 1 was replaced by PROSO millet (*Panicum miliaceum*) in yr 2. All species except TEFF were planted no-till from June 25 to July 2. TEFF was planted after minimum tillage. Three 1/1000 ha yield samples were taken from each plot. Pooled samples for each species were analyzed for CP, ADF, NDF, Ca and P. TEFF was sampled at 50 d post planting (haying) with all species sampled after killing frost (September 8 and 16, yr 1 and 2, respectively). Heifers grazed the plots during November and December, and animal grazing days were recorded. Yield data were analyzed by ANOVA with means compared using a *t*-test. Data for each yr were analyzed separately. Species affected DM yield ($P = 0.10$ yr 1; $P < 0.02$ yr 2). Yields (DM; Mg ha^{-1}) were not different ($P = 0.22$) for CORN (5.5 ± 1.6, 10.7 ± 1.0), GERMAN (5.4 ± 0.4, 5.8 ± 1.0), and SUDEX (7.0 ± 0.7, 7.1 ± 1.8) in yr 1 and 2, respectively, and TEFF (6.1 ± 0.2; yr 1 only). In yr 1, yields of SUDEX and TEFF exceeded ($P < 0.01$) PEARL (3.9 ± 1.2 Mg ha^{-1}). CORN yields were greater ($P < 0.01$) than GERMAN or PROSO (3.9 ± 1.6 Mg ha^{-1}) in yr 2. Nutrient content of all forages exceeded NRC requirements for cows in mid-gestation. TEFF, PROSO, and PEARL produced fewer ($P = 0.10$) animal grazing days than the other species. In conclusion, CORN, SUDEX, and GERMAN produce acceptable fall and winter grazing for the Intermountain West.

Key Words: cattle, grazing, fall

M119 Biological parameters by spring and fall-calving cows grazing with full access, limited access, or no access to endophyte-infected tall fescue–2 year summary. J. Caldwell*[1], K. Coffey[1], M. Looper[2], D. Kreider[1], E. Kegley[1], J. Jennings[3], C. West[1], D. Hubbell III[1], J. Tucker[1], A. Young[1], T. Hess[1], M. Popp[1], M. Savin[1], D. Philipp[1], C. Rosenkrans Jr.[1], [1]*University of Arkansas*, *Fayetteville,* [2]*USDA-ARS*, *Booneville, AR,* [3]*University of Arkansas Cooperative Extension Service*, *Little Rock*.

Cattle consuming *Neotyphodium coenophialum*-infected tall fescue (E+) may have altered physiological responses. Replacing E+ with non-toxic endophyte-infected fescue (NE+) may help this problem, but acceptance of NE+ by producers has been slow. Our objective was to determine the extent limited access to NE+ will alter biological parameters by spring (S) and fall-calving (F) cows grazing E+ or NE+ at different percentages of the total pasture area. Crossbred cows (n = 178) were stratified by BW and age within calving season and allocated randomly within calving season to 1 of 14 groups representing 5 treatments: 1) F on 100% E+ (F100; n = 3); 2) S on 100% E+ (S100; n = 3); 3) F on 75% E+ and 25% NE+ (F75; n = 3); 4) S on 75% E+ and 25% NE+ (S75; n = 3); and 5) S on 100% NE+ (NE100; n = 2). Cow serum K, Cu, NEFA, and prolactin (PRL) concentrations at breeding, and serum Na and PRL concentrations at the end of breeding were greater ($P < 0.05$) for S vs. F. Serum Ca, Mg, and Fe concentrations at breeding and serum Fe, Zn, Cu, and NEFA concentrations at the end of breeding were greater ($P < 0.05$) for F vs. S. Serum P and PRL concentrations at breeding were greater ($P < 0.05$) for S75 and F75 vs. S100 and F100; serum NEFA concentrations at the end of breeding were greater ($P < 0.05$) for S100 and F100 vs. S75 and F75. At breeding, serum NEFA concentrations were lower ($P < 0.05$) for NE100 vs. S75, and serum PRL concentrations at the end of breeding were greater ($P < 0.05$) for NE100 vs. S75. Calf serum Zn concentrations at weaning were greater ($P < 0.05$) for F vs. S, but serum Fe and Cu concentrations at weaning were greater ($P < 0.05$) for S vs. F. Serum Fe concentrations at weaning were also greater ($P < 0.05$) for S75 and F75 vs. S100 and F100. Therefore, calving season may alter biological parameters for cows grazing E+ during critical stages of production. Limited access to NE+ may improve cow PRL concentrations at breeding, and may affect calf serum Zn concentrations at weaning.

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Key Words: cow, fescue

M120 Immune function responses by spring and fall-born calves weaned from wild-type or non-toxic endophyte-infected tall fescue. M. A. Ata*[1], K. P. Coffey[1], J. D. Caldwell[1], E. B. Kegley[1], M. L. Looper[2], A. N. Young[1], D. Philipp[1], C. P. West[1], G. F. Erf[1], D. S. Hubbell III[1], and C. F. Rosenkrans Jr.[1], [1]*University of Arkansas*, *Fayetteville,* [2]*USDA-ARS*, *Booneville, AR*.

Cattle grazing *Neotyphodium coenophialum* infected tall fescue (E+) may have reduced immune function. Recently, non-toxic endophyte-infected fescues (NE+) were shown to enhance cattle performance. A 3-years study (2007–2009) was conducted using Gelbvieh x Angus calves (558 ± 9.2 lb, n = 500) to determine how limited access to NE+ affects immune function in calves weaned from E+ pastures. Prior to weaning, groups of spring (S) and fall-born calves (F) grazed E+ continuously (S100 and F100, respectively), or E+ for much of the year, but grazed NE+ for 1 mo. before weaning (S75 and F75, respectively). Groups of spring-born calves also grazed NE+ continuously (NE100). Blood samples were collected at weaning for all 3 years and analyzed for whole blood cell counts (K/µl). Starting in 2008, calves (1 fall and 2 spring groups, n = 266) were injected at weaning with 200 µ g of phyto-hemagglutinin (PHA) in the caudal fold underneath the tail head. Blood samples were collected for serum prolactin (PRL) analysis. Skinfold thickness was measured before injection (0 h) and at 6, 12, 24, 48 h after injection. Statistical analyses performed by using PROC MIXED procedure of SAS. Concentrations of neutrophils, hemoglobin, and hematocrit were greater ($P < 0.05$), while concentrations of eosinophils and basophils were lower ($P < 0.05$) for F vs. S. lymphocytes Concentrations were greater ($P < 0.05$), and that of red blood cells were lower ($P < 0.05$) for NE100 vs. S75. Concentrations of total white blood cells and neutrophils were greater ($P < 0.05$) for S75 and F75 vs.S100 and F100. Within spring-born calves, skinfold thickness was greater ($P < 0.05$) for NE100 vs. S75 at 0h, and 6, 12, and 24 h after injection with PHA. Serum PRL concentrations were greater ($P < 0.05$) for S75 vs. S100 at 24 h post-weaning. Within fall-born calves, serum PRL concentrations were greater ($P < 0.05$) for F75 vs. F100 at weaning. Therefore, allow-

ing calves limited access to NE+ before weaning may enhance certain aspects of immune function.

This project supported by the National Research Initiative of the National Institute of Food and Agriculture, USDA, grant # 2006–55618–17114.

Key Words: fescue, immunity, calves

M121 Antagonism of 5-hydroxytryptamine$_{2A}$ receptor results in decreased contractile response of bovine lateral saphenous vein to tall fescue alkaloids. J. L. Klotz*[1], J. R. Strickland[1], L. P. Bush[2], B. H. Kirch[1], K. R. Brown[1], and G. E. Aiken[1], [1]*USDA-ARS, FAPRU, Lexington, KY*, [2]*University of Kentucky*, *Lexington*.

Pharmacologic profiling of 5-hydroxytryptamine (5HT) receptors of bovine lateral saphenous vein has shown that cattle grazing endophyte-infected (*Neotyphodium coenophialum*) tall fescue (*Lolium arundinaceum*) have altered responses to ergovaline (ERV), 5HT, $5HT_{2A}$ and $5HT_7$ agonists. To determine if 5HT receptor binding of tall fescue alkaloids is affected by grazing endophyte-free (EF), wild type (WT), or novel endophyte-infected (NE) tall fescue, contractile responses of lateral saphenous veins biopsied from cattle grazing these different fescue-endophyte combinations were evaluated in presence or absence of antagonists for $5HT_{2A}$ (ketanserin; KET) or $5HT_7$ (SB-269970; SB). Biopsies were conducted over 2 years on 35 mixed breed steers (361.5 ± 6.3 kg) grazing KY31 (WT; n = 12), EF (n = 12), MAXQ (NE AR542; n = 6) or KYFA9301 (NE AR584; n = 5) pasture treatments (3 ha) between 84 and 98 d (Yr 1) or 108–124 d (Yr 2). Segments (2–3 cm) of vein were surgically biopsied, sliced into 2–3 mm cross-sections, and suspended in a myograph chamber containing 5 mL of oxygenated Krebs-Henseleit buffer (95% O_2/5% CO_2; pH = 7.4; 37°C). Veins were exposed to increasing concentrations of 5HT, ERV, and ERV+1 × 10^{-5} M KET, or +1 × 10^{-6} M SB in Yr 1. In Yr 2, ergotamine (ERT) and ergocornine (ERO) were evaluated in presence or absence of 10^{-5} M KET. Data were normalized to a reference addition of 1x10^{-4} M norepinephrine and analyzed as a CRD factorial with steer as experimental unit. In Yr 1, contractile response to 5HT and ERV were lowest in WT KY31 pastures ($P < 0.05$) and the presence of KET greatly reduced the response to ERV in all pastures ($P < 0.05$). The presence of SB did not alter contractile response to ERV. In Yr 2, there was no difference in response to ERO or ERT across pastures, but KET again reduced the contractile response ($P < 0.05$). The $5HT_{2A}$ receptor is involved in alkaloid-induced vascular contraction and alkaloid binding may be affected by exposure to different endophyte-fescue combinations.

Key Words: alkaloid, bovine, 5-hydroxytryptamine

M122 Tall fescue alkaloids cause vasoconstriction in equine medial palmar artery and vein. J. L. Klotz*[1] and K. J. McDowell[2], [1]*USDA-ARS, FAPRU*, *Lexington, KY*, [2]*University of Kentucky*, *Lexington*.

Mares grazing endophyte-infected (*Neotyphodium coenophialum*) tall fescue (*Lolium arundinaceum*) typically exhibit reproductive dysfunction rather than peripheral vasoconstriction as a primary sign of the fescue toxicosis syndrome. Recent work using Doppler ultrasonography demonstrated that consumption of endophyte-infected tall fescue seed causes measurable vasoconstriction in the medial palmar artery (PA). The objective of this study was to evaluate contractile responses of medial palmar artery and vein (PV) to increasing concentrations of tall fescue alkaloids. Medial PA and PV were collected immediately following euthanasia from 18 horses of mixed breed, age and gender along the third metacarpal proximal to the fetlock joint from both forelimbs. Vessels were separated, cleaned of excess connective and adipose tissue, divided into 2–3 mm cross-sections and suspended in a multimyograph chamber with continuously oxygenated Krebs-Henseleit buffer (95%O_2/5%CO_2; pH = 7.4; 37°C). Following a 90-min equilibration and recovery from a 1x10^{-4} M NE reference addition, additions of ergotamine (ERT), ergonovine (ERN), ergocryptine (ERP), ergocristine (ERS), ergocornine (ERO), lysergic acid (LSA), norepinephrine (NE) and 5-hydroxytryptamine (5HT) occurred every 15 or 20 min for PV and PA, respectively. Data were normalized as a % contractile response induced by the 10^{-4} M NE addition and analyzed as a completely randomized design with significance set at $P = 0.05$. Response between PA and PV for alkaloid or biogenic amine did not differ. All alkaloids produced a contractile response, except neither PA nor PV responded to LSA. Both NE and 5HT had a 2-fold greater ($P < 0.05$) maximal response than all alkaloids in both PA and PV, ERN had the greatest PV response ($P < 0.05$), and ERN and ERO had greatest PA maximal responses ($P < 0.05$). Although horses do not outwardly appear to be affected by peripheral vasoconstriction as observed in cattle, these data indicate that tall fescue alkaloids are vasoactive and suggest that potential exists for peripheral vascular effects of tall fescue alkaloids in horses.

Key Words: alkaloids, equine, vasoconstriction

M123 Comparison of management strategies commonly used to lessen or alleviate the symptoms of fescue toxicosis in cattle using meta-analysis. J. Hawley*, J. D. Caldwell, E. B. Kegley, and K. P. Coffey, *University of Arkansas*, *Fayetteville*.

Cattle consuming toxic endophyte-infected fescue (E+) may develop fescue toxicosis, causing production losses exceeding $600 million annually. Currently, there is no cure for fescue toxicosis; however, management strategies that are primarily designed to limit the amount of toxin ingested by the animal are available to producers. This review of data compared cattle performance effects (ADG and DMI) of management strategies used to lessen or alleviate the symptoms of fescue toxicosis. Management strategies evaluated were novel endophytes (NE), diet supplementation, interseeding, and other inventive remedies. For inclusion in the analysis, studies (n = 38) were conducted in the United States from 1985 to present, reported randomization to treatment and untreated control groups, used cattle, were sourced from peer-reviewed journals, and reported sufficient information to calculate correlation coefficients (r). Dot plots were used to examine the data for trends toward a uniform effect of management strategy on cattle performance. Management strategies displaying a uniform response on the dot plot compared with negative controls were analyzed using mixed models. Examination of dot plots for NE, diet supplementation, and other inventive remedies revealed performance advantages for treated cattle relative to cattle in negative control groups. An insufficient number of studies met the inclusion criteria to conduct meta-analyses comparing interseeding with negative controls. Studies comparing NE to E+ indicated a large (r and 95% confidence interval [CI] = 0.63 [0.52, 0.75], $P < 0.05$) effect on cattle performance. Studies comparing diet supplementation to no diet supplementation indicated a medium (r and 95% CI = 0.35 [0.24, 0.46], $P < 0.05$) effect on cattle performance. Similarly, studies comparing other inventive remedies to no other inventive remedies indicated a medium (r and 95% CI = 0.35 [0.24, 0.46], $P < 0.05$) effect on cattle performance. The data discussed herein illustrate that the negative effects of fescue toxicosis on cattle performance may be mitigated by altering management strategies.

Key Words: cattle, fescue toxicosis, meta-analysis

M124 Yield potential of eastern gamagrass in central Wisconsin. W. K. Coblentz*[1], W. E. Jokela[1], M. G. Bertram[2], and P. C. Hoffman[2], [1]*US Dairy Forage Research Center*, *Marshfield, WI*, [2]*University of Wisconsin*, *Madison*.

Recently, perennial warm-season grasses have received considerable interest, largely through bioenergy initiatives, but their suitability for limiting caloric intake by ruminants has not been explored. Our objective was to assess the yield potential of eastern gamagrass [*Tripsacum dactyloides* (L.) L.] for potential incorporation into dairy-heifer diets offered throughout the north-central US. Replicated plots of 'Pete' eastern gamagrass were arranged in a split-plot design, where 9 harvest systems (wholeplots) and 4 N fertilization regimens (subplots) were evaluated over a 3-yr period. Harvest systems included one-time cuts on 1 June, 15 June, 1 July, 15 July, 1 August, and 15 August, plus 3 2-cut systems with harvests spaced at 45-d intervals (1 June/15 July, 15 June/1 August, and 1 July/15 August). Nitrogen fertilization was applied as ammonium nitrate (34–0-0) at rates of 0, 67, 134, or 202 kg N/ha annually. For 1-cut harvest systems, yields of DM increased across harvest dates, reaching numerical maximums of 7192, 9764, and 7554 kg/ha by mid-August of 2007, 2008, and 2009, respectively. During each year, there was a strong linear ($P < 0.001$) effect of harvest date; however, higher-ordered effects varied within year. Relatively large yield increases (≥1812 kg/ha) between 1 and 15 August during 2008 and 2009 suggested that improved yields could be achieved by delaying 1-cut harvests beyond 15 August. Yields of DM from 2-cut harvest systems were not competitive with 1-cut harvest systems timed in mid-August. Nitrogen fertilization rate affected ($P < 0.001$) yields of DM, but did not interact with other treatment effects ($P \geq 0.082$). Overall, yields of DM increased with N fertilization, exhibiting both linear ($P < 0.001$) and quadratic ($P = 0.027$) effects, but efficiencies were reduced at greater application rates. Current recommendations for eastern gamagrass generally adopt a conservative philosophy concerning growth-reserve status; therefore, delaying a 1-cut harvest closer to first-frost may improve yields, but also could negatively affect persistence. This approach for further increasing yields of DM might be viable, but it needs to be evaluated critically.

Key Words: eastern gamagrass, N fertilization, DM yield

M125 Nutritive value of pearl millet hay as affected by moisture concentration and bale sampling depth. J. Kanani*, D. Philipp, K. P. Coffey, A. N. Young, R. Rhein, and J. D. Caldwell, *University of Arkansas*, *Fayetteville*.

A study was conducted to evaluate the effects of moisture (15, 21, and 28% DM) and sampling depth (0.2, 0.4, and 0.6 m) on chemical composition and in situ disappearance of pearl millet [*Pennisetum glaucum* (L.) R. Br.] hay stored for 71 d. Seven ha of pearl millet were divided into 3 blocks and 3 subplots to assign moisture treatments of which 3 round bales (1.2 × 1.5 m) were obtained and stored (n = 27). Heating degree days (HDD) were calculated as summation of the daily internal bale temperature above 35°C. Duplicate sample bags for in situ (10 × 20 cm) analysis were incubated in 6 ruminally cannulated cows (BW = 585 ± 37.8 kg) for 0, 6, 12, 18, 24, 36, 48, 72, 96, and 120 h. Data for bale temperature and forage chemical composition were analyzed as a randomized complete block design using Proc Mixed procedures of SAS and tested for moisture, depth, and their interactions. Residual DM weight for each in situ sampling time was fit to a non-linear statistical model using PROC NLIN of SAS to determine DM degradation kinetics. Increasing bale moisture led to increased bale temperature (140.4, 365.3, and 840.8 HDD; $P < 0.01$). Crude protein concentration was not affected ($P > 0.1$) by moisture or sampling depth, but increasing moisture tended ($P = 0.07$) to affect NDF, OM, and ADF negatively. Increasing moisture increased ($P < 0.05$) NDIN (40.8, 47.5, and 49.8% of total N), ADIN (7.0, 9.5, 22.8% of total N), and ADL (3.0, 2.9, and 6.0% DM); however, hemicellulose decreased ($P < 0.05$) with increasing moisture (31, 31, and 25% DM). Increasing bale moisture also reduced the rate of DM disappearance (K_d; 0.047, 0.043, 0.036 h^{-1}; $P = 0.03$). Sampling depth did not affect ($P > 0.1$) any of the digestion variables, but the immediately degradable fraction (A), potentially degradable fraction (B), and effective disappearance were affected ($P < 0.05$) by a moisture × sampling depth interaction. Storing pearl millet at high moisture concentrations appeared to result in heat damage and reduced forage quality and digestibility.

Key Words: pearl millet, moisture and sampling depth, nutritive value

M126 Characterization of plant cuticular wax markers in native grazing pastures of southwest Virginia. A. E. Tanner*[1], S. R. Blevins[1], E. Green[2], R. W. Mayes[2], and R. M. Lewis[1], [1]*Virginia Tech*, *Blacksburg,* [2]*The Macaulay Land Use Research Institute*, *Aberdeen, Scotland, UK*.

Plants contain cuticular wax compounds in varied concentrations, and can be used to estimate intake and diet composition of grazing animals. Native plant species available to pasture-raised beef cattle were evaluated during the production season on a southwest Virginia farm. Our objectives were to: i) determine forage heterogeneity; ii) quantify *n*-alkane and long chain alcohol (LCOH) concentrations; and iii) investigate changes over time. Six 0.73 ha paddocks were selected randomly and sampled bi-monthly (April to September 2009). A 0.5m x 0.5m quadrat was thrown in random directions within each paddock. Plants within quadrats were harvested and separated according to species. Milled oven-dried (85°C) samples were heated with ethanolic KOH (90°C, 16h), extracted into heptane and separated into *n*-alkane and LCOH fractions before being quantified by GC. Patterns of *n*-alkane and LCOH concentrations were analyzed for 3 plant categories: grass, legume, and weed, with ANOVA. Plant species, carbon chain length, their interaction, and sampling period were fitted as fixed effects. Plant *n*-alkane C29 and C31 concentrations were higher in May (294 ± 8 mg/kg DM; $P < 0.001$) then declined to 1/3 that amount. Plants differed in C27, C29, C31 and C33 concentration ($P < 0.001$), although orchardgrass and dandelion were difficult to differentiate. *N*-alkane patterns were not specific to a plant category. Orchardgrass had extremely high concentrations of 1-C26-OH from July onward (18447 to 19670 mg/kg DM), 10 times that of other plants, inflating variance. There was no change in LCOH over time ($P = 0.09$) for other species. Plants differed in 1-C26-OH, 1-C28-OH, and 1-C30-OH concentrations ($P < 0.001$), but LCOH patterns were not specific to a plant category. Plant total LCOH concentration was more consistent than *n*-alkane concentration (CV 17.9% and 69.9%, respectively), suggesting greater utility to delineate plant species. Plant heterogeneity limits the usefulness of grouping plants by category. Combined *n*-alkane and LCOH data delineates plants. Plant patterns remain fairly static over time, which will be important for investigating foraging patterns in cattle.

Key Words: cuticular wax, *n*-alkane, LCOH

M127 Statistical variation in predicting dry matter intake of Brahman bulls using the n-alkane technique. A. D. Aguiar*[1,4], L. O. Tedeschi[1], F. M. Rouquette[2], T. D. A. Forbes[3], C. M. Hensarling[3], and R. D. Randel[2], [1]*Texas A&M University*, *College Station,* [2]*Texas AgriLife Research*, *Overton,* [3]*Texas AgriLife Research*, *Uvalde,* [4]*University of Florida*, *Gainesville*.

The objectives of this study were to determine the variation structure within and across days when determining DMI using C_{32} alkane as an external marker, to determine the optimum fecal collection periods, and to compare C_{31} and C_{33} as plant markers in estimating DMI. Brahman bulls (n = 16) stratified by previous residual feed intake (RFI) rankings were placed in 4 groups. Each group had 2 high (inefficient) and 2 low (efficient) RFI bulls. Groups were randomly assigned to 4 Coastal bermudagrass [*Cynodon dactylon* (L.) Pers.] pastures and stocked at moderate to low grazing pressure. Corn gluten was marked with C_{32} n-alkane and bulls were individually fed 400 g twice daily to estimate DMI. There were 3 periods (P1, P2, P3) of collection from mid-July to late-Aug; each period was divided into 2 sub-periods in which fecal samples were collected 4 times a day for 5 d (0700, 1100, 1500, and 1900 h). Gas chromatography was used to determine n-alkanes. A double repeated measure design in a completely randomized block design was used. During P1 and P2, the prediction of DMI using C_{33} had a better fit (smaller $-2 \times$ Log) than C_{31} either with or without adjustments for forage C_{32}. The variation in DMI decreased when adjustments for forage C_{32} were not used. The variances of DMI were similar using C_{31} across days, but the correlations between days were low, suggesting that several days of collection were needed to accurately predict DMI. Correlations between times of fecal collection were medium to high for all periods and varied from 0.65 to 0.97 for C_{31} and from 0.26 to 0.96 for C_{33}. When all periods were analyzed together, estimates of DMI using either C_{31} or C_{33} had low correlations between days of collection. In addition, the adjustment for forage C_{32} did not improve the variance and (co)variance matrix. In conclusion, C_{33}/C_{32} had the lowest variation in predicting DMI and at least 5 d of continuous fecal collection were needed to decrease the variability of DMI. The optimum times for fecal collection were 0700 and 1500 h and it was important to adjust for forage C_{32} concentration to predict DMI of Brahman bulls grazing Coastal bermudagrass.

Key Words: cattle, correlation, grazing

M128 A comparison of anatomical and compositional differences of residual feed intake (RFI)-indexed Brahman bulls under grazing conditions. T. D. A. Forbes*[1], F. M. Rouquette[2], L. O. Tedeschi[3], R. D. Randel[2], and F. R. B. Ribeiro[4], [1]*Texas AgriLife Research*, *Uvalde,* [2]*Texas AgriLife Research*, *Overton,* [3]*Texas A&M University*, *College Station,* [4]*Texas A&M University-Commerce*, *Commerce*.

This study compared gastrointestinal tract (GIT) measures, carcass composition, and ADG of Brahman bulls grazing Coastal bermudagrass at 2 stocking rates (SR) for 60 d. Prior to the grazing trial, bulls were fed a high roughage diet for 70 d, stratified as efficient (LRFI) or inefficient (HRFI), and randomly assigned to high (HSR) or low (LSR) SR pastures. Shrunk BW (SBW) was recorded after animals fasted for 18 h before harvest. Carcass was weighed; KPH and internal organs were separated; the GIT was dissected and emptied; small and large intestine lengths were recorded, and internal fat (excluding KPH) was separated from the GIT; all components were then weighed. After a 48 h chill, the 9–11th rib section (RIB) was removed from the left carcass. Lean, fat, and bone were physically separated. Fat and lean tissues were analyzed for moisture and fat. Independent variables were expressed as amount and percent of SBW. Data were analyzed using a split-plot design in a 2×2 factorial arrangement with pastures within SR as random factors. There was no effect of RFI ($P = 0.74$) or SR ($P = 0.74$) on initial BW. Low RFI bulls had heavier SBW ($P = 0.04$) and HCW ($P = 0.01$) (393 and 217 kg, respectively) than HRFI bulls (381 and 203 kg, respectively). There was no effect of RFI ($P = 0.09$) on ADG (0.66 and 0.50 kg/d for LRFI and HRFI, respectively). There was a tendency ($P = 0.08$) for an interaction between RFI and SR for fat thickness (FT). Low RFI bulls at LSR had less FT compared with LRFI bulls at HSR (1.7 vs 2.94 mm). There was an interaction between RFI and SR ($P = 0.02$) on the lipid content of the RIB which was greater (17.9%) in LRFI bulls at HSR. Low SR bulls had greater ($P = 0.03$) liver % BW than HSR bulls while HRFI tended to have greater ($P = 0.07$) liver % BW than LRFI bulls. Low RFI bulls had lighter ($P = 0.02$) small intestine % BW and more ($P = 0.06$) internal fat % BW than HRFI bulls. These initial results suggest that efficient bulls tend to gain more and may deposit more fat when forage availability does not limit DMI, but when forage is limited there may be no influence of RFI on carcass composition.

Key Words: cattle, efficiency, carcass

M129 *Cenchrus ciliaris* in a silvopastoral system with *Prosopis juliflora*. T. Clavero* and R. Razz, *Centro de Transferencia de Tecnologia en Pastos y Forrajes. Universidad del Zulia.*, *Maracaibo, Estado Zulia, Venezuela*.

Buffelgrass (*Cenchrus ciliaris*) planted under and outside the canopies of mesquite (*Prosopis juliflora*) in Venezuela's semi- arid region were evaluated to determine dry matter production, forage quality, and soil chemical characteristics. Harvested buffelgrass was analyzed for dry matter yield (DM), crude protein (CP), neutral detergent fiber (NDF), acid detergent fiber (ADF), and lignin. Transects extending from the tree trunk to open grass areas were established and soil samples (0–15 cm) and buffelgrass cv. Biloela (standing live biomass in one square meters plots) samples were taken at 5 sites (0, 20, 80, 150, 200% of the average canopy radius) during growing season. A randomized block design was used with 5 replications. The results showed that DM decreased as shading increased ($P \leq 0.05$). The DM production was about 21% lower in the understory areas. The shaded plants exhibited a trend for larger, thinner, wider leaves and developed larger leaf area ($P \leq 0.05$). Tree canopies had a positive effect on CP content on buffelgrass ($P \leq 0.05$). Overall, soil moisture content was greater ($P \leq 0.05$) under mesquite, and leaf blade increased, which is highly correlated to CP (r = 0.87) . Grass samples showed no significant differences ($P \geq 0.05$) in NDF, ADF, and lignin under mesquite compare with open pasture. Greater levels of soil C, N, P, Ca, Mg and K were found under the canopies of mesquite ($P \leq 0.05$), with differences of 0.64% C, 0.46% N, 2.40 ppm P, 2.10 ppm Ca, 1.27 mEq/100 g Mg and 0.57 mEq/100 g K. Soil analyses showed no significant differences ($P \geq 0.05$) in Na and Mn under mesquite compared with open grassland. Results suggest that mesquite has a lot of potential for use in a silvopastoral system with buffelgrass. Fodder availability of buffelgrass was lower under the trees; however, canopies had a positive effect on nutritional value and improved soil chemical conditions.

Key Words: *Prosopis juliflora*, *Cenchrus ciliaris*, silvopastoral

M130 Quantifying terpenes in rumen fluid, serum, and plasma from sheep. R. E. Estell*[1], S. A. Utsumi[2], and A. F. Cibils[3], [1]*USDA, ARS, Jornada Experimental Range*, *Las Cruces, NM,* [2]*Michigan State University, Kellogg Biological Station*, *Hickory Corners,* [3]*New Mexico State University*, *Las Cruces*.

Determining the fate of terpenes consumed by browsing ruminants require methods to quantify their presence in blood and rumen fluid. Our objective was to modify an existing procedure for plasma terpenes to quantify 25 structurally diverse mono- and sesquiterpenes in serum, plasma, and rumen fluid from sheep. The terpenes examined were tricyclene, α-pinene, camphene, sabinene, β-pinene, myrcene, 2-carene, 3-carene, α-terpinene, *p*-cymene, limonene, 1,8-cineole, *cis*-β-ocimene, γ-terpinene, *cis*-sabinene hydrate, terpinolene, linalool, camphor, borneol, terpin-4-ol, α-terpineol, longifolene, β-caryophyllene, α-humulene, and caryophyllene oxide. Terpenes were extracted with SPE columns and quantified using gas chromatography (n = 8 per terpene/fluid combination). Data were analyzed with the MIXED procedure of SAS with fluid as the independent factor, and means were separated by LSD in the event of a significant *F* test (α = 0.05). Recovery estimates were 100 ± 5% for 14, 7, and 4 terpenes from serum, plasma, and rumen fluid, respectively. Recovery from plasma and serum differed for 12 terpenes ($P < 0.05$), although typically differences were <10%. Recovery from rumen fluid differed ($P < 0.05$) from both serum and plasma for 16 compounds (lower in each case except linalool). Recovery did not differ ($P > 0.05$) among the 3 matrices for only 2 compounds (*p*-cymene and terpinolene). Greater recovery was generally observed for oxygenated terpenes than hydrocarbon compounds, particularly for monoterpenes. This procedure is applicable to a wide array of terpenes in fluids from sheep, but differential recoveries among terpenes and fluids require that estimated concentrations of each analyte be corrected for recovery using that specific compound in the same matrix collected under the same set of experimental conditions, and that caution be exercised in generalizing responses among different compounds with this procedure.

Key Words: terpene, serum, rumen fluid

M131 The effect of supplementing corn by-products or mesquite twigs on daily gain of Creole x Zebu young steers: A simulation model. J. M. Tapia-González*[1], A. Tewolde-Medhin[2], W. E. Grant[3], J. C. Martinez-González[2], H. Diaz-Solís[4], A. Moreno-Valdéz[5], O. D. Montañez-Valdez[1], J. A. Martínez-Ibarra[1], and G. Rocha-Chavez[1], [1]*CUSUR, U de G*, *Ciudad Guzman, Jalisco, Mexico*, [2]*Unidad Académica Multidisciplinaria Agronomía y Ciencias. UAT*, *Cd. Victoria, Tamaulipas, México*, [3]*Wildlife and Fisheries Sciences, Texas A&M University*, *College Station,* [4]*Área de Recursos Naturales, UAAAN*, *Saltillo Coahuila, México*, [5]*Área de Recursos Naturales, Instituto Tecnológico de Ciudad Victoria*, *Cd. Victoria, Tamaulipas, México*.

The Software STELLA II Version 5 was used for predicting a potential beef cattle daily gain scenario out of a conceptual mathematical model. Type of feed (hay or hay + supplement) was used to examine the effect on daily gain of Creole-Zebu steers. The model was created using real data coming out of several types of production systems totaling up to 30,000 cases. A total of 20 repetitions during 48 mo were represented in the model to predict daily gain of 8-weeks old steers up to 48 mo of age. The growing sector of steers was evaluated under the effect of supplementing several types of ingredients included in 4 experimental groups: (1) hay only, (2) hay + silage, (3) hay + nutritional blocks and (4) hay + mesquite twigs. Two types of corn were used for groups 2 and 3 (local creole maize or hybrid) and 2 types of crops were considered (raised either with or without cultural management practices). Blocks are made of chopped dry corn plant (including grain and straw), molasses and minerals pressed together to form a brick. Mesquite twigs include small branches and leaves of *Prosopis farcta* and *Celtis spinosa*. ANOVA was used to compare means and significance was set to $P < 0.05$. Higher gains were observed in steers supplemented with something more than hay because they had 14 to 21% of crude protein (CP) whereas hay had only 4.4 to 14% of CP with 30% digestibility. The highest gain was observed in group 4 probably because *Celtis spinosa* may have up to 21% CP and digestibility of 46% while nutritional blocks only have 14% CP and silage 14.6% of CP. There was no effect of corn type or rising method on total gain of steers (Table 1). Since all these parameters (coming exclusively out of the simulation model) are similar to those obtained in the field by several researches, we can conclude that simulation models are useful for predicting beef production scenarios.

Table 1. Total gain of 48-month steers with several types of feed regimen

Treatment	Cycles[1]	Total gain of steers (kg, mean ± SE)
Hay only	20	144.91 ± 16.92[c]
Hay + corn silage	20	182.30 ± 17.71[b]
Hay + corn blocks	20	179.29 ± 35.95[b]
Hay + mesquite twigs	20	224.80 ± 9.60[a]

[1]All values evaluated for each treatment representing a cycle of 48 months totalizing 80 years of evaluation.
[a–c]Different letters in the same column differs significantly ($P < 0.05$).

Key Words: mesquite, daily gain, steers

M132 Effects of dietary beta-glucan on the T helper cytokine balance in the intestine of broiler chicks. C. M. Cox*[1], L. H. Stuard[1], S. Kim[1], A. P. McElroy[1], M. Bedford[2], and R. A. Dalloul[1], [1]*Virginia Tech*, *Blacksburg*, [2]*AB Vista Feed Ingredients*, *Marlborough, UK*.

Immunomodulators like β-glucans have attracted considerable attention as potential alternatives to the prophylactic use of antibiotics. Despite increasing research, little is known about their regulatory influence on immune function in poultry. Two studies were conducted to evaluate the effects of a yeast-derived β-glucan (Auxoferm YGT) on gene expression of T helper cytokines in the intestine. Day old chicks were fed a diet containing 0, 0.02, or 0.1% β-glucan. For the first study, small intestinal sections were collected on d 7 and d 14 to evaluate gene expression by quantitative real-time PCR. On d 7, interleukin (IL)-18 expression was upregulated in the jejunum but decreased on d 14 in the duodenum of the 0.02% β-glucan birds. Expression of IL-18 also decreased on d14 in the ileum of both β-glucan groups when compared with control. On d 7, IL-4 expression was downregulated in both β-glucan treated groups in the duodenum and in the 0.1% treated group in the jejunum and ileum. In contrast, IL-4 was upregulated in the duodenum of treated birds and in the ileum of 0.1% fed birds on d 14. Similarly, IL-13 was downregulated in all intestinal sections of 0.1% β-glucan fed birds on d 7. The second study included a mixed *Eimeria* infection on d 8 and samples were collected on d 10, 14, and 21 post-hatch. Despite the fact that no significant differences were seen among treatment groups, IL-18 expression was consistently upregulated in the *Eimeria* challenged birds due to β-glucan exposure. IL-4 expression was downregulated in the non-challenged birds fed the 0.1% β-glucan diet. Mucin-1 expression was significantly decreased due to 0.1% β-glucan supplementation. On d 14, mucin-2 expression was decreased due to the *Eimeria* infection in the 0.1% β-glucan fed birds. Though not significant, there was a tendency for birds fed 0.1% β-glucan to express lower levels of IL-13 than the control birds. Taken together, the data provided from these trials strongly suggest that β-glucans downregulate T helper type 2 cytokines and thus favor a T helper type 1 cell response.

Key Words: β-glucan, poultry, cytokines

M133 Effect of capsicum and turmeric oleoresins with betaine on the performance of broilers challenged with coccidiosis. V. Brito[1], C. Moynat*[2], A. Casarin[3], M. Forat[3], and D. Bravo[1], [1]*Euronutec*, *Queretaro, Mexico*, [2]*Pancosma*, *Geneva, Switzerland*, [3]*Instituto Internacional de Investigacion Animal*, *Mexico*.

During coccidiosis, vaccination acquired immunity is insufficient to keep broiler performance. Studies showed that betaine (BE), capsicum (CA) and turmeric (TU) positively impact innate immunity. The combination of these 3 products should positively affect immunity and therefore improve performance of birds infected with coccidiosis. The objective was to evaluate the efficiency of a mixture of CA and TU oleoresins (PF = Proflora / XT 6986) combined with 2 levels of BE on performance of vaccinated broilers challenged with coccidiosis. Day-old broilers were allotted to 4 treatments and challenged with *Eimeria* spp. at d 14 (48 birds * 10 cages/treatment). The treatments were set as follow, doses in ppm, with bacitracin (BA), Nicarbazin (NI), salinomycin (SA), nitrofuran (NO). Starter Diet (d 1 to 14): T1 = 55 BA + 125 NI; T2 = 50 PF; T3 = 50 PF; T4 = 50 PF. Grower diet (d 15 to 42): T1 = 55 BA + 65 SA + 50 NO; T2 = 50 PF; T3 = 50 PF + 500 BE; T4 = 50 PF + 1000 BE. Finisher (d 43 to 52): T1 = 55 BA + 65 SA + 50 NO; T2 = 100 PF; T3 = 100 PF + 500 BE; T4 = 100 PF + 1000 BE. All birds except in T1 were vaccinated against coccidiosis at d 1. BW, BWG, FCR were recorded. Data were analyzed using GLM procedure of SAS. Before the challenge, there was no difference between treatments in FCR ($P = 0.23$). After the challenge, FCR of T1 was lower than T4 (−3.4%, $P = 0.02$) and tended to be lower than T2 (−2.6%, $P = 0.08$). FCR was similar between T1 and T3 (2.50 kg/kg, $P = 0.93$). No difference between treatments was observed in terms of BWG ($P = 0.65$) and final BW ($P = 0.68$). In spite of different modes of action, anticoccidials or vaccine combined to PF and BE lead to similar performance. These results show that a mixture of capsicum and turmeric oleoresins with 500 ppm of BE can be used associated to vaccination to maintain broiler performance in case of coccidiosis infection.

Key Words: essential oils, betaine, coccidiosis

M134 Excess dietary amino acids reduce splenic pro-inflammatory cytokine mRNA abundance and increase anti-inflammatory cytokine mRNA abundance during an acute phase response. A. Diaz[1], N. Hamel[1], K. Martorana[1], R. Angel[2], and B. D. Humphrey*[1], [1]*California Polytechnic State University*, *San Luis Obispo,* [2]*University of Maryland*, *College Park*.

The objective of this experiment was to determine the effect of dietary amino acid levels on the catabolic response to infection. Catabolic responses to infection are coordinated through the pleiotropic effects of cytokines, thus mRNA abundance of interleukin (IL)-1β, IL-6, IL-18, IL-4, IL-13 and transforming growth factor (TGF)-β4 were quantified in the spleen. Male Cobb 500 hatchlings were raised in pens (n = 15/pen) for 14 d and were fed a diet that met NRC requirements. On d 14, birds were fed 1 of 2 diets (n = 20/diet) that contained adequate (A) or excess (E) amino acid levels. The E diet contained excess Phe (+0.43%), Trp (+0.14%), Thr (+0.30%) and Arg (+0.35%). On d 21, half of the pens per dietary treatment (n = 10) were either not injected or injected with 1 mg/kg BW of *E. coli* lipopolysaccharide (LPS). The spleen from one bird per pen was collected at 3, 12, 24, 48, 96 and 168 h post-injection for measurement of cytokine mRNA abundance using quantitative real-time PCR. IL-4 and IL-13 mRNA were not detected at any time point. At 3 h, LPS-injected chicks fed the E diet had 2.6-fold higher TGF-β4 mRNA abundance compared with LPS-injected chicks fed the A diet ($P < 0.05$). At 12 and 168 h, LPS-injected chicks fed the A diet had 2-fold and 7.8-fold higher IL-1β mRNA abundance compared with LPS-injected chicks fed the E diet, respectively ($P < 0.05$). At 24 h, LPS-injected chicks fed the E diet had 3-fold higher IL-18 mRNA abundance compared with LPS-injected chicks fed A diet ($P < 0.05$). At 168 h, LPS-injected chicks fed the A diet had 12.6-fold higher IL-6 mRNA compared with LPS-injected chicks fed the E diet ($P < 0.05$). Taken together, the changes in cytokine profiles in response to LPS-injected birds fed the E diet indicate that feeding specific amino acids in excess of their growth requirement may mitigate the catabolic response to LPS-injection.

Key Words: amino acid, cytokine, inflammation

M135 Effects of repeated intravenous lipopolysaccharide injection on hematological characteristics of chicken blood. O. T. Bowen, R. F. Wideman, R. L. Dienglewicz, and G. F. Erf*, *Department of Poultry Science, Division of Agriculture, University of Arkansas*, *Fayetteville*.

Lipopolysaccharide (LPS) is a cell-wall component of gram-negative bacteria and an important pathogen-associated molecular pattern

recognized by pattern-recognition receptors of innate immunity. LPS stimulates monocytes/macrophages via Toll-like receptor-4 to produce vasoactive factors including nitric oxide, a potent vasodilator. In previous in vivo studies we established that in chickens, intravenously (i.v.) administered LPS induced a transient pulmonary hypertensive response within 1 h, increased plasma nitric oxide (NO) reaching peak levels by 6 h, and resulted in greatly reduced monocyte levels in blood samples collected 1 h post-LPS injection. Examination of the effects of a repeat i.v. injection of LPS revealed a lack of response of the pulmonary vasculature to a second LPS injection that lasted 5 d post-primary LPS injection. The objective of this study was to examine in vivo effects of a second i.v. LPS injection on cells in the systemic circulation using the 6 h peak in plasma NO levels and the 1 h drop in monocytes as end-point measurements of in vivo LPS effects. The second i.v. LPS injection was administered at 1 (24 h), 2, 3, 4, 5, 6, or 7 d post-initial LPS injection. Additionally, LPS-specific antibody titers in the plasma were also monitored post-primary LPS injection. While the drop in monocyte concentrations at 1 h and the increase in plasma NO at 6 h were observed with all second LPS administrations, the LPS-stimulated rise in plasma NO levels was, however, attenuated when LPS was injected at 5- or 6-d post-initial LPS injection. This attenuation in the increase in plasma NO following a second LPS administration at 5- and 6-d post-primary LPS injection may be explained by the presence of LPS-specific antibodies which reached peak plasma levels 4- to 6-d post-primary LPS injection. Hence, it appears that unlike the pulmonary vasculature, cells in the systemic circulation continue to be responsive to LPS stimulation administered 24 h to 7 d post-primary LPS injection.

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Key Words: lipopolysaccharide, nitric oxide, chicken leukocytes

M136 Effects of dietary conjugated linoleic acid on macrophage functions in broilers immunosuppressed with cyclophosphamide. D. Liu*, F. Y. Long, Y. M. Guo, Z. Wang, and J. M. Yuan, *China Agriculture University*, *Beijing, China*.

This study was carried out to investigate the effects of conjugated linoleic acid (CLA) on macrophage functions in broilers immunosuppressed with cyclophosphamide (CY). The experiment was designed as a 3 × 2 factorial arrangement, i.e., 3 CLA levels (0, 1.0% and 2.0%) in the diet and with or without CY injection as an immunosuppressive challenge. Two hundred and 16 1-d-old male Arbor Acres broiler chickens were randomly allocated into 6 treatments with 6 replicates. CLA was the mixture of 2 CLA isomers (c9,t11-CLA:t10,c12-CLA = 20:80). CY was injected into the femoral muscle of broilers at a dose of 80 mg/kg of body weight for 3 consecutive days (14, 15 and 16). On d 21, the peritoneal exudate macrophages from 12 broilers per treatment were collected for in vitro culture. Phagocytic rate and phagocytic index of macrophages were detected through ingesting sheep red blood cells. The levels of nitric oxide (NO) and the cytokine interleukin (IL)-1 in the culture supernatants of macrophages were assayed by Griess reagent and bioassay method, respectively. Statistical analysis of all data was performed by 2-way ANOVA with SPSS. Individual treatment means were compared using Duncan′s multiple comparison when the significant ($P < 0.05$) interaction between the main effects was observed. The results showed that the immunosuppressive challenge with CY significantly decreased the phagocytic rate and index of macrophages ($P < 0.05$), and the addition of 2% CLA significantly increased the phagocytic rate and index of macrophages ($P < 0.05$). There was a significant interaction between CLA levels and immunosuppressive challenge on the secretion of NO and IL-1 of macrophages ($P < 0.05$). But 1% dietary CLA had no influence on phagocytic functions and the secretion of NO and cytokines of macrophages. These results suggest that the dietary supplementation of 2% CLA alleviates the suppressive effects of CY on macrophage phagocytic functions and has the effects of bidirectional regulation on the secretion of NO and IL-1 of macrophages in broilers.

Key Words: conjugated linoleic acid, macrophage function, broilers

M137 Broiler breeder feeding programs and trace minerals on cytokine gene expression response in progeny. N. M. Leandro[1,2], R. Ali[1], M. Koci[1], V. Moraes[1], M. J. Wineland[1], J. Brake[1], and E. O. Oviedo-Rondón*[1,3], [1]*North Carolina State University*, *Raleigh,* [2]*Universidade Federal de Goiás*, *Goiania, GO, Brasil*, [3]*Universidade Estadual Paulista, UNESP*, *Jaboticabal, SP, Brasil*.

This study examined how feed allocation programs during breeder pullet rearing and dietary trace mineral (TM) sources during lay could affect the immune response of broiler progeny. Cobb 500 breeders were fed according to 2 feed allocation programs, either sigmoid late fast (LF) or sigmoid late slow (LS) until peak of production. From 56 to 62 wk of age, breeders were fed corn-soybean diets with 5% DDGS with either inorganic TM or an organic source (Mintrex P) to replace 30% of Cu, Zn, and Mn. Total dietary levels of the TM evaluated were 25, 125, and 125 ppm, respectively. Fertile eggs were collected for 4 d, incubated, and placed in pedigree bags at 19 d of incubation. Thirty 6 chicks/treatment were identified with neck tags to track hen effects, and placed in 2 isolation rooms, each with 6 floor pens. Three broilers per treatment were placed in each pen for 12 broilers per pen total. All broilers were fed the same diet. At 7 d of age, La Sota Newcastle disease virus (NDV) vaccine was applied by ocular route in one room only. Whole blood cells were collected at 4 d after vaccination to assay for cytokine (interleukin (IL)-2, IL-4, and interferon-γ) gene expression and serum was collected at 14 d post vaccination to assay for humoral response to NDV. Data were analyzed as a 2 × 2 × 2 factorial design considering breeder feeding programs, TM sources in breeder diet, and broiler vaccination as main factors. Broiler vaccination increased gene expression of all cytokines evaluated. Broiler progeny from breeders fed diets with 30% organic TM increased IL-4 expression after NDV vaccination, while vaccination did not cause significant upregulation of this gene in broiler progeny when breeders were fed 100% inorganic. Expression of IL-2 was found to be increased following vaccination in broilers from LF breeders fed diets with 30% organic TM. However, there was no significant change in IL-2 expression post vaccination in broilers from LS breeders fed the same diet. It was concluded that breeder feeding programs during rearing and dietary TM source during egg production influences the type and magnitude of cytokine expression in broiler progeny.

Key Words: breeder effects, trace minerals, cytokines

M138 Copy number variants in two genetically distinct chicken lines. X. Li*[1], W. Chou[1], S. J. Lamont[2], R. Croomjmas[3], and H. Zhou[1], [1]*Texas A&M University*, *College Station,* [2]*Iowa State University*, *Ames,* [3]*Wageningen University*, *PO Box 338, 6700 AH, Wageningen, the Netherlands*.

Genomic copy number variation (CNV) is another important source of genetic variation besides single nucleotide polymorphisms and microsatellites. In humans, CNVs are associated with Mendelian disease and complex traits. The high-throughput array has provided a powerful tool to discover copy number variation at the genome level. Two genetically distinct highly inbred chicken lines (Fayoumi and Leghorn G-B1) were used in this study. Previous study has shown that Fayoumi is resistant,

while Leghorn is susceptible, to avian influenza virus (AIV) infection. The Agilent 244K chicken CGH array was utilized to identify the potential CNVs associated with host response to pathogen. Six biological replicates from each line, in total, 12 biological replicates, were used. Red Jungle fowl was used as a reference to normalize the microarray data. There were 241 and 269 CNVs identified in Fayoumi and Leghorn, respectively, of which 116 and 119 were located in known chicken QTLs based on chicken QTLdb database. The CNVs identified in this study have also generated strong candidate CNVs potentially associated with host response to AIV infection in chickens.

Key Words: copy number variation, host response, avian influenza virus

M139 Phage display selection and characterization of a single-chain antibody (scFv) against chicken CD40. D. Abi-Ghanem*[1], C-H. Chen[1], L. Njongmeta[1], J. Bray[1], W. Mwangi[1], S. D. Waghela[1], J. L. McReynolds[2], and L. R. Berghman[1], [1]*Texas A&M University*, *College Station*, [2]*U.S. Department of Agriculture, Agricultural Research Service*, *College Station, TX*.

CD40, an integral membrane glycoprotein of the tumor necrosis factor-receptor super family, is mainly expressed on antigen-presenting cells (APCs), including B-cells, macrophages, and dendritic cells. The interaction between CD40 and its ligand CD154 (CD40L) mediates specific $CD4^+$ T-cell help to APCs in response to T-cell dependent antigens, and provides crucial signals for antigen-specific T-cell priming and expansion, as well as heightened antibody production and immunoglobulin class switching in B-cells. In contrast to the extensive characterization of mammalian CD40 by use of agonistic anti-CD40 monoclonal antibodies, which can mimic $CD4^+$ T-cell help to APCs, investigation of chicken CD40 (cCD40) has been limited. In this study, we describe the production of a dimeric single-chain antibody fragment (scFv) against cCD40. An immune antibody library against cCD40 was constructed by phage display. Following 3 rounds of panning against cCD40, specific, likely high-affinity antibodies were obtained. Soluble anti-cCD40 scFv (~35 KDa) was purified by nickel affinity chromatography and characterized by immunoblotting. This scFv recognized cCD40 in ELISA, and agglutinated chicken DT40 B-cells in vitro. We are currently investigating the biological activities of this scFv, particularly the induction of nitric oxide synthesis in chicken HD11 macrophages and proliferative stimulation of serum-starved chicken DT40 B-cells. These activities will evaluate the extent to which the anti-cCD40 scFv can mimic the effects of CD40L, providing the signals needed to induce activation of chicken APCs in vitro. Such an agonistic anti-cCD40 scFv may therefore constitute a powerful tool to study the role of CD40 in the chicken immune system.

Key Words: chicken CD40, single-chain antibody fragment, co-stimulation

M140 Functional characterization of the avian macrophage migration inhibitory factor (MIF). S. Kim*[1], K. B. Miska[2], M. C. Jenkins[2], R. H. Fetterer[2], C. M. Cox[1], L. H. Stuard[1], and R. A. Dalloul[1], [1]*Animal & Poultry Sciences, Virginia Tech*, *Blacksburg,* [2]*Animal Parasitic Diseases Laboratory, ARS, USDA*, *Beltsville, MD*.

Macrophage migration inhibitory factor (MIF) is recognized as a soluble factor produced by sensitized T lymphocytes and inhibits the random migration of macrophages. Recent research shows a more prominent role of MIF as a multi-functional cytokine mediating both innate and adaptive immune responses. This study describes the cloning and functional characterization of avian MIF in an effort to better understand its function and potential in poultry health applications. The full-length avian MIF gene was amplified from stimulated chicken lymphocytes and cloned into a prokaryotic expression vector. The confirmed 115 amino acid sequence of avian MIF has 71% identity with human and murine MIF. The bacterially expressed avian recombinant MIF (rChMIF) was purified, the endotoxins removed, and a 4 h-chemotactic assay performed using a 48-well chemotaxis chamber. Diff-Quick staining results showed sharply decreased migration of macrophages in the presence of 10 ng/ml rChMIF. Further, the expression of various cytokines was measured in peripheral blood mononuclear cells (PBMCs) or splenocytes using quantitative real-time PCR (qRT-PCR). Isolated PBMCs or splenocytes were cultured in the presence or absence of rChMIF, with or without lipopolysaccharide (LPS) or Concanavalin A (Con A) for 6 or 12 h. qRT-PCR analysis revealed that rChMIF alone did not induce transcription of interleukin (IL)-1β or induced-nitric oxide synthase (iNOS). However, the presence of rChMIF enhanced levels of IL-1β and iNOS during PBMCs stimulation with LPS. Similarly, there was no effect of rChMIF alone on splenocytes; however, the Con A-stimulated lymphocytes showed enhanced interferon (IFN)-γ and IL-2 transcripts in the presence of rChMIF. Interestingly, addition of rChMIF to the stimulated PBMCs, in the presence of lymphocytes, showed anti-inflammatory function of rChMIF. To our knowledge, this study represents the first report for the functional characterization of avian MIF, which inhibits migration of macrophages similarly to mammalian MIF, and it also mediates inflammatory responses during antigenic stimulations.

Key Words: MIF, avian immunity, real-time PCR

M141 US Veterinary Immune Reagent Network. H. Lillehoj*[1], S.-H. Lee[1], D.-K. Kim[1], M.-S. Park[1], D. Tompkins[2], C. Baldwin[2], J. LaBresh[3], and B. Wagner[4], [1]*USDA-ARS*, *Beltsville, MD,* [2]*University of Massachusetts*, *Amherst,* [3]*Kingfisher Biotech*, *St. Paul, MN,* [4]*Cornell University*, *Ithaca, NY*.

To advance veterinary immunology and animal disease research, a CSREES-funded NRI consortium grant (#2005–01812) was established in 2005 to develop immunological reagents specific for poultry, ruminants, swine, equine and aquaculture species (http://www.umass.edu/vetimm). Immunological reagents to be developed through this grant include monoclonal antibodies (mAb) and polyclonal antibodies that identify the major leukocyte subpopulations (T and B lymphocytes, NK cells, neutrophils, macrophages, and dendritic cells) for many animal species including fish. In addition, recombinant cytokines and chemokines as well as antibodies to them and to their receptors, will be developed and these immune reagents will be valuable in research to understand the major components of immune system which are involved in inflammation, innate and adaptive immunity. These immunological reagents will be used to (1) evaluate changes associated with diseases and vaccination, and (2) manipulate various lymphocyte subpopulations to evaluate their roles in protective immunity as well as in immunopathology. In this report, progress in poultry immune reagent development will be discussed.

This project is funded by USDA-CSREES proposal 2005-01812 and was carried out as part of the US Veterinary Immune Reagent Network. For commercially available immune reagents from this consortium, go to http://kingfisherbiotech.com

Key Words: poultry, immune reagent, diseases

M142 Expression of the development gene CAMK2G in the virgin mammary gland of the dairy goat. L. N. Wang, C. Li, Q. Z. Li*, and C. Y. Yuan, *Key Laboratory of Dairy Science of Education Ministry, Northeast Agricultural University*, *Harbin, China*.

Identification of the key genes related to mammary gland development in the dairy goat is important for optimizing milk production. In this research, after comparing the expression of ESTs in 7 Long-SAGE libraries corresponding to different stages of development (early virgin, late virgin, early pregnancy, late pregnancy, middle lactation, early involution and late involution) and sequence alignment with BLAST in the sheep library, we found the gene CAMK2G to be an important gene that affected the development of the mammary gland in virgin dairy goats. mRNA was extracted from healthy virgin mammary glands of dairy goat, and then amplified by RACE (rapid amplification of cDNA ends). We synthesized the 3′- and 5′-RACE-fragments by using the CAMK2G's EST from the virgin mammary gland long-SAGE library as the gene-specific primer, then cloned and sequenced RACE fragments to obtain the full-length gene. The anticipated length of the 3′cDNA of gene CAMK2G was about 500 bp, and 5′cDNA was about 1500 bp. Comparing the homology with the sheep EST library provided by NCBI GenBank confirmed that the cloned gene was CAMK2G. We next performed an RNAi (RNA interference) experiment. The synthesized siRNA was based on the full-length of the gene CAMK2G and transfected into cells that were subcultured from primary epithelial cells of the virgin mammary gland. After the detection of cell viability analyzer and flow cytometry, both the proliferation and the activity of mammary epithelial cells were inhibited ($P < 0.05$). Real-time PCR showed that the expression of CAMK2G was lower after RNAi ($P < 0.01$). Addition, Western blotting showed that the expression of β-casein was decreased ($P < 0.05$). The experiments above were repeated 3 times. Thus, the gene CAMK2G may be important in mammary gland development of the virgin goat.

This work was supported by the National High Technology Research and Development Program of China (Grant No. 2006AA10Z1A4).

Key Words: dairy goat, mammary gland development, CAMK2G

M143 Effects of thyroxine, glucagon and insulin on mRNA levels of heat shock proteins in bovine mammary epithelial cells under heat stress in vitro. R. L. Cui[1], J. Q. Wang*[1], H. Y. Wei[1], D. P. Bu[1], H. Hu[1,2], and L. Y. Zhou[1], [1]*State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences*, *Beijing, China*, [2]*Faculty of Animal Science & Technology, Gansu Agriculture University*, *Lanzhou, China*.

The objective of this study was to establish the effects of thyroxine (T4), glucagon and insulin on the mRNA levels of heat shock proteins (HSPs) in bovine mammary epithelial cells under heat stress in vitro. The mammary epithelial cells were cultured in DMEM/F12 media containing 10% fetal bovine serum (FBS) at 38°C until they reached 80% confluence. T4 (0, 0.01, 0.1, 0.5, 1 and 2 μmol/L), glucagon (0, 0.01, 0.1, 0.5, 1 and 2 μmol/L) and insulin (0, 0.005, 0.01, 0.1, 0.5 and 1 μmol/L) were separately added into the media then cells were exposed at 42°C for 12 h as a heat stress model and 38°C for 12 h as the control. Levels of HSP mRNA were detected by RT-qPCR. Each treatment had 3 replicates in this experiment, and one-way ANOVA of SAS was used to analyze the experimental data. The results indicated that (1) At 38°C, HSP90 did not significantly change with insulin (0.005, 0.01, 0.1, 0.5 and 1 μmol/L) and T4 (0.01, 0.1, 0.5 and 1 μmol/L) ($P > 0.05$); HSP70 increased markedly with 0.005 and 1 μmol/L insulin ($P < 0.05$), and did not change markedly with 0.01, 0.1 and 0.5 μmol/L insulin ($P > 0.05$); However, other treatments all significantly decreased the mRNA levels of HSP27, 70, 90 and heat shock factor-1 (HSF-1) ($P < 0.05$). (2) The mRNA levels of HSP27, 70, 90 & HSF-1 were all significantly lower after cells were cultured with different concentrations of T4, glucagon and insulin separately at 42°C for 12 h ($P < 0.01$). In conclusion, T4, glucagon and insulin could inhibit mRNA levels of HSPs in mammary epithelial cells under heat stress.

Key Words: bovine mammary gland epithelial cells, heat shock proteins, FQ-PCR

M144 Immunodetection of the secreted forms of osteopontin in bovine milk. N. Bissonnette[1,3], C. Thibault[1], and G. Robitaille*[2], [1]*Agriculture and Agri-Food Canada, Dairy and Swine Research and Development Centre*, *Sherbrooke, Qc, Canada*, [2]*Agriculture and Agri-Food Canada, Food Research and Development Centre*, *Saint-Hyacinthe, Qc, Canada*, [3]*Université de Sherbrooke*, *Sherbrooke, Qc, Canada*.

Osteopontin (OPN), a phosphoglycoprotein, presents in human a complex pattern of gene expression (splicing variants) which is tissue and physiological state-dependent. The concentration reaches 1 g/L and varies during lactation. Bovine OPN is secreted in lower but substantial amounts (10 mg/L) in bovine milk. The aim of this study was to monitor bovine OPN and to identify the different isoforms in milk. Four human and one mouse commercial anti-OPN targeting different portions of the human OPN were tested on bovine OPN. In addition, 2 antisera were raised against synthetic peptides designed from the NCBI refseq bovine sequence and one was raised against the protein that was purified from milk by HPLC; the purification method allows the isolation of a significant amount of pure protein. Purified and commercial bovine OPN were characterized by silver coloration and ECL Western blot analysis. The signature of both sources was identical as detected by silver coloration. One of the 3 human anti-OPN, which targeted the N-terminal part of the protein, profiled 2 bovine OPN isoforms at 65 and 40 kDa, whereas 3 human anti-OPN failed to detect purified OPN. The bovine anti-OPN (synthetic peptide) and the anti-mouse-OPN, which are highly specific to the C-terminal part of the protein, detected only the 65 kDa isoform. The bovine antisera (purified OPN from milk) recognized both forms and other forms in milk. Preliminary ELISA assays allowed a specific detection of bovine OPN. Using these antibody preparations it is possible to determine the abundance of each of these isoforms in milk. In conclusion, analysis of the bovine OPN reveals the presence of 2 isoforms. The immunodetection of the respective isoforms will allow to determine their relative abundance during lactation and to speculate on their local bioactivity.

Key Words: osteopontin, bovine, milk

M145 Differentiated immortalized porcine mammary epithelial cells grown on polysulfone hollow fiber provide a potential cell culture system for expression of recombinant proteins. T. C. Kuan*[1], Y. L. Sun[2], C. Y. Yen[1], and C. S. Lin[1], [1]*Department of Biological Science and Technology, National Chiao Tung University*, *Hsinchu, Taiwan*, [2]*Division of Biotechnology, Animal Technology Institute Taiwan*, *Miaoli, Taiwan*.

Spontaneously immortalized porcine mammary epithelial cells (PMEC) isolated from the mammary gland of lactating sows can express milk

proteins following differentiation into mammary gland-like structures (gland ducts, lateral buds, and alveoli). Hollow fiber bioreactors have been used for large-scale mammalian cell culture to produce monoclonal antibodies or recombinant proteins. The hollow fibers provide a culture system with a high surface to volume ratio. The system allows extremely efficient exchange of nutrients and waste products across the fiber wall. Therefore, we attempted to culture PMEC transformed with recombinant DNA in these hollow fiber bioreactors to produce recombinant proteins. In the present study, we investigated the optimum conditions for culturing the PMEC onto polysulfone hollow fibers (PHF). The results showed that the seeded PMEC could attach, grow and form monolayers on the surface of PHF. The PMEC could differentiate into mammary gland-like structures when the cells were grown on PHF coated with Matrigel. The regulatory region of the milk gene, α lactalbumin, was inserted upstream of luciferase cDNA to generate a recombinant DNA, pAL-luc. The pAL-luc was transformed into PMEC and used to test the potential for recombinant protein production by PMEC cultured on PHF. Luciferase activity expressed from the PMEC grown on the PHF coated with 2.5 mg/ml and 5 mg/ml Matrigel were increased by 2.7-fold and 7.0-fold compared with that of the cells grown on the PHF without Matrigel (n = 3). Moreover, prolactin supplementation enhanced the luciferase expression. In this established PHF-cell culture approach, the PMEC could be continuously cultured for one week and potentially express recombinant protein. In conclusion, we have provided a potential PHF-cell culture approach in which PMEC can differentiate and express recombinant protein.

Key Words: mammary epithelial cells, polysulfone hollow fiber, recombinant protein

M146 Effects of nutrient restriction on mammary cell activity and hormonal statement in lactating dairy cows. F. Dessauge*[1,2], V. Lollivier[1,2], E. Cutullic[1,2], J. Portanguen[1,2], C. Disenhaus[1,2], S. Barbey[3], B. Ponchon[1,2], and M. Boutinaud[1,2], [1]*INRA UMR 1080 Dairy Production*, *35590, Saint Gilles, France*, [2]*Agrocampus UMR 1080 Dairy Production*, *35000, Rennes, France*, [3]*INRA UE 326 Domaine Experimental du Pin au Haras*, *61310, Le Pin au Haras, France*.

Feed restriction results in milk yield (MY) decrease. However the consequences on mammary activity and the involvement of prolactin (PRL) in the lower mammary synthesis are not known. The aim of the study was to investigate the effects of nutrient restriction on mammary epithelial cell activity in lactating dairy cows. We used 15 Holstein × Normande crossbred dairy cows, divided into 2 groups submitted to 2 feeding levels. From calving to wk 11 postpartum, the cows were fed a total mixed ration composed either of 55% maize silage, 15% dehydrated alfalfa and 30% concentrate (Basal diet-group as control, n = 7) or of 60% grass silage and 40% hay (Restricted diet-group, n = 8). Cows were milked twice daily. MY and composition were measured. Blood samples were harvested at wk 11 postpartum for the determination of PRL concentration. After 11 weeks of lactation, cows were slaughtered and mammary glands were removed and weighted. Expression of proteins involved in secretory activity was evaluated on mammary tissue by real-time qPCR and immunohistochemical staining was performed. Restricted diet-group cows had lower 11-week average daily MY (20.5 kg/d vs. 35.5, $P < 0.001$) and lower milk protein and lactose content from calving to slaughter than Basal diet-group cows. The size of the mammary acini were lower (−41%, $P < 0.01$) in the Restricted diet-group. Nutrient restriction decreased kappa-casein ($P < 0.01$) and α-lactalbumin ($P < 0.01$) mRNA levels in the mammary gland. The decrease in mean PRL concentration was not significant (−27%, $P = 0.15$) in Restricted diet-group compared with Basal diet-group. In conclusion, nutrient restriction resulted in a lower MY in lactating dairy cows. This was partly due to a modulation of mammary epithelial cells activity regulated at mRNA level.

Key Words: nutrient restriction, mammary epithelial cell, prolactin

M147 Effects of incremental sunflower seed supplementation on milk composition and mammary expression of genes regulating fatty acid uptake and lipogenesis. J. W. Møller, T. Bjørn, P. K. Theil, M. T. Sørensen, and K. Sejrsen*, *Faculty of Agricultural Science, Aarhus University*, *Tjele, Denmark*.

Dietary supplementation with unsaturated fatty acids is a well-established strategy for enhancing milk fat content of unsaturated fatty acids. The objective was to examine the effects of increased sunflower seed supplementation (SFS) on milk fat composition and mammary expression of genes regulating fatty acid uptake and lipogenesis. Twenty 4 lactating Holstein Friesian cows (186 ± 20 DIM; 25.3 ± 2.5 kg/d) were randomly assigned to 4 groups and fed a control diet or diets supplemented with 5%, 10%, or 15% sunflower seeds (% of DM) for a 5 week experimental period. DM intake and milk yield was reduced in cows fed 10% and 15% SFS when compared with control, whereas 5% SFS did not differ from control. All levels of SFS tended to increase milk fat content ($P = 0.08$). SFS decreased content of C4–14 ($P = 0,008$) and C16 fatty acids ($P = 0.014$). Content of ≥ C18 fatty acids was increased ($P = 0.015$). SFS increased the level of unsaturated fatty acids ($P < 0.001$) when compared with control and increased in a linear manner ($P < 0.001$) the content of rumenic acid (C18:2 c9t11) from 0.3% to 0,9%. Gene expression was analyzed by RT-PCR on RNA from mammary biopsies using the ΔΔCT method. SFS (5–15%) reduced mRNA abundance of SREBP-1 ($P = 0.034$), SCAP ($P = 0.0075$), FASN ($P = 0.035$), FADS1 ($P = 0.006$), and SCD ($P = 0.046$). mRNA abundance of ACC tended to be reduced ($P = 0.06$). SFS did not affect expression of the lipid uptake and transport genes LPL ($P = 0.189$), FABP3 ($P = 0.862$), and FAT ($P = 0.403$). In conclusion, our results show that dietary supplementation with high levels of unsaturated fatty acids in form of sunflower seeds leads to increased milk fat content in spite of decreased de novo milk fat synthesis as substantiated by a reduction in lipogenic genes. Furthermore, the expression of genes regulating fatty acid uptake and transport were unaffected although the amount of dietary fat present in milk was increased.

Key Words: dietary supplementation, mammary gene expression, conjugated linoleic acid

M148 Principal component analysis of milk fatty acid composition and the relationships between stearoyl CoA desaturase genotype and conjugated linoleic acid production in dairy cattle. J. Thomson*, L. Clark, M. Oba, and S. Moore, *University of Alberta*, *Edmonton, AB, Canada*.

The objectives of this study were to assess the relationships between individual milk fatty acids and conjugated linoleic acid (CLA) concentration in bovine milk fat and to assess the relationship between a single nucleotide polymorphism in the stearoyl CoA desaturase gene and CLA production using principal component analysis (PCA). 215 cows from an Alberta commercial dairy farm were genotyped and milk samples were collected for milk fatty acid analysis. Forty-three variables including milk production parameters, individual fatty acid concentrations, and indices of desaturation were analyzed. The first 3 principal components explained 47.61% of the total variance (PC 1, 24.13%; PC 2, 13.95%; and PC 3, 9.53%). The first PC had high loadings for most of the short chain fatty acids, the second PC had high loadings for the yield

measurements, and the third PC had high loadings for long chain fatty acids. Thus, the majority of the variables were described by 3 principal components. There was a positive correlation among the short chain or de novo synthesized fatty acids (C4-C16) ($P < 0.05$), and a negative correlation between the de novo synthesized fatty acids and the long chain fatty acids which primarily come from peripheral circulation (C18 and C20 isomers) ($P < 0.05$). CLA concentration had a positive correlation with C18:1 t6–8, C18:1 t9, C18:1 t10, C18:1 t12, C18:1 t13–14 and 18:1 t11 ($P < 0.05$). CLA was negatively correlated with C18:1 c9 ($P < 0.05$). A high positive correlation between the concentration of C12:0 with CLA yield (coefficient of 0.85, $P < 0.0001$) was observed. The CLA desaturation index (CLA /18:1t11 + CLA) was positively correlated to C8:0, C10:0, C12:0, C14:0, C14:1, and C16. This relationship may warrant further research. Genotype did not explain a significant amount of the variation in these data. This suggests that fatty acid origin (de novo synthesized fatty acids vs. fatty acids from circulation) had a much bigger impact than genotype on fatty acid variation in milk.

Key Words: stearoyl CoA desaturase, milk fatty acids

M149 Improved lactation persistence and altered milk composition in growth hormone-treated mice is not linked to dramatic changes in mammary mitochondrial biogenesis or the degree of mTOR or AMP kinase phosphorylation. W. Olea*[1], A. Parlow[2], R. Collier[3], and D. Hadsell[1], [1]*Baylor College of Medicine*, *Houston, TX*, [2]*Harbor-UCLA Medical Center*, *Torrance, CA*, [3]*University of Arizona*, *Tucson*.

Previous work in our lab has shown that mice treated with growth hormone (GH) under both ad-libitum (AL) and reduced (4X) nursing frequency can support greater litter gain during prolonged lactation. However, the mechanism of this response is not well understood. Our hypothesis was that GH treatment would increase milk production or alter milk composition through effects on signaling pathways regulating protein synthesis or mitochondrial biogenesis. To test this hypothesis we compared milk concentrations of fat, protein, and lactose, mammary mitochondrial (mt) DNA copy number, and the phosphorylation of mammalian target of rapamycin (mTOR) and AMP kinase (AMPK) in mammary tissue from lactating mice treated (n = 6/treatment) with either saline (SAL) or recombinant murine GH (18 mg/kg/day) under conditions of either AL or 4X nursing frequency during prolonged lactation. GH treatment increased (main effect, $P < 0.05$) milk triglyceride (172.47 ± 25.42, 321.50 ± 33.33, 185.27 ± 51.75, and 271.45 ± 52.07 mM for AL-SAL, AL-GH, 4X-SAL, and 4X-GH, respectively), and protein concentrations (93.68 ± 7.02, 109.63 ± 9.84, 81.68 ± 6.32, 106.64 ± 9.78 mg/mL for AL-SAL, AL-GH, 4X-SAL,4X-GH, respectively). Mitochondrial DNA copy number, measured as the ratio of cytochrome-B to β-Actin by real time qPCR, was not significantly impacted by nursing frequency or GH treatment. Immunofluorescent staining for Phospho-mTOR and phospho-AMPK were also not significantly affected by nursing frequency or GH treatment. Staining for total mTOR, however, was higher in GH treated animals than SAL (main effect, $P < 0.01$). These results support the conclusion that although GH treatment increases milk production and alters milk composition during prolonged lactation in mice, this response is not mediated through dramatic alterations in the phosphorylation of mTOR or AMPK or through affects on mitochondrial biogenesis.

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Key Words: growth hormone, persistence, mitochondria

M150 Beef quality of bovines supplemented with vitamin E. G. Aranda-Osorio*[1], H. Barragan-Gonzalez[1], M. Huerta-Bravo[1], O. Hernandez-Mendo[2], E. Maldonado-Siman[1], and J. C. Garcia-Ortiz[1], [1]*Universidad Autonoma Chapingo*, *Chapingo, Mexico*, [2]*Colegio de Posgraduados*, *Montecillos, Mexico*.

The aim of this study was to establish the feeding duration and dietary level of vitamin E offered to young bulls which does not affect performance but positively improve shelf-life of beef. Three experiments were carried out: E1) 1,000 IU vitamin E/animal per d fed during 37, 49, and 63 d; E2) 2,000 IU vitamin E/animal per d fed for 77 d and E3) 3,000 IU vitamin E/animal per d fed for 55 d. In E1, E2 and E3 a total of 36 (12, 549 ± 22.44; 12, 510.42 ± 27.48; and 12, 480.25 ± 19.99 kg), 24 (396.21 ± 24.39), and 24 (432.50 ± 23.81 kg) crossbred (*Bos taurus* × *Bos indicus*) young bulls were used, respectively. Average daily weight gain (ADG), dressing percentage (DP) as well as pH, water retention capacity (WRC), L* and chroma values and hue angle (hue°) of the rib eye (obtained between the 12th and 13th rib) were determined. Data were analyzed as a randomized block (E1) and completely randomized (E2 and E3) design using PROC GLM of SAS. Neither ADG nor DP were negatively affected ($P \leq 0.05$) by the feeding duration or the dietary vitamin E level (E1, E2 or E3). Differences ($P \leq 0.05$) in pH, L*, chroma and hue° in beef until d 63 (E1) of supplementation were observed in animals offered vitamin E. There were no ($P \geq 0.05$) differences in beef quality traits on d 1 post-mortem, but differences ($P \leq 0.05$) were found on d 8 and 16 post-mortem (E2), when the beef color was more stable. In E3 the beef quality traits were similar to those found in E2, suggesting that supplementing 3,000 IU of vitamin E/animal per day during 55 d had a similar effect than supplementing 2,000 IU vitamin E/animal per d during 77 d. In conclusion, it is feasible to supplement 1,000, 2,000, or 3,000 IU of vitamin E/animal per d without compromising the finishing performance. However, the vitamin E supplement has to be offered for at least 45 d before the slaughter to improve beef quality.

Key Words: beef cattle, vitamin E, meat traits

M151 Effect of vitamin E supplementation on the finishing of beef cattle. G. Aranda-Osorio*[1], P. De la Cruz-Honorato[1], R. Hernadez-Arrieta[1], O. Hernandez-Mendo[2], and J. C. Garcia-Ortiz[1], [1]*Universidad Autonoma Chapingo*, *Chapingo, Mexico*, [2]*Colegio de Posgraduados*, *Montecillos, Mexico*.

The objective of this study was to evaluate the effect of vitamin E supplementation on performance (dry matter intake (DMI), average daily gain (ADG), feed conversion (FC), feed efficiency (FE), backfat depth (BFD), trimming fat (TF), hot carcass yield (HCY), and profitability of finishing young bulls. Two experiments were carried out. In experiment 1 (E1), 36 young bulls (*Bos taurus* × *Bos indicus*) were assigned to 3 BW blocks (549.50 ± 22.44, 510.42 ± 27.48 and 480.25 ± 19.99 kg) and offered 1000 IU vitamin E /head per d for 37, 49 or 63 d during the finishing period. To each BW block 12 animals were assigned (6 with and 6 without vitamin E supplementation). Each bull was the experimental unit, with 6 replicates per treatment. In experiment 2 (E2) 24 young bulls (*Bos taurus* × *Bos indicus*) with an ILW of 396.21 ± 24.39 were used. Half of them were offered 2000 IU vitamin E/head per d during 77 d. They were vaccinated against *Clostridium*, dewormed, vitamined, implanted and individually penned (2 × 2 m). The diet was based on corn (42.2%), bakery waste (24.6%), barley straw (22.9%), soybean meal (7.93%), minerals (2%), and $CaCO_3$ (0.4%), with 13.1% crude protein, 1.79 Mcal ENm, 1.16 Mcal ENg and 11.6% crude fiber. The animals were slaughtered the d after they finished their fattening period. Data were analyzed as a randomized block (E1) and completely randomized (E2) design using PROC GLM of SAS. In E 1, vitamin E supplementation for 37 d enhanced ($P \leq 0.05$) DMI, ADG, FC, FE, BFD, and TF but decreased ($P \leq 0.05$) HYC. However, vitamin E supplementation for 49 or 63 d enhanced ($P \leq 0.05$) DMI but affected ($P \leq 0.05$) ADG, FC, FE, BFD, and HCY. In E 2, 2000 IU vitamin E supplementation improved ($P \leq 0.05$) feedlot performance but decreased ($P \leq 0.05$) FC. However, due to the high costs of dietary vitamin E profitability was reduced. It is concluded that vitamin E supplementation in the finishing period of young bulls did not negatively affect animal performance and therefore can be used to improve beef quality.

Key Words: young bulls, vitamin E, performance

M152 Influence of different forms of lipid supplements on physical characteristics of heifers' meat fed on feedlot system. M. C. A. Santana*[1], T. T. Berchielli[1], R. A. Reis[1], G. T. Pereira[1], and R. C. Canesin[1], [1]*São Paulo State University*, *Jaboticabal, São Paulo, Brazil*, [2]*Bellman Animal Nutrition Mineral Supplements*, *Jaboticabal, São Paulo, Brazil*.

Physical quality of meat products can be influenced by the feed offered to the animal. The evaluation of beef quality indicators is important because it is able of determining the product which will be offered to the consumer. The focus areas in this experiment are colors (a, b, L), shear force (WBSF), water-holding capacity (WHC), pH and cooking loss percentage (CLoss) in meat from heifers fed under different lipid supplements in feedlot system. The experiment design was completely random, using 3 supplements. The supplements came from soya lipid-based supplements, offered in different forms (soybean grain, soybean oil and protected fat - Megalac-E), 60:40 concentrate:corn silage. The treatments were compared by analyzing variables using the GLM procedure (SAS 9.1, SAS Institute, Inc., Cary, NC). Mean values were compared using the Tukey test at a significance level of 0.05. Using a colorimeter, the color of the longissimus muscle (LM) at the 12th and 13th rib interface in the L*a*b* color space (CIE system) was determined. A time span of 30 min was awaited before color analysis. The WBSF was obtained from steaks previously thawed and roasted using an insert thermometer until 70°C was obtained. Later, the samples were cut into cubes; the data collected was achieved using a Warner-Bratzler shear machine. The muscle pH measurements were taken from the interior of the LM at 24 h and 48h postmortem using a portable pH meter. The water holding capacity was obtained by determining the difference of the sample weights under 10 kg of pressure for 5 min. The cooking loss value was determined according to the reduced percentage rate before and after the meat was cooked. The results of this research suggest that the physical indicators of meat quality were not influenced by the supplements, offered in different forms (soybean grain, soybean oil and protected fat - Megalac-E).

Table 1. Means for the colors a, b and L, meat pH, water-holding capacity (WHC), and percentage cooking loss (CLoss) and shear force (WBSF) of heifer's meat from feedlot.

	Soybean grain	Soybean oil	Protected fat	Mean	CV (%)
WBSF (kgf/cm^3)	6.5	8.2	7.9	7.6	21.7^{NS}
WHC (%)	73.8	71.8	71.2	72.2	6.6^{NS}
CLoss (%)	34.7	33.7	32.7	33.6	5.1^{NS}
Color L (%)	35.0	34.0	34.7	34.5	7.4^{NS}
Color A (%)	16.6	16.7	16.4	16.5	13.5^{NS}
Color B (%)	3,5	3.5	3.6	3.6	33.6^{NS}
pH (48 h)	6.1	6.1	6.2	6.1	3.2^{NS}
pH (24 h)	5.6	5.6	5.7	5.6	2.2^{NS}

NS = nonsignificant.

Key Words: soybean grain, soybean oil, protected fat

M153 Effect of maternal nutritional status on muscle development and carcass characteristics in heifer progeny. L. V. Nicodemus*, K. R. Underwood, J. F. Tong, P. L. Price, B. W. Hess, S. I. Paisley, W. J. Means, R. J. McCormick, and M. Du, *Department of Animal Science, University of Wyoming*, *Laramie*.

In the Western United States, cow herds commonly experience nutrient deficiency due to frequent drought conditions. Mid to late gestation is an important time for skeletal muscle and adipose tissue development. The objective of this study was to evaluate the effects of maternal nutrient deficiency during mid gestation on the growth performance and carcass traits of heifer progeny. Thirty-two heifers, born to crossbred cows from 2 years were evaluated for the effects of dietary treatments from d 45 through d 180 of gestation on muscle development, meat quality, and carcass characteristics. At d 45 of gestation cows were randomly allotted to 1 of 3 dietary treatments consisting of individually fed native grass hay plus a soybean meal-based supplement: control (C, 100% NRC requirements), nutrient restricted (NR, 70% NRC requirements), and nutrient restricted plus ruminally undegradable protein supplementation (NRP, 70% NRC requirements with essential amino acids supplemented to the control level), and that 11 C, 7 NR and 14 NRP offspring heifers were produced from the herd. Following weaning, heifers from all treatments were back-grounded, and then place in the feedlot where they received a high concentrate diet until slaughter. Carcass characteristics were measured at 48 h postmortem. Steaks were removed 14 d postmortem for Warner-Bratzler Shear Force and proximate analysis. The 12th rib fat thickness of C heifers was less ($P \leq 0.05$) than that of NR. The Semitendinosus muscle weight was reduced in NR compared with C carcasses ($P \leq 0.05$). There was no difference in LM area, percent KPH fat, or marbling scores between treatments. Data show that a low plane maternal nutrition during early to mid-gestation increased fatness and reduced muscling of heifer progeny, and protein supplementation had no major impact on carcass composition of offspring heifers.

Key Words: maternal nutrition, beef, fetal development

M154 Nutrient restriction during early prenatal growth and carcass characteristics of beef steers. T. A. Pye*, B. H. Boehmer, R. P. Wettemann, and G. W. Horn, *Oklahoma Agricultural Experiment Station*, *Stillwater*.

To evaluate the effect of prenatal nutritional restriction on carcass characteristics, Angus heifers (15 mo of age) were AI, and after 32 ± 1 d, pregnancy was determined. Heifers were stratified by BW and BCS and allotted to low (L, 55% of NRC requirements) or moderate nutritional (M, > 100% NRC requirements) treatment groups. After 86 d of treatment (128 d of gestation), heifers were managed in a single pasture and received a common diet (>100% of NRC requirements). Bulls were castrated at birth, weaned at 230 d, and maintained as a group before and after weaning. At 14 (rep 1) or 18 mo (rep 2) of age, L (n = 13) and M (n = 10) steers were fed a high-energy finishing diet and gained 2.1 ± 0.2 kg/d to a BW of 592 ± 7 (rep 1) or 631 ± 6 kg (rep 2). Steers were harvested at 1.3 ± 0.2 cm backfat. Data were analyzed using PROC GLM procedures of SAS. There was no treatment × rep effects ($P > 0.32$). At onset of treatment, BW ($P = 0.37$) and BCS ($P = 0.30$) were similar for L and M heifers. During early gestation M heifers gained 68 ± 7 kg and L heifers lost 54 ± 8 kg ($P < 0.001$). After treatment, M heifers had greater BCS (5.5 ± 0.1) compared with L heifers (4.3 ± 1; $P < 0.001$). Hot carcass weight ($P < 0.001$), dressing percentage ($P < 0.001$), REA ($P < 0.02$), marbling ($P < 0.001$) and KPH fat ($P < 0.001$) were influenced by replication but not by prenatal nutritional treatment ($P > 0.15$). Neither treatment nor replication influenced yield grade or fat thickness at the 12th rib. Major nutritional restriction of young bovine dams during 32 to 118 d of gestation, that resulted in 1.2 BCS units difference, did not influence carcass characteristics of steer progeny at normal harvest weights.

Key Words: beef cattle, carcass characteristics, prenatal programming

M155 Residual feed intake in three-cross beef heifers: color and chemical composition of *Longissumus dorsi* muscle. S. F. Reis[1], P. V. R. Paulino*[1], S. R. Medeiros[2], S. C. Valadares Filho[1], G. L. D. Feijó[2], R. A. A. Torres Júnior[2], R. O. Cristaldo[2], R. A. Silva[2], D. A. Fausto[3], and J. Cavali[1], [1]*Universidade Federal de Viçosa*, *Viçosa, MG, Brazil*, [2]*EMBRAPA Gado de Corte*, *Campo Grande, MS, Brazil*, [3]*Universidade de São Paulo*, *Piracicaba, SP, Brazil*.

Residual feed intake (RFI), as an index for feed efficiency selection, is promising because it is independent of growth traits of the animal. However, studies have shown that efficient animals (low RFI) tend to produce beef with less intramuscular fat (IMF). This trial aimed to evaluate the color and chemical composition of *Longissumus dorsi* (LD) muscle of 31 3-cross beef heifers. The same diet (ME = 2.73 Mcal/kg DM, CP = 11.90% DM) was fed during 84 d. The experiment was conducted according to a completely randomized design. The animals were classified in 3 groups according to their RFI value (high, medium or low). The RFI was calculated as the difference between an animal's actual and predicted feed intake – Predicted DMI = −3.82593 + 0.15438 × MBW + 1.09531 × ADG. At the end of the trial all animals were slaughtered. After 18 h of chilling, color (L*, a *, b *) of the LD was evaluated, according to CIELAB system. A sample of the LD was collected to assess the chemical composition. Data were analyzed using the PROC GLM of SAS and the effects of treatments were considered significant at $P < 0.05$. Chemical composition and color of the LD was similar ($P > 0.05$) among RFI groups. The mean chemical composition of the LD obtained was 4.28% fat; 18.3% CP and 77.42% moisture. The mean L*, a* and b* values were 40.47, 24.74 and 16.13, respectively. The L* and a* values were greater than those commonly reported for

beef (35.00 – 38.00 and 18 – 22, respectively). The b* value found in this study (16.13) was greater than the values reported for cattle under feedlot conditions (3.00 to 5.00). The yellow intensity is related to the amount and color of IMF in the meat. Thus, one can hypothesize that it might have been influenced by the high proportion of IMF (4.28%) found in this study as well as to a greater carotene incorporation, once the animals were raised on pasture for approximately 2 years before being placed in a feedlot. We conclude that efficient animals (low RFI) produce beef with color attributes and chemical composition similar to that produced by less efficient animals (high RFI).

Key Words: feedlot, feed efficiency, meat color

M156 Residual feed intake in three-cross beef heifers: Sensorial traits of *Longissimus dorsi* muscle. S. F. Reis[1], P. V. R. Paulino*[1], R. A. Silva[3], S. R. Medeiros[2], S. C. Valadares Filho[1], G. L. D. Feijó[2], R. A. A. Torres Júnior[2], F. A. Curci[2], and M. A. Rezende[2], [1]*Universidade Federal de Viçosa*, *Viçosa, MG, Brazil*, [2]*EMBRAPA Gado de Corte*, *Campo Grande, MS, Brazil*, [3]*Universidade Federal do Mato Grosso do Sul*, *Campo Grande, MS, Brazil*.

Studies have indicated that animals selected for residual feed intake (RFI) may produce lean carcasses which can result in changes in sensory traits of meat. This trial aimed to evaluate sensorial traits (flavor, texture and juiciness) of *Longissumus dorsi* (LD) muscle of 31 3 cross beef heifers. A same diet (ME = 2.73 Mcal/kg DM, CP = 11.90% DM) with roughage:concentrate ratio of 40:60 was fed during 84 d. The experiment was conducted under a completely randomized design. The animals were classified in 3 groups according to its RFI value (high, medium or low). RFI was calculated as the difference between an animal′s actual and predicted feed intake – Predicted DMI = −3.82593 + 0.15438 × MBW + 1.09531 × ADG. At the end of the trial all animals were slaughtered and the carcasses chilled for about 18 h. After chilling, a sample was removed from LD muscle to evaluate sensorial traits and shear force (SF). The sensorial panel was composed by trained individuals (regular consumers of beef, up to 3 times / week). The sensory panel scores were attributed for each sample, following a scale ranging from 1 (low meat quality) to 9 (high meat quality). Data were analyzed using the GLM procedure of SAS. No differences ($P > 0.05$) between classes of efficiency for the sensorial traits and SF of LD muscle were detected. Sensory panel score means for flavor, texture and juiciness were 5.6; 6.1 and 5.4. As all traits were analyzed by a subjective method (sensory panel), only very contrasting results would be detected as different. In this study, animals with low RFI produced meat tenderness similar to those from other classes of efficiency. The mean value of SF was 5.3 kg, which was above those usually reported to crossbred animals (about 4.0 kg) and it may be accounted to the fact that the heifers had 25% of zebu breeds in their composition. The hypothesis that animals with better RFI produce tougher and less desirable meat was not proven in this study, thus RFI is as an interesting tool to select animals in breeding programs.

Key Words: feed efficiency, feedlot, tenderness

M157 Ageing process influence on fatty acids relations in yearling bulls fed different sources of omega-3 and omega-6. A. A. M. Sampaio[1], T. M. Pivaro[1], E. A. Oliveira*[1], W. Henrique[2], B. L. Rosa[1], and A. R. M. Fernandes[3], [1]*FCAV/Unesp*, *Jaboticabal, SP, Brazil*, [2]*APTA*, *São José do Rio Preto, SP, Brazil*, [3]*UFGD*, *Dourados, MS, Brazil*.

The aim of this study was to investigate the effects of oil supplemented diets on the fatty acids levels of bovine *Longissimus thoracis* muscle aged for different days. Thirty-five yearling Nellore bulls were kept in feedlot during 96 d during which 5 dietary fat sources were tested: control (without oil), soybean oil, soybean oil rumen-protected, linseed oil and linseed oil rumen-protected. Sugarcane was the exclusive roughage source for all diets. Sections of loin meat (2.5 cm of thickness) were removed from each left half-carcass, vacuum packed and submitted to aging for 7, 14 and 21 d, followed by lyophilization, lipid extraction and methylation. Fatty acid methyl esters were analyzed using gas chromatography. All data were subjected to ANOVA and Student's *t*-test. The interaction treatment × aging period was not significant in this experiment. There were no ($P > 0.05$) differences for variables related to total amount of saturated and unsaturated fatty acids, neither for the saturated/unsaturated fatty acids ratio when comparing aging periods and *in natura* meat. Aged meat monounsaturated fatty acids values (46.66, 46.76 and 47.23%), monounsaturated:saturated ratio (1.04; 1.03; 1.04) and omega-6:omega-3 ratio (3.85; 3.76 and 3.99) for 7, 14, and 21 d, respectively, were lower ($P < 0.05$) when compared with non-aged meat (48.29%, 1.08, 4.12). However, the amount of polyunsaturated fatty acids was higher ($P < 0.05$) in aged (8.62, 7.89 and 7.44%, respectively) than in non-aged meat (6.18%). Aged meat values for omega-3 (1.24, 1.70 and 1.57%), omega-6 (6.14, 5.56 and 5.23%) and polyunsaturated:saturated ratio (0.19; 0.17 and 0.16) were also higher ($P < 0.05$) than in non-aged meat (1.44%, 4.88% and 0.13, respectively). Independently of the oil source, oil supplementation improves the fatty acid composition of meat aged for 7 and 14 d.

Key Words: fatty acids ratio, saturated fatty acids, unsaturated fatty acids

M158 Feeding flaxseed to beef cows increases concentrations of omega-3 fatty acids and linolenic acid biohydrogenation intermediates in subcutaneous fat. M. L. He[1,3], T. A. McAllister*[1], J. P. Kastelic[1], Y.-H. Chung[1], K. A. Beauchemin[1], P. S. Mir[1], J. L. Aalhus[2], M. E. R. Dugan[2], and N. Aldai[2], [1]*Lethbridge Research Centre, Agriculture and Agri-Food Canada*, *Lethbridge, AB, Canada*, [2]*Lacombe Research Centre, Agriculture and Agri-Food Canada*, *Lacombe, AB, Canada*, [3]*University of Saskatchewan, Saskatoon*, *Saskatoon, SK, Canada*.

This study was conducted to investigate changes in fat deposition and fatty acid profiles in beef cows fed hay or silage based diets, with or without flaxseed supplementation. Crossbred cull beef cows (64, > 30 mo of age, 620 ± 5 kg) were removed from grassland pastures, randomly assigned to 16 pens and given ad libitum access to 50:50 (wt:wt, DM basis) forage:concentrate diets containing 0 or 15% ground flaxseed (DM basis, 5.2% added fat). The diets were: hay control, HC; hay+flaxseed, HF; silage control, SC; silage+flaxseed, SF. Flaxseed improved ($P < 0.01$) feed conversion ratio and tended to increase body weight gain ($P = 0.10$) and back fat thickness ($P = 0.07$), as assessed by ultrasonography. Compared with hay, silage increased ($P < 0.01$) feed intake, body weight gain, fat thickness ($P = 0.07$) and improved ($P < 0.01$) feed conversion. Subcutaneous fat contained 0.65% omega-3 fatty acids (wt:wt) at arrival, which reached concentrations of 0.69, 0.81, and 0.93% in HF cows, and 0.65, 0.77, and 0.90% in SF cows, after 6 wk, 12 wk, and at slaughter, respectively. In contrast, at these same sampling points, omega-3 fatty acids had decreased in HC and SC cows, to 0.50, 0.47, and 0.43%, and to 0.39, 0.36, and 0.33%, respectively. Flaxseed also improved ($P < 0.01$) wt:wt of conjugated linoleic acids in plasma and fat and resulted in an accumulation of non-conjugated, non-methylene interrupted dienes in fat. This was more pronounced ($P < 0.01$) in cows fed with hay- than with silage-based diet. In summary, a 15% flax supplement in hay- or silage-based diets fed to cows coming off fall pastures increased omega-3 fatty acid concentrations,

which was accompanied by increased concentrations of linolenic acid biohydrogenation intermediates.

Key Words: cull beef cow, flaxseed, omega-3 fatty acids

M159 Effect of finishing system on subcutaneous fat melting point and fatty acid composition. S. K. Duckett*[1], J. P. S. Neel[2], W. S. Swecker[3], J. P. Fontenot[3], and W. Clapham[2], [1]*Clemson University*, *Clemson, SC,* [2]*USDA-ARS*, *Beaver, WV,* [3]*Virginia Tech University*, *Blacksburg*.

Angus-cross steers (n = 69) were used to determine the effect of finishing system on subcutaneous fat melting point and fatty acid composition. Three finishing systems were evaluated: 1) mixed pasture for 134 d [MP], 2) mixed pasture for 93 d and alfalfa for 41 d [AL], or 3) concentrate finishing for 134 d [CONC], in a 2-yr study. Subcutaneous fat samples at the 12th rib were obtained at 24 h postmortem. Melting point was determined using the OptiMelt Automated Melting Point System. Total saturated fatty acid (SFA) and omega-3 fatty acid contents were greater ($P < 0.05$) for AL and MP than CONC. Monounsaturated fatty acid and omega-6 polyunsaturated fatty acid contents were greater ($P < 0.05$) for CONC than AL and MP. The ratio of omega-6 to omega-3 fatty acids was higher for CONC (8.81) than forages (1.64), regardless of forage species grazed. Average temperature for onset point, start of melting point where liquid first appears, was higher ($P < 0.05$) for MP and AL than CONC. Average temperature for clear point, melting point where fat is completely liquid, was higher ($P < 0.05$) for MP and AL than CONC. Melting point was highly, positively correlated with SFA (r = 0.73) and highly, negatively correlated with MUFA (r = −0.78) and omega-6 (r = - 0.60). Prediction equations for s.c. fat melting point included MUFA and SFA contents, and explained 83% or 93% of the variation for AL and MP, respectively. Prediction equations for s.c. fat melting point included omega-3, omega-6 and SFA, and explained 57% of the variation for CONC. Finishing system altered subcutaneous fat composition and melting point. Finishing on forages (MP and AL) increased SFA by 17% and decreased MUFA by 24%, which translated to a higher subcutaneous fat melting point (42.35 vs. 38.64 C).

Key Words: beef, forages, fatty acids

M160 Effects of supplemental dietary lipid sources on fatty acids compositions of *Longissimus* muscle in yearling bulls. E. A. Oliveira*[1], A. A. M. Sampaio[1], W. Henrique[2], B. L. Rosa[1], T. M. Pivaro[1], and A. R. M. Fernandes[3], [1]*FCAV/Unesp*, *Jaboticabal, SP, Brazil*, [2]*APTA*, *São José do Rio Preto, SP, Brazil*, [3]*UFGD*, *Dourados, MS, Brazil*.

The aim of this study was to improve fatty acids composition of bovine *Longissimus* muscle by adding different sources of fat in the diet of Nellore yearling bulls. Thirty-five animals, averaging 18 mo of age (402.69 ± 14.90Kg), were housed during 96 d in individual pens at Jaboticabal Campus of São Paulo State University. Five different diets were tested: control (without oil), soybean oil (3.8% of diet), rumen-protected soybean oil (4.5% of diet), linseed oil (3.8% of diet) and rumen-protected linseed oil (4.5% of diet). All diets included sugarcane as exclusive roughage source. The experiment was a randomized block design with 7 blocks and 5 replications and means were compared by orthogonal contrasts. After 24 h of carcass cooling process, *Longissimus thoracis* (<b < LT) muscle sections were removed at the 12–13th rib level and submitted to lyophilization, lipid extraction and methylation. Samples were analyzed by gas chromatography. The LT of animals fed the oil-supplemented diets had higher ($P < 0.05$) levels of conjugated linoleic (CLA) (0.72% vs 0.35%) and linolenic acid (LLA) (0.66% vs. 0.32%) and lower levels ($P < 0.05$) of saturated fatty acid. Among oil-supplemented diets, there was no ($P > 0.05$) difference for CLA when comparing soybean and linseed oil (0.77% and 0.67%, respectively). However, the LT of animals fed linseed oil had higher ($P < 0.05$) levels of LLA (1.21% vs. 0.44%). There was no ($P > 0.05$) difference between control and other diets concerning saturated and unsaturated fatty acids concentrations. Omega6:omega3 ratio was lower ($P < 0.05$) and closer to ideal for linseed oil when compared with the other diets (2.36 vs. 3.77, respectively). Soybean or linseed oils supplementation to feedlot cattle provides better fatty acids composition and improve their relationship, leading to a healthier and more balanced meat, independently of being protected or not.

Key Words: beef, fatty acids, health

M161 Fatty acid profile of intramuscular fat of young bulls grazing tropical pasture and supplemented with different strategies. J. Cavali[1], P. V. R. Paulino*[1], I. M. Oliveira[1], M. M. C. Silva[1], H. J. Fernandes[2], R. Mezzomo[1], J. F. H. Rodrigues[1], É. E. L. Valente[1], S. F. Reis[1], and L. A. M. Gomide[1], [1]*Universidade Federal de Viçosa*, *Viçosa, MG, Brazil*, [2]*Universidade Estadual do Mato Grosso do Sul*, *Aquidauana, MS, Brazil*.

Grass fed beef gathers desirable nutritional characteristics that are valuable to the final consumer. The objective of this study was to evaluate the fatty acid profile of intramuscular fat (IMF) of young bulls grazing *Brachiaria decumbens* pastures and supplemented with different strategies. Fifty 2 Nellore young bulls were used, being distributed, in a completely randomized design, into 4 treatments (13 replicates): control, when the animals had free access only to mineral mixture throughout the experiment; and 3 protein supplementation strategies, when the animals were creep-fed with supplements containing 10, 20 and 30% CP, respectively. After weaning the creep-fed animals received isonitrogenous supplements designed to supply 0.50 and 0.66 g of CP/day during growing and finishing, respectively. After 580 d, the animals were slaughtered and a sample of the *Longissimus dorsi* was taken at the level of the last rib and the fatty acid profile of the IMF was determined by gas chromatography. IMF of bulls of the control group (pasture + mineral mixture) had greater ($P < 0.10$) contents of palmitic (C16:0), oleic (C18:1), linoleic (C18:3) and eicosapentaenoic acid (EPA), more monounsaturated fatty acids (MUFA) and lower estearic acid (C18:0) when compared with the other groups, but did not differ ($P > 0.10$) from the supplemented counterparts regarding total saturated fatty acids (SFA) content. Protein supplementation improved ($P < 0.10$) the amount of polyunsaturated fatty acids (PUFA) and n-6/n-3 ratio of the IMF of the animals, when compared with the control group. However, the MUFA and EPA content of the IMF of the supplemented animals were lower ($P < 0.10$) than the values observed in the animals that received only mineral mixture. Different strategies of protein supplementation of young bulls grazing tropical pastures can modify the fatty acid profile of intramuscular fat and thus be used as a tool to produce beef that meets specific niche markets.

Key Words: beef cattle, pasture, protein supplementation

M162 How do n-3 fatty acids affect human perception of ground beef? T. Jiang*, J. R. Busboom, M. L. Nelson, and R. Mengarelli, *Washington State University*, *Pullman*.

Our objective was to determine the impact of increasing levels of Eicosapentaenoic acid (EPA; C20:5n-3) and Docosahexaenoic acid (DHA; C22:6n-3) on beef palatability. Two commercial supplements of EPA and DHA (GNC DHA 250 with DHA: EPA = 2.5:1 and GNC Triple Strength Fish Oil with EPA: DHA = 2.6:1) were added to patties

(176.2 ± 3.76 g) made from 85% lean ground beef with different levels (0, 0.3, 0.4, 0.5, 0.6, 0.7, and 1% as-is). Olive oil was added so that a total of 1% lipids were added to all treatments. A control treatment was prepared with no fatty acid supplement or olive oil. Patties were aged for 72 h at 3°C, frozen at –20°C and vacuum packaged. A 9-member trained sensory panel was conducted to evaluate beef aroma, off-aroma, beef flavor, off-flavor, tenderness, juiciness, and overall acceptability of ground beef on a 10-cm unstructured line scale labeled at each end. Six tasting sessions were conducted with 6 patties served in each session. Patties were assigned across the sessions in a randomized complete block design, with the first 3 sessions as block 1 and the next 3 as block 2. Control and 0% supplement (1% olive oil) patties were served in each session. Results indicated that increasing levels of DHA did not impact ground beef palatability. Similarly, increasing levels of EPA had no impacts on most sensory attributes. However, off-aroma and off-flavor scores vs. EPA levels fit a non-linear plateau model ($P < 0.0001$). The slopes (β_1) of the models for off-aroma and off-flavor were 4.4 ± 0.62 and 9.0 ± 0.95, respectively. The maximum scores (D) were 1.9 ± 0.35 and 4.2 ± 0.53 for off-aroma and off-flavor, respectively. In conclusion, n-3 long chain polyunsaturated fatty acid EPA had a greater negative impact on ground beef palatability than DHA. Furthermore, the panelists seemed to be more sensitive to EPA in off-flavor perception than off-aroma.

Key Words: EPA, DHA, ground beef palatability

M163 Geometrical isomers of octadecenoic, octadecadienoic and octadecatrienoic acids from subcutaneous fat of British or Continental versus Nellore crossbred cattle slaughtered at different end points. R. Mello*[1], A. C. de Queiroz[2], F. D. de Resende[3], D. P. D. Lanna[4], M. H. de Faria[3], and E. da Costa Eifert[4], [1]*Universidade Federal de Santa Maria*, *Santa Maria, RS, Brazil*, [2]*Universidade Federal de Viçosa*, *Viçosa, MG, Brazil*, [3]*Agência Paulista de Tecnologia dos Agronegócios*, *Colina, SP, Brazil*, [4]*Universidade de São Paulo – Escola Superior de Agricultura 'Luiz de Queiroz'*, *Piracicaba, SP, Brazil*.

The study was carried out to evaluate the effect of genetic group (GG) and slaughter weight on C18:1, C18:2 and C18:3 fatty acids isomers in subcutaneous fat sampled at the 13th rib. Thirty 6 young (20 mo) bulls, 18 crossbred F1 Red Angus × Nellore (1/2 RA 1/2 N) at 447.7 ± 5.8 kg of shrunk body weight (SBW) and 18 F1 Blonde D′Aquitaine × Nellore (1/2 BA 1/2 N) at 444.3 ± 6.5 kg of SBW were used. The animals were in compensatory growth. The young bulls were feedlot finished and slaughtered at 480, 520 and 560 kg of SBW. A completely randomized experimental design in a 2 × 3 (2 genetic groups × 3 slaughter weights) factorial arrangement with 6 replicates was used. Data were analyzed with SAS software using initial SBW as a covariate. The backfat thickness increased ($P < 0.05$) as slaughter weight rised, being 2.1, 2.7 and 4.4 mm, respectively, for animals slaughtered at 480, 520 and 560 kg. The 1/2 RA 1/2 N young bulls had a higher ($P < 0.05$) *cis*-12 C18:1, *cis*-9,12 C18:2, and *cis*-9,12,15 C18:3 levels than 1/2 BA 1/2 N young bulls. As the slaughter weight rised the *cis*-15, *trans*-9, *trans*-11, and *trans*-12 C18:1 levels decreased ($P < 0.05$); while *cis*-11 C18:1 level increased. The *trans*-11 *cis*-15 C18:2, *cis*-9 *trans*-11 C18:2 (CLA), and *cis*-6,9,12 C18:3 levels also decreased ($P < 0.05$) as the slaughter weight increased. The interaction between GG and SW was significant ($P > 0.05$) for *cis*-9, *cis*-13 and *trans*-16 C18:1 levels. The 1/2 RA 1/2 N young bulls slaughtered at 520 kg had lower *cis*-9 and *cis*-13 C18:1 levels and the 1/2 RA 1/2 N slaughtered at 560 kg had lower *trans*-16 C18:1 level than others. Thus, crossbred F1 Red Angus × Nellore young bulls had higher *cis*-9,12,15 C18:3 ($\alpha = n$-3) level in the subcutaneous fat (0.41) than F1 Blonde D′Aquitaine × Nellore young bulls (0.37). Animals slaughtered at lighter weights had higher *cis*-9 *trans*-11 C18:2 (CLA, 0.50) and *cis*-6,9,12 C18:3 ($\gamma = n$-6, 0.13) levels in the subcutaneous fat than animals slaughtered at heavier weights (0.32 and 0.10 respectively).

Key Words: conjugated linoleic acid, fatty acids, *trans* stereoisomer

M164 Fatty acid profiles of subcutaneous adipose tissue from cross young bulls produced by different genetic groups sires and slaughtered with distinct weights. R. Mello*[1], A. C. de Queiroz[2], F. Dutra de Resende[3], D. P. D. Lanna[4], M. H. de Faria[3], and E. da Costa Eifert[4], [1]*Universidade Federal de Santa Maria*, *Santa Maria, RS, Brazil*, [2]*Universidade Federal de Viçosa*, *Viçosa, MG, Brazil*, [3]*Agência Paulista de Tecnologia dos Agronegócios*, *Colina, SP, Brazil*, [4]*Universidade de São Paulo – Escola Superior de Agricultura 'Luiz de Queiroz'*, *Piracicaba, SP, Brazil*.

In the present study the aim was to investigate fatty acid profiles of subcutaneous adipose tissue from *Longissimus dorsi* muscle at 13th rib of crossbred bulls at different body masses. Thirty 6 young (20 mo) bulls, 18 crossbred F1 Red Angus × Nellore (1/2 RA 1/2 N) at 447.7 ± 5.8 kg of shrunk body weight (SBW) and 18 F1 Blonde D′Aquitaine × Nellore (1/2 BA 1/2 N) at 444.3 ± 6.5 kg of SBW were used. The animals were in compensatory growth. The young bulls were feedlot finished and slaughtered at 480, 520 and 560 kg of SBW. A completely randomized experimental design in a 2 × 3 (2 genetic groups × 3 slaughter weights) factorial arrangement with 6 replicates was used. Data were analyzed with SAS software using initial SBW as a covariate. The table below shows the least squares means of dependent variables. The backfat thickness increased ($P < 0.05$) as slaughter weight raised, being 2.1, 2.7 and 4.4 mm, respectively, for animals slaughtered at 480, 520 and 560 kg. The 1/2 RA 1/2 N young bulls had a higher ($P < 0.05$) content of long-chain fatty acids, polyunsaturated fatty acids and *n*-6 than 1/2 BA 1/2 N young bulls. On the other hand, the 1/2 BA 1/2 N young bulls had a higher ($P < 0.05$) content of medium-chain fatty acids than 1/2 RA 1/2 N young bulls. As the slaughter weight raised the content of odd-chain fatty acids decreased ($P < 0.05$); whereas the animals slaughtered at 520 kg had a smaller ($P < 0.05$) content of *n*-3. The interaction between genetic group (GG) and slaughter weight (SW) was significant ($P > 0.05$) for saturated fatty acids and monounsaturated fatty acids (data not shown). The 1/2 BA 1/2 N young bulls slaughtered at 520 kg had smaller content of saturated fatty acids, while 1/2 RA 1/2 N young bulls slaughtered at 520 kg had smaller content of monounsaturated fatty acids than others. Thereby, crossbred F1 Red Angus × Nellore young bulls and lighter animals had better fatty acid profiles in the subcutaneous fat than F1 Blonde D′Aquitaine × Nellore young bulls and heavier animals.

Table 1. Least squares means

	Genetic Group		Slaughter Weight		
Fatty acids	½ RA ½ N	½ BA ½ N	480	520	560
Short-chain	0.1	0.1	0.1	0.1	0.1
Medium-chain	41.0^{B}	43.4^{A}	42.7	42.9	41.0
Long-chain	56.4^{A}	54.0^{B}	54.4	54.6	56.6
Very long-chain	0.1	0.1	0.1	0.1	0.1
Odd-chain	2.3	2.4	2.7^{a}	2.2^{b}	2.2^{b}
Saturated	49.2	49.3	50.0	49.1	48.6
Monounsaturated	47.3	47.7	46.9	47.6	48.1
Polyunsaturated	3.4^{A}	3.0^{B}	3.1	3.3	3.3
n-3	0.8	0.7	0.8^{a}	0.7^{b}	0.8^{a}
n-6	3.0^{A}	2.5^{B}	2.5	2.8	2.8

Within a row, means followed by different capital and small letters differ ($P < 0.05$), respectively, among GG and SW by Tukey test.

Key Words: beef cattle, feedlot, *Longissimus dorsi*

M165 Meat quality of Nellore heifers finished at pasture, in tropical conditions, supplemented with crushed sunflower. S. L. N. Cerilo*, R. H. de Tonissi e Buschinelli de Goes, H. L. Lima, A. R. M. Fernandes, K. A. de Souza, D. de Faria Pereira, K. C. da Silva Brabes, and A. F. Marquez, *Universidade Federal da Grande Dourados*, *Dourados, MS, Brasil*.

Meat quality traits of Nellore Heifers finished on pasture of *Brachiaria humidicola* and fed crushed sunflower, in partial substitution of soybean meal, were evaluated. Twenty animals, slaughtered at a 378.5 kg BW were used. The supplements contained 20% CP and was composed of corn, soybean meal and minerals. The soybean meal was replaced by crushed sunflower in the proportions of 0, 20, 40 and 60% and its lipid content was 2.5, 4.7, 7.0 and 9.2%, respectively. The supplement was offered at 0.8% BW/animal per d, which corresponded to 3.31, 3.35, 3.28 and 3.25 kg of supplement/d. The experimental design was completely randomized and mean values were compared using the Tukey's test at $P < 0.05$. After slaughter the carcasses were cooled for 20 h. Subsequently, from the left carcass at the 12nd to 13rd rib level, a 2.5 cm thick LM sample was removed and pH, L*a*b*-values, water holding capacity, cooking loss, and shear force were determined. There was no ($P > 0.05$) effect of replacing soybean meal by crushed sunflower for pH, L*, a* and b* values, water holding capacity, cooking loss and shear force. The mean values were for pH = 5.59, L* = 37.48, a* = 18.42, b* = 10.01, water holding capacity = 65.86%, cooking loss = 31.94% and shear force = 7.70 kg/cm^2. Partial substitution of soybean meal by crushed sunflower does not alter the qualitative characteristics of meat from Nellore heifers finished on pasture under tropical conditions.

Key Words: shear force, luminosity, pH

M166 *Longissimus dorsi* muscle fiber profile in young bulls grazing tropical pasture and supplemented with different strategies. J. Cavali*[1], P. V. R. Paulino[1], I. Lage[2], C. A. Neves[1], M. V. Santos[1], M. F. Paulino[1], R. Justino[3], J. F. H. Rodrigues[4], and D. Melo[1], [1]*Universidade Federal de Viçosa*, *Viçosa, MG, Brazil*, [2]*Universidade Federal dos Vales do Jequitinhonha e Mucuri*, *Diamantina, MG, Brazil*, [3]*JBS Friboi*, *Barretos, SP, Brazil*, [4]*Universidade Estadual Paulista*, *Jaboticabal, SP, Brazil*.

The objective of this study was to evaluate the muscle fiber profile of young bulls grazing *Brachiaria decumbens* pastures and supplemented with different strategies. Fifty 2 Nellore young bulls were used, being distributed, in a completely randomized design, into 4 treatments (13 replicates): control, when the animals had free access only to mineral mixture throughout the experiment; and 3 protein supplementation strategies (T1, T2 and T3), when the animals were creep-fed with supplements containing 10, 20 and 30% crude protein (CP), respectively. After weaning the creep-fed animals received isonitrogenous supplements designed to supply 0.50 and 0.66 g of CP/day during the growing and finishing phases, respectively. The supplements used during growing and finishing contained different urea levels: 0; 4.0; 8.0 and 0; 3.0; 6.0% for T1, T2 and T3 respectively. After 580 d, the animals were slaughtered and a sample of LD muscle was taken at the last rib, frozen at −80°C. Later on histological cuts were obtained to assess the muscle fiber profile. T2 and T3 supplementation strategy elicited an increase ($P < 0.10$) in the frequency of IIB muscle fiber (61.00 and 59.80%) when compared with control and T1 treatments (54.00 and 56.15%). Probably, a modulation of intermediate muscle fibers (type IIA) into glycolitic fibers (IIB) occurred, as the increase in the proportion of IIB muscle fiber observed in T1 and T2 treatments was accompanied by a decrease ($P < 0.10$) in the frequency of IIA muscle fibers (31.17a; 31.03a; 27.57b and 25.32% for control, T1, T2 and T3 treatments, respectively). The frequency of type I muscle fiber was equal ($P > 0.10$) among treatments (19.50%). Probably, the protein supplementation strategies T2 and T3 might have provided a higher energy intake by the animals, leading to muscle modulation into more glycolitic fibers. The change observed in muscle fiber metabolism due to the different protein supplementation strategies can alter important beef quality attributes. However, it still has to be investigated in beef cattle grazing tropical pastures.

Key Words: muscle fiber, protein supplementation, tropical grass

M167 Effect of concentrate- vs. forage-based finishing diet on carcass traits, beef palatability, and color stability of longissimus muscle from Angus heifers. A. J. Garmyn*, D. L. VanOverbeke, R. G. Mateescu, and G. G. Hilton, *Oklahoma State University*, *Stillwater*.

The objective of the study was to determine the effect of finishing diet on carcass traits, beef palatability, and color stability of longissimus from Angus heifers. Half-siblings were obtained from a herd involved in selection for increased intramuscular fat, ribeye area, and retail product, and decreased back fat and alternatively assigned to a forage- or concentrate-based finishing diet. Longissimus muscle samples (n = 155) were obtained and fabricated into steaks for trained sensory panel, Warner-Bratzler Shear force (WBS), thiobarbituric acid reactive substances (TBARS), and simulated retail display. ANOVA was conducted through the MIXED procedure of SAS using harvest age as a covariate. Carcasses from heifers finished on concentrate had greater adjusted fat thickness (1.86 vs. 0.87 cm), higher percentage KPH (2.14 vs. 1.35%), higher numerical yield grades (3.38 vs. 2.25), and higher marbling scores (modest 90 vs. traces 70; $P < 0.05$) than forage-finished heifers. There was no difference in longissimus muscle area between diets ($P > 0.05$). Steaks from concentrate-fed heifers had lower WBS values (3.67 vs. 5.05 kg), higher tenderness ratings, higher beef flavor intensity, lower grassy/cowy flavor intensity, and higher painty/fishy flavor intensity than steaks from forage-fed heifers ($P < 0.05$). There was no difference ($P > 0.05$) between diets for initial or sustained juiciness and livery/metallic flavor intensity. Initial TBARS were higher ($P < 0.05$) in steaks from concentrate-fed heifers when compared with grass-fed heifers, but TBARS were not different ($P > 0.05$) between diets following 7 d in retail display. Diet did not have an effect on instrumental or subjective color, except L* values (0 = black and 100 = white) were higher (38.36 vs. 32.25; $P < 0.05$) for steaks from concentrate-fed heifers than from forage-fed heifers. This study points to several disadvantages of forage-based finishing diets in relation to beef palatability, especially tenderness and beef flavor.

Key Words: beef palatability, color stability, diet

M168 Does creep feed and backgrounding energy source affect lifetime growth performance and carcass characteristics of nursing calves pastured on annual ryegrass? M. S. Gadberry*[1], P. A. Beck[2], B. Barham[1], W. Whitworth[3], and J. Apple[4], [1]*University of Arkansas*, *Little Rock*, [2]*University of Arkansas*, *Hope*, [3]*University of Arkansas*, *Monticello*, [4]*University of Arkansas*, *Fayetteville*.

Angus sired, fall born steer (n = 36) and heifer (n = 24) calves (BW = 153 kg) with their dams were randomly assigned to 1 of 3 creep feeding treatment pastures (2 pastures/treatment) 93 d before weaning. Annual ryegrass (*Lolium multiflorum*) pastures were stocked at 2.47

cow/calf pair per ha. Treatments included no creep (NC), soybean hull (SC) based creep, or corn (CC) based creep offered at 1% BW (as-fed). After weaning, calves were allocated to 1 of 12 backgrounding pens receiving either a soybean hull or corn based diet for 63 d. Following the backgrounding phase, calves were fed a common finishing diet for 133 d. Pasture and pen were considered the experimental units. Post-weaning data were analyzed as a split-plot with pre-weaning treatments as the whole plot and backgrounding treatments and pre-weaning by backgrounding interaction as the subplot. Creep feed did not affect ADG pre-weaning ($P = 0.41$). Pre-weaning ADG averaged 1.3, 1.4, and 1.4 kg/d for NC, SC, and CC, respectively. Backgrounding BW gain was not affected by pre-weaning diet ($P = 0.14$), backgrounding diet ($P = 0.38$), or their interaction ($P = 0.54$). Backgrounding ADG averaged 1.2 kg/d among treatments. Over the 133 d finishing period, calves averaged 1.8 kg/d BW gain which was not affected by pre-weaning diet ($P = 0.88$), backgrounding diet ($P = 0.52$), or their interaction ($P = 0.86$). Calves were harvested with an average back fat thickness of 1.6 cm. Hot carcass weight (339 kg), back fat thickness, calculated yield grade (3.6), and percentage USDA Choice (56.4%) were not significantly affected by pre-weaning diet, backgrounding diet, or their interaction. These results suggest that neither creep feed nor source of energy in creep or backgrounding diets affect lifetime performance when calves are developed on a high plain of nutrition beginning pre-weaning.

Key Words: creep feed, backgrounding, carcass characteristics

M169 Does creep feed and backgrounding energy source affect lifetime growth performance and carcass characteristics of nursing calves pastured on improved warm-season grasses? B. Barham*[1], P. A. Beck[2], M. S. Gadberry[1], W. Whitworth[3], and J. Apple[4], [1]*University of Arkansas*, *Little Rock*, [2]*University of Arkansas*, *Hope*, [3]*University of Arkansas*, *Monticello*, [4]*University of Arkansas*, *Fayetteville*.

Angus sired, spring born steer (n = 78) and heifer (n = 42) calves (BW = 141 kg) with their dams were randomly assigned to 1 of 3 creep feeding treatment pastures (2 pastures/treatment) 90 d before weaning. Mixed warm-season, grass pastures were stocked at 2.47 cow/calf pair per ha. Treatments included no creep (NC), soybean hull (SC) based creep, or corn (CC) based creep offered at 1% BW, as-fed basis. After weaning, calves were allocated to 1 of 12 backgrounding pens receiving either a soybean hull or corn based diet for 45 d. Following the backgrounding phase, calves were fed a common finishing diet for either 147 or 183 d. Pasture and pen were considered the experimental units. Post-weaning data were analyzed as a split-plot with pre-weaning treatments as the whole plot and backgrounding treatment and pre-weaning by backgrounding interaction as the subplot. Creep fed calves gained 0.3 kg/d more than NC calves ($P = 0.002$); however, there was no difference between SC and CC ($P = 0.28$). Creep feed conversion averaged 5.2 kg feed per kg additional BW gain. Average daily gain during the backgrounding phase was not affected by creep diet ($P = 0.45$), backgrounding diet ($P = 0.93$), or their interaction ($P = 0.46$). At feedlot entry, creep fed calves continued to weigh more than NC calves ($P = 0.03$); however, by the conclusion of the finishing phase, there were no significant treatment effects on finished BW. Calves were finished at an average back fat thickness of 1.4 cm after an average 173 d finishing period. Hot carcass weight (319 kg), days on feed, back fat thickness, calculated yield grade (3.7), and percentage USDA Choice (73.6%) were not significantly affected by pre-weaning diet, backgrounding diet, or their interaction. These results suggest that improvements in BW gain may occur with calves offered creep feed during summer months; however, the benefit of additional BW may diminish by the end of feedlot finishing. In addition, creep feeding showed no beneficial effect on carcass characteristics.

Key Words: creep feed, backgrounding, carcass characteristics

M170 Genetic group and slaughter weight influence on meat quality of feedlot cattle. R. Mello*[1], F. D. de Resende[2], A. C. de Queiroz[3], M. H. de Faria[2], R. A. Possenti[2], and G. F. Alleoni[2], [1]*Universidade Federal de Santa Maria*, *Santa Maria, RS, Brazil*, [2]*Agência Paulista de Tecnologia dos Agronegócios*, *Colina, SP, Brazil*, [3]*Universidade Federal de Viçosa*, *Viçosa, MG, Brazil*.

The purpose of this study was to investigate the genetic group and slaughter weight influence on meat quality of the cattle. Thirty 6 young (20 mo) bulls, 18 crossbred F1 Red Angus × Nellore (1/2 RA 1/2 N) and 18 F1 Blonde D′Aquitaine × Nellore (1/2 BA 1/2 N) were used. The young bulls were finished in a feedlot and slaughtered at 480, 520 and 560 kg of shrunk body weight (SBW). A completely randomized experimental design of a 2 × 3 (2 genetic groups × 3 slaughter weights) factorial arrangement with 6 replicates was used. The animals were slaughtered in a commercial slaughter-house. Data were analyzed with SAS software using initial SBW as a covariate. The table below shows the least squares means of pH at 24 h after slaughter in the *Longissimus dorsi* muscle (LM), tenderness (WBSF) and cooking loss in the LM at 12th rib, and chemical composition (humidity, ash, crude protein, crude fat) in the LM at 13th rib. There was no effect ($P > 0.05$) of genetic group (GG) and the interaction between GG and slaughter weight (SW) was not significant ($P > 0.05$) for all measured traits. The tenderness, cooking loss, and chemical composition (humidity, ash, crude protein, crude fat) of meat were similar for all treatments. On the other hand, as the slaughter weight raised the pH 24 h increased ($P < 0.05$). Therefore, finishing of crossbred F1 Blonde D′Aquitaine or Red Angus versus Nellore young bulls on feedlot and slaughtered at 480, 520 and 560 kg produced meat with similar and suitable quality.

Table 1. Least squares means

	Genetic Group (GG)		Slaughter Weight (SW)		
	½ RA ½ N	½ BA ½ N	480	520	560
pH 24 hours	5.8	5.8	5.7^{c}	5.8^{b}	5.9^{a}
Shear (WBSF), kgf/cm ^{2}	4.41	4.72	4.88	4.47	4.35
Cooking loss, %	26.0	24.3	23.3	25.0	27.2
Humidity, %	75.3	74.5	75.4	75.1	74.1
Ashes, %	1.0	1.0	0.9	1.0	1.0
Crude protein, %	19.5	20.0	19.2	20.0	20.1
Crude fat, %	4.3	4.5	4.4	3.9	4.8

Within a row, means followed by different capital and small letters differ (P<0.05), respectively, among GG and SW by Tukey test.

Key Words: chemical composition, *Longissimus dorsi*, young bulls

M171 Animal health effects on carcass quality. T. M. Jeske*, R. J. Maddock, and K. R. Carlin, *North Dakota State University*, *Fargo*.

The objective of this study was to investigate the effects of medical treatment and lung condemnations on carcass quality of feedlot cattle. Steers and heifers (n = 1974) were individually identified in one of 3 cooperating feedlots, and all health issues and treatments were noted. When cattle reached market weight, they were slaughtered at one location and USDA yield and quality grade was obtained for all carcasses. In addition, complete carcass traits were recorded from 276 head. Data were

analyzed using ANOVA to compare between carcasses with or without condemned lungs, and to compare between treated and untreated. Difference in grading percentages were evaluated using chi-squared. Lung condemnations were noted for 1297 carcasses at slaughter, of which 109 lungs (8.4%) were condemned for some defect related to the heart, lung or trachea. USDA Quality grades of cattle with condemned lungs were 0% Prime, 69.7% Choice, 27.5% Select and 2.7% as No Rolls. Complete carcass data on 38 of the carcasses with condemned lungs found an average ribeye area of 80 cm^2 (SD = 3.4) marbling score of 459 (Sm59) (SD = 28), fat thickness of 1.26 cm (SD = 0.12). Cattle with lungs not condemned (n = 1185) had a USDA Quality grade breakdown with 1% Prime, 68% Choice, 28% Select and 2.1% as No Rolls. Average carcass data for carcasses without lung condemnations was a ribeye area of 83 cm^2 (SD = 4.1) marbling score of 437 (Sm37) (SD = 41) and a fat thickness of 1.17 cm (SD = 0.16). No significant differences in carcass traits were noted between carcasses with or without condemned lungs. Cattle treated at the feedyard consisted of 84 out of 1974 head or 4.25%. USDA Quality grades for treated cattle were 0% Prime, 56% Choice, 37% Select and 7% as No Roll, and an average USDA Yield grade of 2.54. Comparatively, overall carcass data was 1.1% Prime, 67.3% Choice, 29.5% Select, 2% as No Rolls, and average USDA Yield grade was 2.51. A strong trend ($P = 0.08$) was found for treated cattle to have inferior USDA quality grading percentages. These data indicate that health status may be related to USDA Quality grade of steer and heifers.

Key Words: beef, health, carcass quality

M172 Effect of garlic and onion on the thiobarbituric acid reactive substances (TBARS), volatile compounds and sensory evaluations of irradiated cooked ground beef. H. S. Yang*, G. D. Kim, K. Y. Seo, E. Y. Jung, and S. T. Joo, *Division of Applied Life Science (BK21 Program), Graduate School of Gyeongsang National University, Jinju, Gyeongnam 660-701, Republic of Korea.*

The effects of adding garlic and onion on the lipid oxidation, volatile compounds, and sensory evaluations of irradiated ground beef patties were investigated during storage. Beef rounds were ground, added with none (control), 0.1% garlic or 0.5% onion, packaged in oxygen permeable bags, irradiated at 0 or 2.5 kGy, and cooked to an internal temperature of 75Â°C. Data was analyzed by the procedures of generalized linear model (GLM) of SAS (2000). SNK (Student-Newman-Keuls) multiple-range test was used to compare the mean values of treatments. Differences in sensory values were compared using the Tukey's honestly significant differences. Irradiated ground beef had significantly higher TBARS values than nonirradiated ones regardless control and garlic treatment at 3 d. However, at d 5, the TBARS values of irradiated ground beef with 0.5% onion (0.78) sample was lower than nonirradiated control (1.04 mg malonaldehyde/kg meat) ($P < 0.05$). Addition of garlic greatly increased the amounts of all sulfur compounds. In control beef, carbon disulfide was not detected, but methanethiol, dimethyl disulfide, and dimethyl trisulfide were newly produced after irradiation. During storage, the amounts of all S-compounds in ground beef decreased rapidly, and carbon disulfide, 2-propen-1-thiol, 3,3-thiobis-1-propene, methyl 2-propenyl disulfide, dimethyl trisulfide and di-2-propenyl disulfide were not detected from the irradiated ground beef with 0.5% onion treatment after 3 d storage and no S-compounds were found in both onion alone and control ground beef after 5 d storage. Although, addition of garlic produced large amounts of S-compounds, the intensity of irradiation aroma and flavor in irradiated cooked ground beef with garlic or onion was similar to that of the nonirradiated control ($P > 0.05$). Therefore, addition of 0.5% onion or 0.1% garlic is recommended to mask or prevent off-odor in irradiated ground beef.

Key Words: irradiated, ground beef, garlic and onion

Graduate Student Poster Competition: National ADSA Dairy Foods Poster

M173 Angiostatin-like peptides in milk: Potential development for dairy products capable of cancer prevention. E. Stefanutti* and R. Jiménez-Flores, *California Polytechnic State University*, *San Luis Obispo*.

Angiogenesis, the development of new blood vessels from pre-existing vascularization, represents one of cancer's hallmarks. Blood supply is essential for a tumor to progress toward a malignant condition since this allows the delivery of nutrients and oxygen necessary to support cancerous cells' growth as well as entrance into the circulation causing metastasis to arise. Study on angiogenesis inhibitors has shown promising results on animal models. Blocking cancerous cells' blood access resulted in a reduction on primary tumor size and number of metastatic colonies. One of the peptides that showed interesting results on this study was angiostatin, the internal fragment of the fibrinolytic enzyme plasminogen in blood. It is well known that bovine plasminogen gets transferred into milk during lactation. The objective of this research was to investigate enzymes capable of releasing the antiangiogenic peptide from bovine plasminogen and compare the anticancer activity of the fragment with that of human angiostatin. We tested enzymes such as *Lactobacillus* (*L. casei*, *L. reuteri*, *L. acidophilus*) and *Bacillus* (*B. subtilis*, *B. cereus*, *B. coagulans*) originated proteases, *Bacillus polymyxa* metalloprotease dispase as well as elastase. Techniques such as SDS-PAGE, column chromatography, MALDI-TOF, and Western blot were utilized. After hydrolysis, results from electrophoresis showed bands in the molecular range of 37 kDa, which were confirmed through sequence analysis to belong to the kringle 1–4 region of plasminogen. Test for anticancer activity on melanoma and colon malignant cells, demonstrated a reduced proliferation of cancerous cells for samples treated with angiostatin and plasminogen; interestingly highest inhibition was obtained for treatments from bovine sources. We believe that these results represent a starting point for future development of novel dairy products capable of cancer prevention.

Key Words: plasminogen, angiostatin, proteases

M174 The effect of different inulin types on the formation of rennet-induced gels. A. Foo*, A. R. Hill, and M. Corredig, *University of Guelph*, *Guelph, Ontario, Canada*.

The objective of this research was to determine the effect of the prebiotic fiber inulin on rennet induced gelation of skim milk, and to determine the potential for utilization of inulin in rennet cheese applications. Four chicory inulin types (CLR, ST, XL, and HPX) with different degree of polymerization (DP) were studied. Inulin was added to untreated milk at concentration up to 3% (w/v) and the rennet-induced gelation was followed using dynamic oscillatory rheology and confocal microscopy. Experiments were performed in triplicates and differences were determined statistically using 2-way ANOVA and Tukey ($P < 0.05$). Gelation time, gel stiffness and strain at break changed depending on type and concentration of inulin. XL, and HPX (high DP molecules) significantly increased gelation time at 2 and 3% compared with the control sample. All inulin-fortified gels were stiffer and were less brittle than control milk gels. Rennet-induced gels containing 0.02% FITC were observed after 3h incubation at 30°C with confocal laser scanning microscope, and results showed that type and concentration of inulin affected the gel structure formation. Low DP inulins (CLR and ST) produced similar structures as control, while high DP inulins (XL and HPX) produced more branched structures. The degree of branching seemed to increase with concentration. Syneresis was tested after gel formation at 3h. CLR and ST fortified gels had almost identical syneresis rates as control, while XL and HPX fortified gels showed slower syneresis rates, especially at 3% inulin concentration. A modified HPLC method using an evaporative light scattering detector was used to analyze the amount of inulin present in the whey. Majority of CLR and ST (~90 ± 2–4%) were loss into the whey, while XL and HPX retained ~50 ± 2–4% in gels. The results indicated that high DP inulins were more retained in the gel than low DP inulins, but they also affected the gelling properties of caseins and network formation.

Key Words: inulin, rennet curd, rheological properties

M175 Impact of temperature and fat content on bleaching of liquid whey. M. A. D. Listiyani*[1], R. E. Campbell[1], R. E. Miracle[1], D. M. Barbano[2], and M. A. Drake[1], [1]*North Carolina State University*, *Raleigh,* [2]*Cornell University*, *Ithaca, NY*.

The use of whey protein as an ingredient in foods and beverages is increasing, and thus demands for colorless and mild tasting whey protein are also rising. Bleaching is commonly applied to fluid colored cheese whey to decrease color, and different temperatures and bleach concentrations are applied. The objectives of this study were to compare the effects of hot and cold bleaching and the point of bleaching (before and after fat separation) on bleaching efficacy and volatile components of liquid Cheddar whey. Liquid colored Cheddar whey was produced in triplicate and pasteurized. Part of the whey was collected (no separation, NSE) and the rest was subjected to fat separation (FSE). NSE and FSE whey were then subdivided and bleaching treatments (benzoyl peroxide (BPO) 50 or 100 mg/kg and hydrogen peroxide (HP) 250 or 500 mg/kg) at 68C for 30 min or 4C for 16 h were applied. Control NSE and FSE with no added bleach were also subjected to each time temperature combination. Volatile compounds from wheys were evaluated by gas chromatography mass spectrometry (GCMS) and norbixin (annatto) was extracted and quantified to compare bleaching efficacy. Proximate analysis, including total solids, protein, and fat content were also conducted. Liquid whey subjected to hot bleaching at both concentrations of HP or 100 mg/kg BPO had significantly higher lipid oxidation products (aldehydes) compared with unbleached wheys, 50 mg/kg BPO hot-bleached whey, or cold-bleached wheys. Fat separation had no impact on the relative abundance of volatile lipid oxidation products ($P > 0.05$). Wheys bleached with BPO had lower norbixin recovery compared with wheys bleached with HP ($P < 0.05$). HP bleaching efficacy was decreased at 4C compared with 68C ($P < 0.05$), BPO bleaching efficacy was not impacted by temperature ($P > 0.05$). These results suggest that fat separation has no impact on bleaching efficacy or lipid oxidation and that hot bleaching may result in increased lipid oxidation in fluid whey.

Key Words: whey, bleach, flavor

M176 Bleaching liquid Cheddar whey using ultraviolet radiation. E. J. Kang* and M. A. Drake, *North Carolina State University*, *Raleigh*.

Two of the desirable attributes of whey protein (WP) are a neutral color and bland flavor. The residual annatto colorant from Cheddar cheese production, therefore, has to be removed by bleaching. Currently, in the United States, hydrogen peroxide and benzoyl peroxide are the only bleaching agents approved to bleach colored whey. Recent studies have demonstrated that peroxide bleaching can negatively impact WP flavor.

Alternative bleaching methods may be valuable to the dairy industry. The objective of this study was to investigate the efficacy of UV radiation on bleaching of liquid Cheddar whey. Fluid colored Cheddar whey was manufactured on duplicate occasions. Following pasteurization and fat separation, whey was subjected to UV radiation for 30, 60, 90 or 120 min or cooled with no bleaching (control). The UV reactor consisted of a stainless steel feed tank (4 L), peristaltic pump, and a UV reactor. A 385 mm length low pressure mercury lamp was enclosed in a 24 mm diameter glass tube inside the stainless steel UV reactor. This UV reactor had a 151 mL working volume. Liquid whey circulated through the UV reactor, back into the feed tank and then re-circulated while the feed tank was held at 60°C. Wheys were then subjected to norbixin extraction and quantitation to measure bleaching efficacy. Control Cheddar whey with no UV treatment had 4.12 ppm of norbixin. Whey exposed to UV radiation for 30, 60, 90 or 120 min had 0.65ppm, 0.39ppm, 0.52ppm, and 0.37ppm norbixin, respectively. Norbixin decreased ($P < 0.05$) compared with control whey when exposed to UV light for 30 min; but increasing time up to 2 h did not increase the bleaching effect ($P > 0.05$). Overall norbixin concentration in fluid whey was reduced 84~91% when treated with UV radiation. UV radiation may be an alternative to peroxide bleaching of fluid whey.

Key Words: UV radiation, liquid whey, bleach

M177 Development and analysis of a dairy-based nutrient dense gel food rich in milk bioactives. M. Cleveland* and R. Jiménez-Flores, *California Polytechnic State University*, *San Luis Obispo.*

Milk products are a rich source of nutrients and bioactive compounds beneficial to human health. Some of these include immunoglobulins, phospholipids, casein and whey proteins and peptides, and components of the milk fat globule membrane (MFGM). These products although originally in milk, can be found in higher concentrations in other products, such as colostrum, buttermilk, and whey protein powders. Addition of ingredients such as probiotics add additional value and are apt to be easily incorporated into a dairy system due to their natural residence in milk. The application of dairy ingredients in product development has great potential to create a strong nutrition delivery system with benefits beyond those of fluid milk. Exploitation of dairy ingredients in this way is economical and promotes use of products that still have untapped potential in the marketplace. Development of dairy-based ready-to-eat foods is an excellent way to provide a rich source of the aforementioned milk bioactives. These products would serve as a compact, convenient source of energy and specialized nutrition. The health benefits include immune system development and function, stimulation of gastrointestinal function, and probiotic activity. We have created and biochemically analyzed a dairy-based high nutrient density gel food. It has a pleasing sensory profile, provides significant whey protein, and due to its ingredient profile is an excellent source of milk bioactives. The protein quality and quantity were designed to promote satiety and healthy muscle mass. We have analyzed the gel for immunoglobulin concentration (ELISA), phospholipid content (HPLC method), probiotic survival and binding preference to phospholipids, and basic macronutrient content (FTIR). The results of these assessments show a significantly higher level of milk bioactivity in the gel than in an equivalent gram quantity of fluid milk. From our studies, we conclude that we have created a highly valuable, convenient dairy-based nutrition delivery system with potentially great health benefits. Future work includes design of large-scale manufacture and studies of bioactivity in cell culture.

Key Words: milk bioactives, nutrition, dairy foods

M178 Identification of bioactive peptides derived from fermentation of organic milk. S. R. Pritchard*, M. Phillips, and K. Kailasapathy, *University of Western Sydney*, *East Richmond, New South Wales, Australia*.

The aim was to identify peptides isolated from bacterial fermentations of organic milk that may have antimicrobial, antihypertensive and antioxidant properties. Organic milk was fermented in duplicate with *Lactobacillus acidophilus* LAFTI L10, *Lactobacillus casei* 2603, *Lactobacillus rhamnosus* 2625 (2, 6 and 9 d) and *Lactobacillus helveticus* (10% v/v) (2, 4 and 6 h). The pH was adjusted to 4.6 and soluble and insoluble peptide fractions were extracted by centrifugation followed by filtration. The extracts were screened for the presence of antimicrobial, antihypertensive and antioxidant activity. All analysis was carried out in triplicate. Antioxidant activity was measured by the inhibition of the free radical 1, 1-diphenyl-2-picrylhydrazyl (DPPH). The soluble fractions had the greatest inhibition of DPPH compared with the insoluble fractions. The peptides extract that inhibited DPPH the greatest were derived from organic milk fermented by *L. rhamnosus* for 6 d (42.83% ± 1.26 standard deviation (SD)), followed by the peptide extracts derived from milk fermented by *L. helveticus* for 2 h (34% ± 3.45) and *L. helveticus* for 4 h (32% ± 0.45). Antimicrobial peptides were determined by inhibition of 3 bacteria namely *Escherichia coli* ATCC 8739, *Bacillus cereus* ATCC 11778 and *Staphylococcus aureus* ATCC 6538. Overall, *E. coli* was inhibited the greatest by soluble peptide fractions including the peptide extracts derived from organic milk fermented by *L. acidophilus* for 9 d (108.38% ± 8.85 SD), with *L. rhamnosus* for 6 d (101.13% ± 1.95) and with *L. casei* for 9 d (90.04% ± 3.52). Antihypertensive activity was determined by the inhibition of the angiotensin-converting enzyme (ACE) using RP-HPLC to detect the amount of hippuric acid produced. Overall, the soluble fractions had the lowest IC50 values. The peptide extract derived from organic milk fermented for 9 d by *L. casei* had the lowest IC50 value (0.124mg/ml ± 0.008 SD). This research has shown that peptide extracts derived from fermented organic milk have antimicrobial, antihypertensive and antioxidant properties.

Key Words: bioactive peptide, milk, fermentation

M179 Increasing stringiness of low fat mozzarella cheese using polysaccharides. E. N. Oberg*[1], K. M. Larsen[1], D. A. Irish[1], M. M. Motawee[2,1], and D. J. McMahon[1], [1]*Western Dairy Center, Utah State University*, *Logan*, [2]*National Organization for Drug Control and Research*, *Cairo, Egypt*.

Removing fat from mozzarella cheese decreases fiber formation because protein strands fuse together during stretching and extruding. This study examined the ability of polysaccharides to act as fat mimetics and aid in fiber formation in manufacture of string cheese. Low fat mozzarella cheese curd made from 273 kg of 0.7%-fat milk was salted at a rate of 10 g/kg then divided into 2.7-kg batches that were hand-stretched in 5% (wt/wt) hot brine (80°C) and formed into a homogeneous mass. The hot cheese was hand mixed with a hot (80°C) polysaccharide slurry and then placed into a small piston-driven extruder and cheese forced through a 16-mm die to form the string cheese and cut manually into about 15-cm lengths. Cheeses were analyzed for fat, salt, pH, and moisture. After 1 wk of storage at 4°C, extent of stringiness was measured by pulling apart the cheese longitudinally, visually observing and photographing size and appearance of individual strings of cheese, and measuring their length. In one trial, 3 starches (waxy corn, waxy rice, and instant tapioca starches) were tested using 8% (wt/vol) slurries at a ratio 7% (wt/wt) of stretched curd. Waxy rice and waxy corn starches did not mix well with hot cheese and in a second trial, xanthan gum and guar gum slurries were added at a ratio of 2% (wt/wt), and polydextrose and instant

tapioca starch added at 7%. In the control low fat cheese there was no apparent fiber formation and the cheese was homogeneous in texture. All cheeses made with added polysaccharides had substantial fiber formation and were more similar to regular commercial string cheese. Low fat cheese with added xanthan gum had the most pronounced fiber formation with the longest strings (i.e., the full length of the cheese stick) and best string separation. Adding polydextrose produced cheese with the least string formation and was only slightly better than the control. Overall, extent of stringiness was greatest immediately after extrusion and tended to decrease during storage with string diameter increasing and string length decreasing.

Key Words: mozzarella, string cheese, low fat

M180 Enrichment of low fat Cheddar cheese with dietary fiber. R. Wadhwani*, D. J. McMahon, and D. A. Irish, *Utah State University*, *Logan*.

Dietary fiber intake of 20 to 35 g/d is recommended for lowering coronary heart disease, cancer, and other health benefits such as satiety and improved digestion. However, the average American daily intake is only 12 to 18 g/d. Fiber intake can be increased by enriching more foods and this study examines the feasibility of enriching low fat Cheddar cheese (6% fat) with dietary fibers and their effect on cheese organoleptic acceptability. Low fat Cheddar was made and stored for 15 d, then comminuted to 1.5 mm particle size. Then, inulin, pectin, polydextrose, or resistant starch were mixed into 1.82 kg batches of comminuted cheese at 50 g/kg with or without addition of 50 g/kg of water. The comminuted batches were then repressed individually in cheese molds, vacuum packaged and stored at 4°C. All cheese samples were analyzed at 90 d for composition and fiber was calculated by difference. Texture profile analysis was performed at 90 and 180 d of storage. Sensory flavor analysis was performed at 180 d with a full fat Cheddar cheese comparison. Chewiness was evaluated by counting the number of bites before swallowing cheese. No liquid expulsion from repressed cheese mixed with fiber was observed which resulted in 100% retention of fiber in cheese except for polydextrose which experienced liquid expulsion of < 0.5%. When added with water, cheese mixed with inulin or pectin resulted in better knitting and uniform mixing of cheese particulates which was confirmed by increased cohesiveness from 0.48 to 0.65 for inulin with water and 0.50 for pectin with water. Hardness for inulin (46.41N) and pectin (55.87N) cheeses were significantly lower than non-repressed control cheeses (80.94N) and chewiness was also significantly reduced from 44.18N to 12.45N. Polydextrose and resistant starch cheese were poor in appeal and lacked smooth texture. Chewdown method showed that full fat cheese and comminuted cheeses required 12 bites before swallow whereas non-comminuted cheese control was reported 24 bites by trained panel which is clearly double the number. This study indicated a feasibility to enrich comminuted low fat cheese with fiber contributing to better texture and no impact on overall flavor.

Key Words: fiber, Cheddar, texture

M181 Development of a rapid method for determination of lactose in process cheese using blood glucose meter. A. C. Biswas*, J. Amamcharla, and L. E. Metzger, *Midwest Dairy Foods Research Center, Dairy Science Department, South Dakota State University*, *Brookings*.

The lactose content can influence the functional and textural attributes of process cheese (PC). Hence, the development of a rapid and accurate method for determination of lactose in PC will be beneficial to the industry. Previously, a blood glucose meter method (BGMM) was developed for the determination of lactose in model solutions and raw milk. The current objective was to modify the BGMM for the determination of lactose in PC. The previous method was modified by utilizing a phosphate buffer to dilute the sample and used a new generation of glucose meter for analysis. For sample preparation, 1 g of PC was added to 20 g of 0.01 M phosphate buffer (pH 7.4) and mixed vigorously at 60°C. Five milliliters of the mixture was transferred to a test tube, and 0.01 mL of β-galactosidase was added. The solution was incubated at 40°C for 10 min to hydrolyze the lactose into glucose and galactose, and then analyzed for glucose in duplicate using the ReliOn Confirm glucose meter and its compatible test strips. To evaluate the variation between different test strip lots, 4 lots of test strips were utilized. For all 4 lots of test strips an individual calibration curve was developed using PC with known lactose concentrations between 3.2 and 8.2%. A universal calibration curve was also computed by pooling the data from all 4 lots of test strips. A sample of the original dilution of PC and buffer was also analyzed for lactose using an HPLC based method. The new rapid method was validated using 10 PC. The slopes and intercepts of individual calibration curves ranged from 1.23 to 1.37 and from −105 to −60, respectively. The slope and intercept of the universal curve were 1.32 and 88, respectively. The mean absolute bias was found to be between 0.11 – 0.32% for individual calibration and 0.15 – 0.24% for the universal calibration curve. The observed moderately high bias could be caused by variability in the test strip lots and intrinsic components of PC. Overall the novel rapid method is promising. However, modifications in sample preparation and calibration need to be developed to improve the method.

Key Words: lactose, glucose meter, process cheese

M182 Monitoring changes in the non-casein nitrogen fraction of raw milk during storage using casein/fat standardizer (CFS). P. Salunke*, J. Amamcharla, and L. E. Metzger, *Midwest Dairy Foods Research Center, South Dakota State University*, *Brookings*.

Prolonged storage at refrigerated temperatures causes changes in the nitrogen distribution of raw and pasteurized milk. An increase in the non-casein nitrogen (NCN) fraction during storage is the result of psychrotrophic microorganisms and proteolytic enzymes. This phenomenon has direct implications on both cheese yield and quality. The Casein-Fat-Standardizer (CFS; Tetra Pak CPS, MN and Metron Instruments, OH) is being used as an on-line tool for standardizing the casein and fat of cheese milk. CFS uses a patented Brewster analysis method of laser light scattering to measure the casein and fat in the cheese milk. The objective of this study was to determine if the CFS can be used to follow the increase in the NCN fraction of cheese milk during refrigerated storage. Four raw milk samples (1 L) were collected immediately after milking. Each of the 4 samples was divided into 6 sub-samples and stored at 4°C. On each experimental day (for 6 consecutive days), one of the 6 sub-samples was withdrawn and tempered to 40°C. The sample was analyzed for fat, total protein (TP) and NCN in triplicate using the respective standard methods. The sample was also analyzed using the CFS to measure the casein and fat. It was found that there was no significant ($P > 0.05$) effect of storage time on the TP and fat of raw milk as analyzed by the standard methods. However, the NCN fraction of milks significantly ($P < 0.05$) increased during the storage period leading to a significant ($P > 0.05$) decrease in casein content after 2 d of storage. Similarly, the casein content analyzed by the CFS also showed significant ($P > 0.05$) differences after 3 d of refrigerated storage. The fat content measured in CFS also showed a significant ($P > 0.05$) decrease from d 0 to d 1, but showed no significant ($P < 0.05$) difference between the remaining storage period. Paired *t*-test comparison between the standard methods and CFS measured fat and casein showed

no significant differences for casein ($P = 0.76$) and fat ($P = 0.72$). These results indicate that the CFS instrument is capable of monitoring changes in the NCN content of milk during refrigerated storage.

Key Words: NCN, raw milk storage, CFS

M183 Impact of xylitol on the functional properties of low fat process cheese. A Kommineni*, J Amamcharla, and L. E. Metzger, *Midwest Dairy Foods Research Center, South Dakota State University.*

Process cheese is a dairy food made by blending natural cheese, salt, emulsifying salts and other dairy and non dairy ingredients, and heating with continuous agitation to produce a homogeneous product. Due to increased health concerns the demand for low fat products has increased. Fat is a critical component of process cheese and plays an important role in its functional characteristics. Reducing or lowering the fat content of process cheese results in poor functional properties. The objective of the current study was to evaluate the effect of xylitol on the functional properties of low fat PC. Three different low fat PC formulations were made with 0%, 2% and 4% xylitol. All PC formulations contained 5% fat and 55% moisture and each treatment was manufactured in triplicate. Rheological characteristics including elastic modulus (G′), Viscous modulus (G″) and Temperature at Tanδ = 1 were determined using Dynamic Stress rheometry (DSR). The DSR was carried out at 1.5Hz frequency and 400 Pa stress levels using a temperature sweep from 200C to 900C. The hardness of the samples was also determined with texture profile analysis (TPA). Compositional analysis indicated that all treatments had a similar fat, protein, and moisture content. The elastic (G′) and viscous (G″) modulus results obtained with DSR decreased with increasing xylitol addition. The meltability index temperature was not significantly ($P > 0.05$) different between all treatments. TPA analysis demonstrated that xylitol addition significantly ($P < 0.05$) decreased the hardness of low fat process cheese. Based on the results obtained with DSR and TPA this study has demonstrated that xylitol addition improves the functional properties of low fat PC.

Key Words: process cheese, low fat, xylitol

M184 Application of salt whey in process cheese food made from young Cheddar cheese containing exopolysaccharides. O. Janevski*, A. N. Hassan, and L. Metzger, *South Dakota State University*, *Brookings*.

The objective of this study was to utilize salt whey in making process cheese food (PCF) from young (3-week-old) Cheddar cheese. To maximize the level of salt whey in process cheese, low salt (0.6%) Cheddar cheese was utilized. Since salt reduction causes undesirable physicochemical changes during extended cheese ripening, young Cheddar cheese was used in making process cheese. An exopolysaccharides (EPS) producing culture (JFR) was used to reduce rigidity and improve meltability of young Cheddar cheese. A non-EPS-producing culture (DVS) was applied in making the control cheese. To obtain similar composition in the EPS-positive and negative Cheddar cheeses, the making protocol was modified in the later cheese to increase its moisture level. The composition of Cheddar cheese was determined and used to formulate the corresponding PCF (JFR-PCF and DVS-PCF). Three-week-old Cheddar cheese containing 41.4% moisture, 31% fat, and 21.2% protein, was shredded, and stored frozen until used for PCF manufacture. No differences in pH and level of water-soluble nitrogen were seen between the EPS-positive and negative Cheddar cheeses. The utilization of low salt Cheddar cheese allowed up to 13% of salt whey containing 9.1% salt to be used in process cheese making. The preblend was mixed in the Rapid Visco Analyzer (RVA) at 1000 rpm, heated at 95°C for 3 min, and process cheese was transferred into copper cylinders, sealed and kept at 4°C. Process cheese contained 43.28% moisture, 23.7% fat, 18.9% protein, and 2.1% salt. No difference in composition was seen between the JFR-PCF and DVS-PCF ($P > 0.05$).The texture profile analysis showed that JFR-PCF was softer, and less gummy and chewy ($P \leq 0.05$) than DVS-PCF. The end apparent viscosity and meltability in JFR-PCF were higher ($P \leq 0.05$) than those in DVS-PCF, whereas the emulsification time was shorter ($P \leq 0.05$) in the former cheese. In conclusion, process cheese, containing up to 13% salt whey, with improved textural and melting properties could be made from young EPS-positive Cheddar cheese.

Key Words: process cheese, salt whey, exopolysaccharides producing cultures

M185 Prediction of water activity of natural cheese using a model cheese system. J. Grummer* and T. C. Schoenfuss, *University of Minnesota*, *St. Paul*.

The ability to predict the water activity of natural cheese in modified formulas is critical in developing products such as reduced or low sodium cheese. In published attempts to develop reduced sodium cheese, replacement salts have been added at levels too low to create the equivalent microbial and enzymatic stability of full sodium controls. The objective of this study was to develop a model system that could be used to measure Aw directly to verify samples formulated using predictive equations. Flour, butter and water were blended at levels that represented typical solids, fat, and water levels in Cheddar cheese. Predictive equations were used to calculate the levels of the various salt replacers needed to achieve the same water activity as samples with 600 mg sodium/100g. Sodium chloride and salt replacers (potassium chloride, modified potassium chloride (Nu-tek Products, Minnetonka, MN), magnesium chloride hexahydrate, and calcium chloride dehydrate) were added to the model blends to produce cheese with less than 300 mg sodium/100g of cheese. The measured water activities did not match the predicted values in some cases. This could have been due to differences in purity and moisture levels between the salts or the solubility of the salts at the percent moisture tested. The discrepancy demonstrated the benefit of using this model system for direct testing of water activity in a model system before producing batches of cheese.

Key Words: water activity, prediction, cheese

M186 Optimization of a CO_2 injection method for increasing the permeate flux in cold microfiltration of skim milk. T. J. Tan*, A. Sauer, and C. I. Moraru, *Cornell University, Ithaca, NY.*

Cold microfiltration (MF) was proven effective for microbial removal from skim milk. One of the challenges associated with MF is the low permeate flux, caused by fouling. To address this, a CO_2 injection technique capable to counteract membrane fouling was developed and optimized. The experimental MF unit consisted of a feed tank connected to a variable-speed centrifugal pump, a tubular heat exchanger and a tubular ceramic membrane of Tami design, placed inside a stainless steel housing. The membrane had a nominal pore size of 1.4 µm and total membrane area of 0.35 m^2. Three portable CO_2 injection ports were attached to the membrane housing. The combinations tested included: no CO_2 injection (control), 1 port, and 3 ports. Four combinations of CO_2 injection frequencies and durations were tested: no injection (control), 60s frequency with 2s duration (60s/2s), 60s frequency with 1s duration (60s/1s), and 120s frequency with 1s duration (120s/1s). The MF experiments were performed at a temperature of 6°C, a cross-flow velocity of 7 m/s and a transmembrane pressure of 83 kPa. A data acquisition

port was used to collect the temperature, pressure and permeate weight data; the latter was then used to calculate the permeate flux. In all runs, permeate flux showed an initial rapid decrease followed by a long and gradual decline. A series of 45min experiments were first performed. At similar water flux values of the membrane (1500 ± 50 L/m^{2}h), the combination of 3 ports with 120s/1s produced the highest flux (46.09 L/m^{2}h at 45min) followed by 3 ports with 60s/1s (41.32 L/m^{2}h) and 3 ports with 60s/2s (39.41 L/m^{2}h). Three hour experiments were then conducted: without injection (control), and with optimal CO_2 injection (3 ports, 120s/1s). After 3 h, the flux for the control was 26.36 ± 3.38 L/m^{2}h, while for the optimized CO_2 injection experiment, a flux of 33.65 ± 3.68 L/m^{2}h was obtained. In addition, a smaller drop in flux was observed for the CO_2 injection experiment (23% after 3h) as compared with the control (31.5% after 3h). The developed method is effective and can be used to increase the flux in microfiltration applications.

Key Words: microfiltration, fouling, CO_2 injection

M187 Polysaccharide addition to lowfat Cheddar cheese to improve texture. R. Kumar* and T. C. Schoenfuss, *University of Minnesota*, *St. Paul.*

Fat plays a role in cheese texture by acting as a plasticizer and inhibiting cross-linking between protein chains. Reductions in fat to produce lowfat cheese (less than 3 g fat/50 g cheese) results in texture defects. The objective of this study was to improve the texture of lowfat cheese by incorporating a polysaccharide gel as a filler to disrupt protein cross-links. Polysaccharides examined were alginate, xanthan, pectin, carageenan (Danisco USA Inc., New Century, KS) and Novagel RCN 15 (FMC Biopolymer, Philadelphia, PA). The level of polysaccharide needed to produce a soft gel was mixed with whey protein concentrate (Avonlac 180, Glanbia Nutritionals, Monroe, WI) on a high shear mixer. The gel (calculated at 10% of the pressed cheese if all was retained) was homogenized (Niro panda, GEA, Hudson, WI) at 160 bar with all the cream and a portion of the skim milk. It was then blended with the remaining skim. Control lowfat cheese was made with homogenized cream without polysaccharides. The cheesemaking procedure used a stirred curd method with pre-acidification to pH 6.2, and a final curd pH of 5.7 at salting. Curds were pressed in 0.7 kg Wilson-style hoops overnight. Cheeses were evaluated at 2 mo of age by sensory and texture profile analysis. Untrained panelists were instructed to place cheese samples (treatments and controls presented blindly) spatially on a 61 × 61 cm sheet of paper based on differences they perceived in texture and flavor. The distance of each sample from a full-fat sample was measured in cm. Novagel and pectin treatments were placed significantly closer ($P < 0.05$) to the full fat cheese than low fat control. Samples measured on a TA.XT-Plus Texture Analyzer (Texture Technologies, Scarsdale, NY) showed pectin and carageenan samples were significantly lower in percent energy recovered ($P < 0.05$) than lowfat control. Moistures of the lowfat samples were not significantly different, (52 to 54%). It was concluded that pectin, carageenan and Novagel had a positive effect on cheese texture using this method.

Key Words: lowfat, Cheddar, polysaccharides

M188 Effect of concentration and temperature on the rheological properties of 95% serum protein (SP) reduced micellar casein concentrates (MCC). A. Sauer*, C. Beliciu, and C. I. Moraru, *Cornell University*, *Ithaca, NY*.

The use of casein preparations obtained by membrane separation is receiving increasing interest from the dairy industry, as well as other industries. Currently, there is a lack of knowledge regarding the flow behavior of these protein concentrates under various processing conditions such as temperature and shear. This work focused on evaluating the rheological properties of micellar casein and on understanding how they are affected by concentration, temperature and shear. MCC with 95% SP reduced were obtained from skim milk by microfiltration followed by spray drying. MCC preparations of concentrations ranging from 5% to 12.5% were obtained by dispersing the MCC powders in deionized water, under vigorous stirring. Large amplitude and small amplitude rheological analyses were performed to evaluate the viscosity and flow behavior, as well as the network structure of these protein preparations. Steady shear experiments at temperature ranging from 0C to 80C were performed using an ARES strain controlled rheometer (TA Instruments). The viscosity vs. shear rate curves were used to evaluate the effect of shear on viscosity, and apparent viscosity at a shear rate of 100s-1 was used to make direct comparison between various concentrations and temperature conditions. All protein preparations displayed a shear thinning behavior, which was more pronounced as casein concentration increased. The apparent viscosity of MCC increased exponentially with casein concentration and decreased with temperature. The dependency of apparent viscosity on temperature followed an Arrhenius relationship. The activation energy for viscous flow (Ea) in the Arrhenius relationship increased with concentration. Ea values of 21280 kJ/mol, 26730 kJ/mol and 40167 kJ/mol were obtained for MCC concentrations of 5%, 7.5% and 10%, respectively. The relationships developed will allow the prediction of rheological properties under desired temperature and concentration conditions, which will provide the dairy and food industry with critical rheological data necessary for developing applications of micellar casein preparations.

Key Words: micellar casein, rheology, viscosity

M189 Formation of bacterial biofilms on spiral wound reverse osmosis whey concentration membranes and its influence on retentate quality. M. Avadhanula*, A. C. Biswas, S. Anand, and A. Hassan, *Midwest Dairy Foods Research Center, Dairy Science Department, South Dakota State University*, *Brookings*.

Fouling is a major operational hurdle in the membrane processing of whey. In addition to the deposition of organic matter, bacterial biofilm formation on membranes may play a role in their reduced performance. The present investigation was conducted to study the formation of bacterial biofilms on spiral wound, reverse osmosis (RO) whey concentration membranes using the standards plate counting technique. Membrane cartridges from a commercial whey RO system were drawn at intervals of 2 mo up to a total duration of 12 mo to evaluate the effect of membrane aging on biofilm formation. Swab samples were taken from 1x1cm^2 membrane pieces drawn randomly from each cartridge. Counts of different bacterial groups were monitored in the feed, retentate and on the surface of membranes using selective media. The results confirmed the presence of multispecies bacterial biofilms on the whey RO membranes. Considerable variations were noticed in the distribution pattern of bacterial constituents in biofilms as the membranes aged. The average colony forming units (cfu/cm^2) for mesophiles, coliforms, lactic acid bacteria, staphylococci, and β-hemolytic colonies were 1.16, Nil, 0.78, 0.72, and 1.26 on the 2 mo old membrane, 4.11, 3.15, 4.05, 1.4, and 3.0 on the 6 mo old membrane, and 3.86, 2.38, 4.04, 1.91 and 2.86 on the 12 mo old membrane, respectively. The average log count (cfu/ml) in the feed whey was 5.44, which increased to 7.67 at the end of a 24 h cycle. In comparison to that, the average retentate count (cfu/ml) increased from log 5.30 to log 7.93. The higher increase in the retentate counts than that in the feed may be due to contamination from the membrane biofilms. This study provides a qualitative analysis of bacterial constituents of the

biofilm consortia obtained from whey concentration membranes from active industrial processes and its influence on retentate quality.

Key Words: whey retentate, reverse osmosis membrane, multispecies biofilm

M190 Thermal aggregation of whey proteins in the presence of buttermilk. M. Saffon*[1], M. Britten[2], and Y. Pouliot[1], [1]*STELA Dairy Research Center, Institute of Nutraceuticals and Functional Food (INAF), Université Laval*, *Québec, QC, Canada*, [2]*Food Research and Development Center (FRDC), Agriculture and Agri-Food Canada*, *St-Hyacinthe, Québec, Canada*.

Reincorporating heat-denatured whey proteins in cheese milk is widely used in the cheese industry. The use of buttermilk is however limited because it increases cheese moisture. It was hypothesized that a co-denaturation process involving a mixture of whey and buttermilk proteins increases the use of buttermilk in cheesemaking. In preliminary experiments, mixed dispersions were prepared from powdered concentrates acidified to pH: 4.6; 5.4 and 6.2 using HCl 1N and heated at 2 temperatures (80°C and 90°C). From these trials, heating the mixed dispersions to 90°C and pH 4.6 showed the best results and this condition was chosen to test different ratios of whey to buttermilk protein. Cheese whey and buttermilk were concentrated by ultrafiltration up to 9.5% (w/v) protein content. Mixtures were heated to 90°C for 25min (including come-up time). After cooling, samples were homogenized 5 times at 9500 psi. Aggregated material was separated by centrifugation at 15000g for 20 min. Protein aggregation was calculated from protein content in the supernatant and water holding capacity (WHC) was determined on the pellet. Heat denaturation was also applied to protein mixtures containing thiol blocker (N-ethylmaleimide) to understand the impact of disulfide bonds on the formation of aggregates. All the heating experiments were repeated 3 times, statistical analysis of the data was performed using ANOVA and the results were considered significantly when $P < 0.05$. Increasing temperature significantly increased protein aggregation from 58% to 75% when heating temperature was raised from 80°C to 90°C. Decreasing heating pH significantly decrease WHC. Minimum WHC being observed at pH 4.6. Increasing the fraction of buttermilk protein in the mixture increased significantly protein aggregation and reduced WHC up to a ratio of 25:75 (78% and 1.80 g water/g protein. The use of NEM significantly increased protein aggregation by 6.2% and decreased WHC by 0.73 g water/g protein. Overall, our results show that increasing buttermilk fraction resulted in higher protein aggregation and lower WHC and suggest that disulfide bonds are formed in the early stages of aggregation.

Key Words: cheese whey, buttermilk, aggregation

Graduate Student Poster Competition: National ADSA Production MS Poster

M191 Assessment of tannin-free and tanniniferous legumes in lactating dairy diets using continuous culture. C. M. Williams*[1], C. M. Dschaak[1], J.-S. Eun[1], J. W. MacAdam[2], and A. J. Young[1], [1]*Department of Animal, Dairy, and Veterinary Sciences, Utah State University*, *Logan*, [2]*Department of Plants, Soils, and Climate, Utah State University*, *Logan*.

Dual-flow continuous culture fermentors (700 mL) were used to determine the effects of feeding tannin-free (alfalfa and cicer milkvetch) and tanniniferous (birdsfoot trefoils and sainfoin) legumes in lactating dairy diets on in vitro methane production and ruminal fermentation characteristics by mixed ruminal microbiota. We hypothesized that methane and ammonia-N production would be reduced when alfalfa hay was replaced by cicer milkvetch and tanniniferous legumes as main forages in TMR diets. Fermentors were inoculated with filtered ruminal contents and allowed to adapt to experimental diets for 6 d, followed by 3 d of sample collection. All dietary treatments were formulated for lactating dairy cows in early lactation. Five TMR diets were evaluated, each containing a different forage source as hay: 1) alfalfa (ALF) as a control, 2) cicer milkvetch (CMV), 3) Norcen birdsfoot trefoil (NBFT), 4) Oberhaunstadter birdsfoot trefoil (OBFT), and 5) sainfoin (SF). The experiment was conducted as a 5 × 5 Latin square design, and all data were analyzed using the MIXED procedure of SAS. Culture pH was not influenced when replacing ALF with CMV, NBFT, and OBFT, but increased when feeding SF ($P < 0.01$). Ammonia-N concentration was reduced when feeding CMV and SF ($P < 0.01$), but was not affected when replacing ALF with NBFT and OBFT. Total VFA production and acetate molar proportion were not influenced by treatments. However, molar proportion of propionate increased by feeding CMV, NBFT, and OBFT ($P < 0.01$). Acetate to propionate ratio decreased in cultures offered CMV and OBFT, but increased by SF when compared with ALF ($P < 0.01$). Methane production, as measured in headspace gas, decreased when replacing ALF with all other treatments ($P = 0.01$). The decrease of in vitro methane production when feeding cicer milkvetch, birdsfoot trefoils, and sainfoin may make these forages suitable for mitigating enteric methane emissions by lactating dairy cows, and maintaining potential productive performance.

Key Words: tanniniferous legumes, continuous culture, methane

M192 Post treatment outcomes of clinical mastitis on commercial dairy farms. C. Pinzón-Sánchez*, C. Hulland, and P. L. Ruegg, *University of Wisconsin*, *Madison*.

The objective was to characterize 60 d outcomes after treatment of mild (abnormal milk) and moderate (abnormal milk and abnormal udder) cases of clinical mastitis (CM) occurring on WI farms (n = 4). Duplicate milk samples were collected for microbiological analysis at onset of CM (PRE) and 20 d later (POST). Cows were treated with an intramammary product containing 125mg ceftiofur. Bacteriological cure (BCURE) was defined as absence of pathogens in POST sample, whether or not a causative pathogen was isolated in PRE sample. Recurrence (RECUR) was defined when CM occurred after the milk withholding period. Permanence (PERM) was defined as cows remaining in the herd. Somatic Cell Cure (SCCURE) was defined as SCC at first test after CM below 200,000 cells/ml. Effects of farm, DIM, parity, severity, PRE outcome, BCURE, previous milk yield, previous SCC, previous occurrence of CM and treatment duration were assessed using Chi-squared analysis and logistic regression. Distribution of cases was: *E. coli* (14), *Klebsiella sp.* (11), *Enterobacter sp.* (8), *Serratia sp.* (7), other gram neg. (3), *Strep sp.* (25), CNS (4); *Staph. aureus* (1); *Staph. ag* (1), other gram-positives (9), and culture negative (60). The first case of CM was 8 times more likely to result in BCURE compared with cases preceded by CM ($P < 0.001$). Cases that were culture positive were 3–5 times less likely to experience BCURE as compared with cases that were culture negative ($P = 0.05$). Occurrence of a previous case of CM, parity, and DIM were associated with the probability of RECUR ($P < 0.04$). Older cows and cows in earlier lactation were more likely to RECUR. The odds of RECUR were 5 times greater for the first case of CM as compared with second or greater cases. Greater milk yield ($P < 0.001$) was the most important predictor for PERM. Farm, severity, milk yield and BCURE were associated with probability of SCCURE. SCCURE was more likely to occur when cows presented mild symptoms of CM (Odds ratio = 20) as compared with cows with moderate symptoms and cases that resulted in BCURE were 29 times more likely to result in SCCURE.

Key Words: mastitis, dairy, treatment

M193 Assessment of prior grazing experiences on adaption to pasture and performance of dairy heifers. F. Lopes*[1], D. K Combs[1], P. C. Hoffman[1], N. M Esser[1], and W. Coblentz[2,1], [1]*University of Wisconsin*, *Madison,* [2]*USDA/ARS, US- Department of Agriculture/Agricultural Research Service*, *Marshfield, WI*.

The objective of this study was to evaluate how previous grazing experience affects animal behavior on pasture. Animal behavior was monitored in 32 Holstein (n = 21) and Holstein-Jersey (n = 11) yearlings. Two heifer groups (n = 8 per group) had been exposed to pasture from August through October 2008, while the other 2 groups had been continuously housed in a bedding pack barn since weaning. All 4 groups were housed in the same bedding pack barn from November 2008 until the start of the experiment. In June 2009, heifers were assigned to one of 4 Italian ryegrass pastures. The experimental unit was paddock and the experimental design was a randomized complete block. Each group was allocated approximately 50kg pasture DM/head initially. Animal activity was assessed by visual observation. The same person recorded the activity of each heifer every 15 min from 0700h to1600h during the first 5 d of the study. Heifer's activities were categorized as: walking, drinking water, grazing, lying down or standing but not grazing. Behavior of heifers that grazed in 2008 initially differed from those with no previous grazing experience. During the first day, heifers with grazing experience spent more time grazing than heifers that had no prior grazing experience (57 vs. 43% of the time, $P < 0.05$). By the fourth day no difference between treatments group was observed. After the first week, behavior was monitored every 2 weeks through August 2009 (7 periods, 2 consecutive days per period). After the initial week on pasture, both groups spent approximately 60 percent of the time grazing (60 vs. 59% of the time, $P > 0.05$). At the end of the grazing season animal body weight was not different between experienced and inexperienced animals (451 vs. 442 kg, $P > 0.05$). The data suggests that prior grazing experience initially affected animal behavior on pasture. Time spent grazing increased for both experienced and inexperienced heifers over the first few days of the grazing period. Both groups of heifers adapted to the pastures within one week and there was no evidence that grazing behavior or weight gain were affected after the first week of pasture adaptation.

Key Words: grazing, heifers, behavior

M194 Seasonal variation of nutrients and in vitro dry matter degradability of forage hay. L. Shi*, N. Li, T. Shenkoru, W. Yang, S. McConahey, and T. Wuliji, *University of Nevada*, *Reno*.

Nutrient composition and digestibility change from season to season. It is advantageous to determine which month of the growing season is most nutritious for the forage hay production. The objective of this study is to determine the seasonal variation in the feed composition and in vitro dry matter degradability of forage hay harvested from the irrigated pastures. The forage hay samples were collected at 3 intervals during the growing seasons from the irrigated grazing pastures, namely for interval I, II and III respectively at the end of June, August and October on the Rafter 7 Ranch, Yerington, Nevada. Organic matter (OM), ash, neutral detergent fiber (NDF), acid detergent fiber (ADF) and crude protein (CP) were estimated. The in vitro dry matter degradability (IVDMD) was determined by incubating dried ground samples in tubes with cattle rumen fluid (Tilley and Terry, 1963). The OM and CP of interval I were higher than II and III; Ash, NDF and ADF were increased from June (I) to October (III), except NDF was lower in II than I and III. But ADF was remained the same for both I and II sampling intervals. The IVDMD was significantly ($P < 0.05$) higher for interval I than II and III. The IVDMD of interval II was lower ($P < 0.05$) than III. Data of feed composition were analyzed for mean and standard errors whereas data of IVDMD were analyzed for ANOVA and t Tests (LSD) procedures of SAS. The results showed that forage hay nutrients and IVDMD estimates are highest at June interval, which is also more suitable to produce a high quality forage hay production from grazing pastures.

Table 1. Nutrient composition (mean±SE) and IVDMD (%) of forage hay from Rafter 7 Ranch, Yerington

Interval	OM%	ASH%	NDF%	ADF%	CP%	IVDMD%
I	89.2±0.01	10.8±0.01	52.3±0.19	33.7±0.44	15.7±0.14	66.3[c]
II	86.9±0.02	13.2±0.02	48.8±0.19	33.1±0.05	14.5±0.04	51.2[a]
III	83.6±0.01	16.4±0.01	58.4±0.33	40.1±0.38	12.2±0.03	53.6[b]

[abc]Mean with a different superscript differs significantly at $P < 0.05$ in column.

Key Words: degradability, in vitro, forage hay

M195 Performance of Holstein heifers supplemented with probiotics. J. Graves*[1], S. Hill[1], E. Suever[1], B. Rude[1], J. Brett[2], and Y. Vizzier-Thaxton[3], [1]*Department of Animal and Dairy Science, Mississippi State University*, *Mississippi State*, [2]*College of Veterinary Medicine, Mississippi State University*, *Mississippi State*, [3]*Department of Poultry Science, Mississippi State University*, *Mississippi State*.

Sixty (n = 12) Holstein heifers were used to evaluate growth and health when supplemented with coccidiostat, mannanoligosaccharide (MOS) or β-glucan in milk replacer. Calves were randomly assigned to one of 5 treatments at birth: CX (1 g/d Deccox), MOS (10 g/d MOS), β-g (0.5 g/d β-glucan), CX + MOS (1 g/d Deccox + 10 g/d MOS) and MOS + β-g (10 g/d MOS + 0.5 g/d β-glucan). Heifers received 3.8L milk replacer (22% CP, 20% Fat) once daily until 6 wks of age, but remained on trial for 56d. Calves were fed a non-medicated starter (18% CP) at 0.9 kg/d and increased by 0.9 kg/d when orts = 0. Orts were collected and weighed daily and pooled by week within treatment. Calves had ad lib access to clean water. At birth, calves were fed colostrum via esophageal tube, weighed, and measured. Fecal and respiratory scores were recorded daily; body measurements, blood and fecal samples were collected weekly. Fecal samples analyzed for coccidia bi-weekly after 21 d; at 2, 4, and 8 wks fecal samples were analyzed for E. *coli*. Blood samples were analyzed for CBC w/differential. There were no significant differences in DMI ($P < 0.93$), FE ($P < 0.95$), ADG ($P < 0.79$) or blood analysis ($P > 0.10$) among treatment groups. Given similar diets fed, no changes in growth or intake were expected. No differences in fecal or respiratory scores, CBC, or other health measures indicated that supplementation with MOS, β-g, or a combination supported immune function similarly to CX. Fecal shedding of E. *coli* was not different across treatments ($P < 0.23$), however, orthogonal contrasts showed greater E. *coli* from MOS + β-g (80.4×10^4 CFU/µl feces) compared with β-g (23.2×10^4 CFU/µl feces; $P < 0.04$). There was also a trend for calves fed MOS to shed more E. *coli* compared with the calves fed β-g (70.3 vs. 23.2×10^4 CFU/µl feces, respectively, $P < 0.06$). E. *coli* shedding decreased over time (114.6, 49.4 and 5.0×10^4 CFU/µl feces at wk 2, 4 and 8, respectively; $P < 0.01$).

Key Words: probiotics, growth, Holstein heifers

Graduate Student Poster Competition: National ADSA Production PhD Poster

M196 Effects of condensed tannins supplementation on ruminal fermentation and lactational performance of dairy cows when fed high or low forage diet. C. M. Dschaak*, C. M. Williams, M. S. Holt, J.-S. Eun, and A. J. Young, *Department of Animal, Dairy, and Veterinary Sciences, Utah State University*, *Logan*.

A lactating dairy trial was conducted to determine the influence of water-soluble Quebracho extract containing approximately 75% condensed tannins (CT; DM basis) with 99% solubility (Chemtan Company Inc., Exeter, NH) on intake, digestibility, ruminal fermentation, and lactational performance of dairy cows. The cows were fed high forage (HF) or low forage (LF) diet with forage to concentrate ratio of 59:41 and 41:59 on DM basis, respectively. Eight lactating Holstein cows (DIM = 62 ± 8.8) were used, and 4 cows were surgically fitted with ruminal cannulas. The design of the experiment was a double 4 × 4 Latin square with a 2 × 2 factorial arrangement of treatments, and each period lasted 21 d (14 d of treatment adaptation and 7 d of data collection). Four dietary treatments were tested: HF without CT (HF−CT), HF with CT (HF+CT), LF without CT (LF–CT), and LF with CT (LF+CT). The Quebracho extract was added to the HF+CT and the LF+CT diets at a rate of 3% of dietary DM. Data were analyzed using the MIXED procedure of SAS. Supplementing CT on HF diet decreased DM intake, but not on LF diet. Digestibilities of DM and nutrients were not affected by CT supplementation on HF and LF diets. Milk yield was not influence by CT supplementation, but milk true protein decreased by supplementing CT in HF diet. Milk urea N concentration decreased with CT supplementation regardless of diet type, whereas efficiency of N use for milk N production was not affected by CT supplementation. Supplementing CT decreased total VFA production in HF and LF diets. Molar proportions of acetate ($P = 0.07$) and butyrate ($P = 0.06$) tended to increase by CT supplementation. Acetate to propionate ratio decreased with CT supplementation in HF diet, while conversely increasing the ratio in LF diet with CT supplementation. Ruminal ammonia-N concentration did not differ across treatments. Supplementing Quebracho extract in lactating dairy diets can improve dietary use of N as indicated by lower milk urea N, therefore N excretion can be reduced.

Key Words: condensed tannins, lactating dairy cows, milk urea nitrogen

M197 Relationships between prepartum energy intake and reproductive parameters in Holstein cows. F. C. Cardoso*, M. R. Murphy, and J. K. Drackley, *University of Illinois*, *Urbana*.

A meta-analysis was conducted to determine the effect of prepartum energy intake on days to first artificial insemination (DTFAI), days to conception (DTC), and number of artificial inseminations per conception (NAIC). The database was developed from 6 different experiments completed in our group from 1993 to 2006. Net energy lactation (NE_L) values in the diets varied from 1.21 Mcal/kg to 1.73 Mcal/kg DM. A total of 304 cows (281 multiparous and 23 primiparous) were included in the analyses. Prepartum dry matter intake (DMI) was recorded daily in all experiments. The NE_L intake ($NE_L I$) was calculated from the cow's respective dietary NE_L and average prepartum DMI. Full models were reduced by removing terms that did not contribute significantly to the model. Such terms included body condition score at calving ($P = 0.81$), season of the year at first artificial insemination ($P = 0.40$), and parity ($P = 0.62$). The DTFAI (n = 258) was lower for cows with higher $NE_L I$ ($P = 0.057$) and was not influenced ($P = 0.39$) by postpartal health problems (DISE). In this analysis, DTC (n = 212) was not influenced by $NE_L I$ ($P = 0.66$) or DISE ($P = 0.20$). Similarly, NAIC (n = 212) was not influenced by $NE_L I$ ($P = 0.50$) or DISE ($P = 0.45$). Inferences related to DTC and NAIC should be reevaluated when these results can be incorporated with those of similar experiments, to increase sample size. Based on the variances of DTFAI, DTC and NAIC in these experiments, the suggested number of cows needed to detect a 10% difference in these variables at a 95% confidence level are 88, 257, and 294, respectively. In conclusion, prepartum NE_L intake affected DTFAI.

Key Words: transition cow, energy intake, reproduction

M198 Effectiveness of an herbal remedy compared to control or traditional therapy in dry off treatments. K. A. E. Mullen*, K. L. Anderson, and S. P. Washburn, *North Carolina State University*, *Raleigh*.

Dry cow therapy, administered at the end of lactation, is aimed at eliminating current and preventing future intramammary bacterial infections. Dry cow therapy conventionally uses antibiotics. Certified organic dairies are restricted from antibiotic use and thus must use an alternative or no dry cow therapy. The current study used 150 Holstein, Jersey, and crossbred cattle to compare an herbal treatment (Phyto-Mast) to conventional (Quartermaster and Orbeseal) or no dry cow therapy. Each treatment (conventional, Phyto-Mast, or none) was balanced by breed, age, and due date and included 40 cows and 10 heifers. Milk weights and somatic cell scores (SCS) from the first test date in the first month postpartum were compared among treatment groups; no significant difference was observed between treatments. SCS average from the previous lactation was also recorded. Mean milk production was 22.7 ± 1.2 kg for conventional cows (CC), 14.7 ± 1.9 kg for conventional heifers (CH), 21.1 ± 1.0 kg for no treatment cows (NC), 14.5 ± 1.1 kg for no treatment heifers (NH), 22.9 ± 1.1 kg for Phyto-Mast cows (PC) and 17.1 ± 1.43 kg for Phyto-Mast heifers (PH). Milk production at the first test day postpartum was similar among multiparous cows, but the first-calf heifers in the Phyto-Mast group tended to have higher milk production at the first test than heifers in other groups. SCS were 1.89 ± 0.23 for CC, 3.33 ± 0.83 for CH, 2.15 ± 0.38 for NC, 3.73 ± 0.37 for NH, 2.17 ± 0.32 for PC, and 3.73 ± 0.85 for PH. SCS averages from the previous lactation were 3.74 ± 2.9 for CC, 3.63 ± 2.93 for NC, and 2.94 ± 2.72 for PC. Differences from previous lactation SCS for cows were not significant and remained similar across treatment groups at the start of the subsequent lactation. Also, SCS among first lactation heifers did not differ in early lactation but tended to be higher than for older cows. Neither lack of treatment nor the use of an herbal treatment differed from a conventional dry treatment for milk production or SCS at the start of lactation. More information on specific mastitic organisms in cows of various treatment groups is needed before definitive conclusions can be made.

Key Words: dry cow therapy, mastitis, organic dairy

M199 Serum pregnancy-associated glycoprotein (PAG) and progesterone concentrations after induction of pregnancy loss at day 39 of gestation in lactating dairy cows. J. O. Giordano*[1], J. N. Guenther[1], G. Lopes Jr.[1], M. F. McGrath[2], and P. M. Fricke[1], [1]*University of Wisconsin*, *Madison*, [2]*Monsanto Agricultural Company*, *St. Louis, MO*.

Pregnancy status was evaluated in lactating crossbred (75% Holstein, 25% Jersey) dairy cows (n = 29) by ultrasonography 39 d after TAI, and pregnant cows were randomly assigned to one of 3 treatments: 1)

control cows (CON, n = 10) received an injection of saline (5 mL, i.m.); 2) PGF cows (PGF, n = 10) received an injection of $PGF_{2\alpha}$ (25 mg, i.m.); and 3) infusion cows (INF, n = 9) received an intrauterine infusion of 120 mL hypertonic saline (25%, v/v) into the uterine horn containing the embryo. Blood samples were collected every 12 h for 6.5 d after treatment and daily from 6.5 to 10 d after treatment to assess serum PAG and progesterone (P4) concentrations. Uterine contents were evaluated using ultrasonography every 12 h to determine embryo presence and viability. All embryos from CON cows remained viable based on embryonic heart beat throughout the experiment. Time from treatment to cessation of embryonic heart beat was greater ($P < 0.001$) for PGF than for INF cows (36.0 ± 1.3 vs. 0.3 ± 1.4 h, respectively), and time from treatment to conceptus expulsion was greater ($P < 0.001$) for INF than for PGF cows (7.1 ± 0.8 vs. 1.9 ± 0.7 d, respectively). There was a treatment by day interaction ($P < 0.001$) for serum P4 concentrations in which P4 concentrations were greater for CON and INF than for PGF cows (8.7 ± 0.6, 8.1 ± 0.6, and 0.9 ± 0.6 ng/ml, respectively). Beginning 12 h after treatment, PGF cows had lower P4 concentrations than CON and INF cows. There was a treatment by day interaction ($P < 0.001$) for serum PAG concentrations in which mean PAG was greater for CON (3.5 ± 0.3 ng/ml) than for PGF (1.4 ± 0.3 ng/ml) and INF (1.4 ± 0.3 ng/ml) cows. Serum PAG concentrations differed among CON cows and PGF and INF cows beginning 60 h after treatment. We conclude that although timing of conceptus expulsion occurred 5.2 d later for INF than for PGF cows, serum PAG concentrations for INF and PGF cows decreased at a similar rate from the onset of treatment

Key Words: PAG, pregnancy loss, embryo

M200 Prepartum 2,4-thiazolidinedione alters gene expression of peroxisome proliferator-activated receptor gamma and leptin in the adipose tissue of dairy cows. K. M. Schoenberg*, K. L. Perfield, S. L. Giesy, Y. R. Boisclair, and T. R. Overton, *Cornell University*, *Ithaca, NY*.

Thiazolidinediones (TZD) are potent ligands for peroxisome proliferator-activated gamma (PPARγ). Administration of TZD has been shown to alter lipid metabolism and energy status in transition dairy cows. The objective of this experiment was to determine the effect of prepartum TZD administration on mRNA expression of PPARγ, leptin, fatty acid synthase (FAS), and lipoprotein lipase (LPL) in adipose tissue. Holstein cows entering second or greater lactation were administered 0 (n = 6), 2.0 (n = 5), or 4.0 (n = 4) mg TZD/kg BW by intrajugular infusion once daily from 21 d before expected parturition until parturition. Adipose tissue was collected on d −7 before expected parturition. After 14 d of TZD administration, PPARγ expression was increased ($P = 0.01$) by 24% (2.0 mg TZD/kg BW) and 10% (4.0 mg TZD/kg BW) over control cows. Increased expression of PPARγ is a marker of improved energy status and is consistent with previous data from this study on improved insulin sensitivity, decreased plasma non-esterified fatty acids, and decreased liver triglycerides with TZD administration. Leptin expression was decreased (−34%) in cows administered the 2.0 mg dose, but increased (+7%) in cows administered the 4.0 mg dose ($P = 0.07$); also corresponding with previous data. There were no significant changes in expression of LPL or FAS. It is likely that these results are confounded by changes in body condition scores and variation in time relative to actual calving dates. However, these results offer additional evidence that TZD treatment alters leptin expression. These data indicate that TZD administration increases PPARγ expression in transition dairy cattle. Further investigation is required to characterize the metabolic changes produced by TZD treatment in transition dairy cattle.

Key Words: transition cow, thiazolidinedione, leptin

M201 Effects of cobalt supplementation and vitamin B_{12} injections on energy metabolism of dairy cows. M. S. Akins*[1], S. J. Bertics[1], M. T. Socha[2], and R. D. Shaver[1], [1]*University of Wisconsin*, *Madison*, [2]*Zinpro Corporation*, *Eden Prairie, MN*.

The objective of this study was to determine metabolic responses of primi- and multiparous dairy cows fed different levels and sources (inorganic and organic) of cobalt or given weekly vitamin B_{12} injections. Forty-five primi- and multiparous cows 60 d prepartum were blocked by parity (1 or > 1) and expected calving date, and then randomly assigned to 1 of 5 treatments in a randomized complete block design. The treatments were: no supplemental Co (Control), 25 mg Co from Co carbonate (CoCarb), 25 mg (LcoGH) or 75 mg (HCoGH) Co from Co glucoheptonate, and Control with weekly 10 mg vitamin B_{12} injections. Cows were on trial until 150 DIM. Cobalt (ppm DM) in the lactating diet was 1.0, 1.9, 2.3, and 5.2 for Control and IB12, CoCarb, LCoGH, and HCoGH, respectively. Far-off, close-up, and lactating diets were 13.8, 15.1, and 18.0% CP and 48.8, 40.2, and 32.9% NDF (DM basis), respectively. Intake was not affected ($P > 0.10$) by treatment and was 19.4 ± 0.5 and 23.1 ± 0.8 kg DM/d for primi- and multiparous cows, respectively. Body weight and condition score and calculated energy balance were not affected by treatment ($P > 0.10$). Plasma glucose, non-esterified fatty acids, and β-hydroxybutyrate were not affected by treatment ($P > 0.10$). Effect of sampling day was significant ($P < 0.001$). Glucose decreased from 60 d prepartum (65 ± 1.1 mg/dL) to 30 DIM (55 ± 1.0 mg/dL), and increased at 90 DIM (60 ± 1.0 mg/dL); however, primiparous cows had a larger decrease at 30 DIM and smaller increase thereafter. Non-esterified fatty acids increased from 60 d prepartum (249 ± 39.8 mmol/L) to 1 DIM (724 ± 40.7 mmol/L), then decreased at 30 DIM (398 ± 40.1 mmol/L), with multiparous cows having a larger increase at 1 DIM. Beta-hydroxybutyrate increased from 60 d prepartum (4.2 ± 0.95 mg/dL) to 30 DIM (15.9 ± 0.95 mg/dL). Addition of Co above requirements or vitamin B_{12} did not improve energy metabolism of dairy cows, because vitamin B_{12} status was likely adequate.

Key Words: cobalt, vitamin B_{12}, dairy cow

M202 Genetic analysis of type traits in the Holstein population of Iran. M. R. Bakhtiarizadeh*, M. M. Shahr Babak, and A. Pakdel, *Tehran University, Karaj, Tehran, Iran.*

The objective of this study was to estimate the genetic parameters for 13 linear type traits, in Holstein population of Iran. Type traits records generated for first lactation Holstein dairy cows from 1991 to 2007 over 220 herds, 13 type traits were analyzed: stature (ST), body depth (BD), rump width (RW), chest width (CW), udder depth (UD), fore udder attachment (FU), udder width (UW), udder height (UH), fore teat placement (FTP), rear teat placement (RTP), suspensory ligament (SL), foot angle (FA) and rear leg, side view (RLS). For the analysis of type traits, herd, year and season of calving, age at Classification, age at calving, effect of classifier and days in milk effects were included in the model. The genetic parameters were estimated by ASREML software. Heritabilities ranged from 0.03 to 0.29. The largest value was for ST, the smallest for FA. The largest positive correlations were between ST

and CW (0.83), FTP and RTP (0.64), FU and UD (0.61). The largest negative correlations were between RLS and FA (−0.56), RLS and UD (−0.48), RLS and SL (−0.46). The genetic parameters estimate for type traits was consistent with other studies in different populations. The phenotypic correlations tended to be weaker than their corresponding genetic correlations although the signs of the correlations were generally the same. ST, BD, RW and CW seem to be strongly genetically correlated in the positive direction. Larger cows (taller, deeper cows with more rump width) tended to have stronger SL and more UH. Within the udder traits, FTP, RTP and SL were positively genetically correlated. The highest genetic correlation was between FU and UD. The highest negative genetic correlations were between UW and UH. Cows with shallow udders possess tighter FU. Animals with genetically stronger, shallower udders with superior udder support tended to have more sickled rear legs. A strong negative genetic correlation existed between FA and RLS indicating that cows with a steep FA tended to have straighter rear legs. The results from this study indicate that considerable genetic variation existed for some type traits within this sample in the Holstein population of Iran.

Key Words: genetic parameters, type traits, genetic correlation

M203 Effects of porcine relaxin on motility characteristics of boar sperm as assessed by computer-assisted sperm analysis (CASA). J. C. Rodriguez-Munoz*, J. M. Feugang, M. Crenshaw, S. T. Willard, and P. L. Ryan, *Mississippi State University, Mississippi State.*

Relaxin is a small peptide found in both female and male reproductive tissue. Relaxin is detected in the seminal plasma of various mammals, but its effect on sperm motility is still unclear. Here, we evaluated the role of porcine relaxin (pRLX) on the motility characteristics of boar spermatozoa during storage (~21°C) using a CASA system (IVOS, Hamilton Thorne, Beverly, MA). Diluted semen from several boars was centrifuged and Nidacon products (Mölndal, Sweden) were used to purify spermatozoa. Motile sperm were selected through a discontinuous percoll gradient, washed twice, counted and diluted with BoviExtend to a final concentration of $75x10^6$ sperm/ml. Samples were incubated for 60 min at 37°C with 0, 25, 50 or 100 ng/ml pRLX. Three µl of each treatment group were loaded into 4-chamber Leja slides for CASA analysis. Experiments were conducted on 3 consecutive days using the same batch of semen. Four independent replicates were used and pRLX effects assessed in triplicate for each treatment. All data were analyzed using ANOVA-2 or −3. The threshold of significance was $P < 0.05$. The ANOVA-3 analysis showed that pRLX and storage time affected the proportion of motile, progressive, and rapid spermatozoa ($P < 0.05$). Similar effects were observed on the amplitude of lateral head displacement (ALH), straightness (STR) and linearity (LIN) ($P < 0.05$). Using ANOVA-2, we found no significant effect of pRLX on proportion of motile cells on d 1 and d 3, but a significant increase on d 2 ($P < 0.05$). The presence of 100 ng/ml pRLX increased the proportion of progressive and rapid spermatozoa on all days, while the ALH was decreased on d 2 and d 3 ($P < 0.05$). There was no effect on beat cross frequency (BCF) at all times ($P > 0.05$). Moreover, 100 ng/ml pRLX significantly increased the STR on all days, while 50 and 100 ng/ml enhanced the LIN on d 2 and d 3 ($P < 0.05$). Overall, our study indicates a beneficial effect of relaxin on motility of boar spermatozoa during storage, in particular the proportion of progressive and rapid spermatozoa. Relaxin positively affects STR, LIN, and ALH which are indices of rapid sperm movement.

Key Words: boar, sperm motility, relaxin

M204 Response surface model for broiler chickens performance fed diets varying in digestible protein and amino acids. H. Ahmadi and A. Golian*, *Ferdowsi University of Mashhad*, *Mashhad, Khorasan Razavi, Iran*.

Response surface methodology (RSM) and 5-level-4-factor central composite design (CCD) were used to evaluate the response of broilers (BWG and FCR) to dietary digestible protein (dP), lysine (dLys), methionine+cysteine (dTSAA), and threonine (dThr). Eighty 4 cages of 5 birds each were assigned to feed diets contained 5 levels of dP (18, 19, 20, 21 and 22%), dLys (1.06, 1.12, 1.18, 1.24 and 1.30%), dTSAA (0.81 to 0.86, 0.91, 0.96 and 1.01%), and dThr (0.66, 0.71, 0.76, 0.81 and 0.86%) from 11 to 17 d of age. Diets were prepared using corn, soybean meal (45.2% CP), and corn gluten meal (48.6% CP). Protein and amino acid analyses were performed for these ingredients. All diets were formulated to have 3050 kcal/kg. The experimental results of CCD were fitted with the second-order polynomial equation. A ridge analysis was utilized to compute the optimum response for maximizing BWG and minimizing FCR. The fitted second-order polynomial equations for BWG and FCR are produced as follows: BWG (g/bird/d) = 1222.2 −76.7 dP −2.4 dP^2 −1468.0 dLys −260.0 $dLys^2$ +675.2 dTSAA −522.0 $dTSAA^2$+ 404.0 dThr −793.5 $dThr^2$ +77.6 dP*dLys +41.6 dP*dTSAA +51.5 dP*dThr +145.8 dLys*dTSAA +556.5 dLys*dThr −958.3 dTSAA*dThr; R^2 = 0.70; Root MS error = 4.97. FCR = −124.3 +12.8 dP +0.2 dP^2 +70.8 dLys +44.7 $dLys^2$ −86.5 dTSAA +60.8 $dTSAA^2$ −18.6 dThr +64.3 $dThr^2$ −9.7 dP*dLys −4.5 dP*dTSAA −4.0 dP*dThr +34.3 dLys*dTSAA −24.8 dLys*dThr +34.3 dTSAA*dThr; R^2 = 0.71; Root MS error = 0.53. The ridge max analysis on BWG and ridge min analysis on FCR models revealed that the maximum BWG may be obtained with dP 18.5%, dLys 1.10, dTSAA 0.89, and dThr 0.73 and minimum FCR may be obtained with dP 19.44%, dLys 1.18, dTSAA 0.90, and dThr 0.75. At the optimum point, the predicted BWG and FCR were 40.2 g/bird/d and 1.09, respectively. The combination of CCD and RSM techniques consider simultaneously all investigating factors and their possible interactions. Thus, it appears that the platform may be used to describe relationship between dietary concentration of nutrients and broiler performance to achieve optimal target.

Key Words: response surface model, digestible protein and amino acid, broiler chicken

M205 Partitioning of lysine stable isotopes in broiler breeders during the transition into sexual maturity. R. D. Ekmay*, C. Salas, J. England, and C. N. Coon, *University of Arkansas*, *Fayetteville*.

A study was conducted to determine how lysine is partitioned during the transition into sexual maturity in broiler breeder hens. At 21 wk, 15 Cobb 500 hens were individually housed and fed a 100g meal. Twelve of these hens were, in addition, administered a 15mg oral dose of ^{15}N-lysine daily beginning at wk 22; 3 hens did not receive any ^{15}N-lysine to serve as controls. At first egg, administration of ^{15}N-lysine ceased and a daily 15mg oral dose of ^{13}C-lysine began. When the second egg was laid, 6 hens (Group 1) were slaughtered and the left *Pectoralis major* was excised and snap frozen in liquid nitrogen. The egg contents were also frozen. The remaining 6 hens (Group 2) were slaughtered after the third egg and sampled as described. Molar percent excess (MPE) was determined in the egg and breast samples by GC-MS. The 159 and 160 *m/z* fragments were utilized for determination of ^{13}C enrichment. The 130 and 131 *m/z* fragments were utilized for determination of ^{15}N enrichment. MPE was calculated using the Rosenblatt (1992) approach. Statements of significance are based on testing at $P < 0.05$. No differences in breast weight or the number of days of enrichment between groups were determined. The ^{13}C-lysine enrichment in breast muscle was not significantly higher than in control hens, however ^{15}N-lysine enrichment was higher in groups 1 and 2 compared with the control. The ^{15}N-lysine enrichment of the egg increased significantly by the 3rd egg (Group 2). The ^{13}C-lysine enrichment of the egg did not differ from the control eggs. In summary, skeletal tissue appears to play an increasingly important role in supplying amino acids for egg formation during hen maturation.

Key Words: broiler breeders, amino acids, nutrient partitioning

M206 Varying levels of dietary methionine inclusion on the hematology and serum biochemistry of broilers. G. O. Adeyemo* and A. D. Ologhobo, *University of Ibadan*, *Ibadan, Oyo, Nigeria*.

The influences on hematology and serum biochemistry of graded levels of methionine inclusion in the diets of broilers were researched. One hundred and fifty broiler chicks were divided into 5 treatments consisting of 6 replicates of 5 chicks each. The chicks were kept in floor pens. The study lasted for 56 d at the teaching and research farm of the university of Ibadan Nigeria. No significant differences ($P > 0.05$) were observed in the packed cell volumes (PCV), red blood cells (RBC) and white blood cells (WBC) values of broilers fed the different levels of methionine inclusion, at the finisher phase, but at starter phase significant differences ($P < 0.05$) were observed, with the WBC values increasing as the inclusion rate of methionine increased. Total protein value of 4.80 g/dl and 4.48 g/dl were obtained for treatments 4 and 5 respectively which were not significantly ($P > 0.05$) different from each other. There were wide variations in the glucose concentration of the birds. The highest glucose concentration was observed from birds on diet 2 (220.90 g/dl) while the least was observed for birds fed the control diet though significant differences ($P < 0.05$) were observed, it did not follow a particular order.

Key Words: broilers, methionine, serum biochemistry

M207 Separate response to lysine and methionine in broiler starter diets. C. Lu*[1], C. A. Coto[1], A. Karimi[2], J. H. Park[1], Y. Min[1], and P. W. Waldroup[1], [1]*University of Arkansas*, *Fayetteville*, [2]*University of Kurdistan*, *Kurdistan, Iran*.

A study was conducted to evaluate the separate response to Lysine (Lys) and to Methionine (Met) in diets on live performance of young broiler chickens from 0 to 18 d of age. Corn and soybean meal of known protein and moisture content were used to formulate basal diets to provide 0.90 to 1.40% digestible Lys in increments of 0.10%. The mean of suggested amino acid ratios to Lys suggested by literature values was used in formulation according to the ideal protein concept. All amino acids other than Met and TSAA were calculated to meet or exceed the expected ratio to Lys. Diets were calculated to be isocaloric with 3086 kcal/kg ME and were supplemented with inorganic trace mineral premix to avoid any source of Met from this premix. Experimental diets were prepared by addition of variable amounts of MHA (84% of Met) and cornstarch to the Lys basal diets to provide increments of 0.04% up to 0.28% supplemental Met activity for each level of digestible Lys, with a 6 × 8 factorial arrangement of 6 levels of Lys and 8 levels of supplemental Met resulting in a total of 48 treatments. Each of the 48 experimental diets was fed to 6 replicate pens of 6 male chicks (Cobb

500). Body weights by pen were obtained at 1 and 18 d of age with feed consumption determined during the test period. The ANOVA considered levels of Lys and Met and their interaction. There was significant ($P < 0.05$) effect of the dietary Lys level on feed intake, body weight gain and feed conversion ratio, with optimal level close to 1.2% of digestible Lys for both body weight gain and feed conversion ratio. There was no significant ($P < 0.05$) effect of the added Met level on feed intake, body weight and feed conversion ratio, indicating that the Met level in the basal diet of this study might be sufficient to support body weight and feed conversion ratio. No significant interactions were observed between Lys and Met for these 3 parameters. Results of this study suggest that the response to variation in Lys is a response to itself but not to Met in broiler starter diets.

Key Words: broilers, lysine, methionine

M208 Effect of crude protein and essential:nonessential amino acids ratio on nitrogen balance in broiler. C. C. Goulart[1], F. G. P. Costa*[1], E. T. Nogueira[2], M. Kutschenko[2], H. S. Rostagno[3], C. F. S. Oliveira[1], R. C. L. Neto[1], and V. P. Rodrigues[1], [1]*Federal University of Paraiba*, *Areia, PB, Brazil*, [2]*Ajinomoto Animal Nutrition*, *Sao Paulo, SP, Brazil*, [3]*Federal University of Viçosa*, *MG, Brazil*.

This study aimed to evaluate the effect of crude protein (CP) and for essential amino acids:nonessential amino acids (EAA:NEAA) diet on nitrogen balance in broiler chickens from 18 to 21 d. A total of 480 Cobb broiler chicks, males, distributed in a completely randomized design with 4 treatments and 6 replicates of 20 birds. Was formulated a diet with 18% CP supplemented with lysine, methionine, threonine, arginine, valine, isoleucine, glycine and tryptophan, to meet the requirements of amino acids (AA) digestible. After the formulation, there was the delivery of EAA in total AA (TAA). Added to the total amount of EAA was calculated and compared with the level of dietary protein, considering this value as AAT. Were considered EAA: lysine, methionine + cystine, threonine, arginine, valine, tryptophan, isoleucine, leucine, phenylalanine, histidine and glycine. The other treatments were formed from glutamate supplementation to achieve levels of 19, 20 and 21% CP. Starch, oil and gravel were used in animal feed to make them isocaloric. Relations EAA:NEAA diets with 18, 19, 20 and 21% CP were 55:45, 52:48, 49:51 and 47:53, respectively. In the period of 18 to 21 d were collecting excreta and feed intake was measured for the determination of consumption, excretion and retention of N. It was observed linear increase in the consumption and excretion of N with increasing levels of dietary CP. No significant levels of CP level on N retention by the birds, however, the retention efficiency of N responded quadratically with increasing CP, being higher in the diet with 19% CP ($y = -403.77 + 49.414x - 1.3025x^2$; $r^2 = 0.98$). Diet with 19% CP and EAA:NEAA ratio of 52:48 is recommended in diets for broilers from 8 to 21 d.

Key Words: ideal protein, N excretion, N retention

M209 True ileal amino acid digestibility and protein utilization in broilers fed various levels of canola meal and phytase. C. Kong* and O. Adeola, *Purdue University*, *West Lafayette, IN*.

A total of 384 broiler chicks were used in a 14-d trial to examine the effect of levels of canola meal (CM, 387.5 g/kg CP) and microbial phytase on ileal amino acid (AA) digestibility and protein utilization of broilers. Experimental treatments consisted of 2 factors including phytase at 2 levels (0 or 1500 FTU/kg) and CM at 3 levels (125, 250, or 375 g/kg). The birds received standard starter diet from d 1 to 7 and the assay diet from d 8 to 22. On d 8, birds were allocated to 6 dietary treatments in a randomized complete block design and excreta were collected from d 12 to 14 and 19 to 21 and on d 22, ileal digesta were collected. Regressions of CM-associated digestible AA intake against AA intake without or with phytase were used for determination of true ileal AA digestibility of CM. There was a significant phytase effect ($P < 0.05$) for true ileal digestibility of all indispensable AA except for histidine. On d 15 and 22, there was a linear increase ($P < 0.05$) in N retention as CM increased from 0 to 375 g/kg, whereas there was a linear decrease ($P < 0.05$) in P retention, regardless of phytase addition. Weight gain (WG), feed intake, protein gain (PG), and protein intake (PI) linearly increased ($P < 0.01$) with increasing CM level regardless of phytase supplementation and experimental period. There were phytase effects ($P < 0.05$) on WG and protein efficiency ratio (PER) on d 15, whereas there were phytase effects ($P < 0.05$) on WG and PG on d 22.On d 15, there was a linear increase ($P < 0.01$) in net protein utilization (NPU) of the diets with phytase, whereas on d 22, there was a linear increase ($P < 0.05$) in NPU regardless of phytase supplementation. In conclusion, the result of this study indicated that phytase supplementation improves the true ileal digestibility of indispensable AA and WG, whereas PER was only improved on d 15 by addition of phytase.

Key Words: phytase, true ileal digestibility, protein utilization

M210 Separate response to lysine and methionine in broiler grower diets. C. Lu*[1], C. A. Coto[1], A. Karimi[2], J. H. Park[1], Y. Min[1], and P. W. Waldroup[1], [1]*University of Arkansas*, *Fayetteville*, [2]*University of Kurdistan*, *Kurdistan, Iran*.

A study was conducted to evaluate the separate response to Lysine (Lys) and to Methionine (Met) in diets on live performance of young broiler chickens during the grower period of 14–35 d. Corn and soybean meal were used to formulate basal diets to provide 0.80 to 1.30% digestible Lys in increments of 0.10%. The mean of suggested amino acid ratios to Lys suggested by literature values was used in formulation according to the ideal protein concept. All amino acids other than Met and TSAA were calculated to meet or exceed the expected ratio to Lys. Experimental diets were prepared by addition of variable amounts of MHA (84% of Met) and cornstarch to the Lys basal diets to provide increments of 0.03% up to 0.21% supplemental Met activity for each level of digestible Lys. Two consecutive trials using the same experimental diets were conducted with identical design. Each of the 48 test diets was fed to 2 replicate pens of each trial at 14 d. Body weights by pen were obtained at 14, 28 and 35 d of age with feed consumption determined during the test period. During the period of 14 to 28 d, there were significant effects of the dietary Lys and added Met levels on BWG and FCR, with optimal digestible Lys level ≥0.90% for BWG and ≥ 1.30% for FCR. The optimal level of added Met during this period is ≥0.09% (total Met ≥ 0.33) and ≥ 0.12% (total Met ≥ 0.43) for BWG and FCR, respectively. During the period of 28 to 35 d, there were significant effects of the dietary Lys and added Met levels on BWG and FCR, with optimal digestible Lys level ≥1.00% for BWG and ≥ 1.30% for FCR. The optimal level of added Met during this period is ≥ 0.18% for both BWG (total Met ≥ 0.38) and FCR (total Met ≥ 0.49). No significant interactions between Lys and Met were observed based on BWG and FCR during each of the 2 periods. Results of this study suggest that the response to variation in Lys is a response to itself but not to Met in broiler grower diets.

Key Words: broilers, lysine, methionine

M211 Digestible arginine:lysine ratios for broilers during the starter and finisher periods. A. Campos[1], E. T. Nogueira[2], L. F. Albino[1], and H. S. Rostagno*[1], [1]*Federal University of Viçosa*, *Viçosa, MG, Brazil*, [2]*Ajinomoto of Brazil/Ajinomoto Animal Nutrition*, *Sao Paulo, SP, Brazil*.

The ideal protein concept requires all amino acids to be present in exact levels to provide for maintenance and protein deposition. Arginine (Arg) is an essential amino acid for poultry and also related to immune functions. Little information has been reported on digestible Argl:Lys ratios for starter and finisher broilers. Two experiments were carried out to evaluate digestible Arg:Lys ratios for male Cobb 500 broilers in 2 periods: 7 – 21 (starter) and 28 – 40 (finisher) days of age. A total of 1000 starter and 800 finisher broilers were distributed in a completely randomized experimental design with 5 digestible Arg:Lys ratios and 8 replicates of 25 and 20 birds per experimental unit (pen) in the starter and finisher period, respectively. Diets were formulated to meet or exceed the nutritional requirements in both periods, except for digestible Lys (1.08% and 0.98% for the starter and finisher periods, respectively). Digestible Arg:Lys ratios of 95 (1,026% dig Arg), 100, 105, 110, and 115% were used in the starter period, whereas ratios of 91 (0.892% dig Arg), 98, 105, 112, and 119% were used in the finisher period. Statistical analysis using different models (quadratic, 95% of the quadratic peak, broken line and quadratic and plateau) were applied to the performance data. In the starter period, weight gain and feed conversion presented a quadratic response ($P < 0.05$) to Arg:Lys ratios, as described by the equations $Y = -1530.57 + 39.174\ Arg - 0.1742\ Arg^2$ ($R^2 = 0.96$) and $Y = 5.047 - 0.0649\ Arg + 0.00029\ Arg^2$ ($R^2 = 0.98$), respectively. In the finisher period, there was a quadratic effect ($P < 0.05$) on weight gain ($Y = -926.96 + 38.09\ Arg - 0.172\ Arg^2$; $R^2 = 0.94$) and feed conversion ($Y = 4.323 - 0.0468\ Arg + 0.000205\ Arg^2$; $R^2 = 0.95$). These results suggest that a dietary Arg:Lys ratio of 108% is adequate for optimal performance of broiler chickens during the starter and finisher periods.

Key Words: arginine, lysine, performance

M212 Effect of a mono component protease on true amino acid digestibility of a corn and soybean meal diet for chicks. R. K. G. Messias[1], L. F. T. Albino[1], J. O. B. Sorbara[2], and H. S. Rostagno*[1], [1]*Universidade Federal de Viçosa*, *Viçosa, MG, Brazil*, [2]*DSM Nutritional Products*, *São Paulo, SP, Brazil*.

Today the utilization of feed additives that improve performance and reduce the impact of pollution generated by intensive broiler chicken production is a concern of every poultry nutritionist. A digestibility trial was conducted to determine the effect of a mono component protease on true ileal amino acid digestibility (TAAD) of a corn and soybean meal diet. The trial was conducted with 168 male chickens placed on 28 wire cages from 12 to 22 d of age, in a complete randomized experimental design with 4 treatments (a corn soy diet and a protein free diet with and without protease supplementation) with 6 replicates of 7 birds each. The mono component protease used was RONOZYME ProAct with 75000 Prot Units/g product (dose of 200 ppm). Acid insoluble ash (Celite) was added to all diets as inert marker. Feed and water were provided ad libitum. At 22 d of age all birds were sacrificed and ileum content collected. Digesta samples were freeze-dried at −40°C for 72 h. The protease improved ($P < 0.05$) TAAD by 4%, 2%, 6%, 11%, 11%, 10%, 6%, 6%, 1%. 5%, 17%, 9%, 6%, 6% and 9% for Lys, Met, M+C, Thr, Val, His, Arg, Ile, Phe, Gly+Ser, Asp, Glu, Ala, Pro and Tyr, respectively. The essential TAAD of the corn soybean basal diet was increased on average 6% by the enzyme supplementation.

Key Words: enzyme, broiler, digestibility

M213 Performance of white commercial layers fed with different of threonine: lysine ratio. F. G. P. Costa*[1], M. R. Lima[1], E. T. Nogueira[2], L. Sá[2], J. H. V. Silva[1], H. S. Rostagno[3], C. C. Goulart[1], R. B. Souza[1], S. A. N. Morais[1], and G. S. Lima[1], [1]*Federal University of Paraiba*, *Areia, PB, Brazil*, [2]*Ajinomoto Animal Nutrition*, *Sao Paulo, SP, Brazil*, [3]*Federal University of Viçosa*, *MG, Brazil*.

The reduction of the crude protein levels of the diets of the commercial layers causes damages to the productive performance, therefore it can make with that other amino acids if become considerably with limits of performance, as the threonine and the tryptophan, for example, thus compelling a supplementation with industrial sources of these amino acids. On the basis of this, this study intended to evaluate the nutritional requirements in digestible threonine for white layer in initial phase of production, being used itself diets with different relations threonine digestible: digestible lysine on the basis of the parameters of productive performance of white commercial layers. A total of 288 chickens with 29 weeks, distributed in delineation randomized, with 6 treatments, 6 repetitions, with 8 birds for experimental unit. The diets had consisted of a basal diet, where the evaluated levels had been 0.446, 0.486, 0.526, 0.565, 0.605 and 0.645% of digestible threonine, generating the threonine digestible: digestible lysine ratios 56, 61, 66, 71, 76 and 81%. With a quadratic behavior, the egg production improved until relation 76%, in accordance with the regression ($\hat{Y} = -0.0112x^2 + 1.6896x + 30.352$; $r^2 = 95$), the maximum point, that is, the best digestible threonine: digestible lysine was 75.43%. For the egg weight (EW), egg mass (EM) and egg mass conversion (EMC), the behavior was similar to the one of the egg production, where its regressions (EW: $\hat{Y} = -0.006x^2 + 0.8728x + 33.256$; $r^2 = 86$; EM: $\hat{Y} = -0.0149x^2 + 2.1964x - 19.562$; $r^2 = 80$; EMC: $\hat{Y} = 0.0005x^2 - 0.0728x + 4.5332$; $r^2 = 96$), had esteem the best relations in 72.73, 73.70 and 72.80%, respectively. These results corroborate with research that evidences the importance of the threonine in the metabolism of the chickens and that its daily necessities of this amino acid had grown with passing of the years and this, conclude that the excellent digestible threonine: digestible lysine ratio for white commercial layers in initial phase of production is of 75%.

Key Words: amino acid, ideal protein, performance

M214 Digestible valine:lysine and isoleucine:lysine ratios for brown egg laying hens. G. Lelis[1], E. T. Nogueira[2], L. F. Albino[1], and H. Rostagno*[1], [1]*Federal University of Viçosa*, *Viçosa, MG, Brazil*, [2]*Ajinomoto of Brazil/ Ajinomoto Animal Nutrition*, *São Paulo, SP, Brazil*.

When formulating minimum cost diets for laying hens it is essential to supply enough valine (Val) and isoleucine (Iso) to allow the hens to express their maximum genetic potential. Val or Iso deficiency may decrease the efficiency of the utilization of methionine + cystine and lysine (Lys), which are the first and second limiting amino acids in layer diets. Two experiments were carried out simultaneously to evaluate 3 digestible Val:Lys and Iso:Lys ratios for brown egg laying hens. In each trial a total of 180 Dekalb Brown layers (25– to 37–wk–old) were evaluated during 3 periods of 28 d with 3 treatments and 10 replicates of 6 birds per experimental unit. The following digestible Val:Lys ratios were tested: 84 (0.554% dig Val), 90 and 96%. The Iso:Lys ratios evaluated were 67 (0.442%), 75 and 83%. To prevent excess, digestible Lys level (0,660%) was calculated to supply 93% of the Brazilian Tables (Rostagno et al., 2005) recommendation. A positive control treatment (60 layers; 0.706% dig Lys; 0.633% dig Val and 0.548% dig Iso) was included to show that Lys was the second limiting amino acid in both experiments. Layers fed the positive control diet presented the best performance when compared with those fed the Val:Lys and Iso:Lys diets. During the period of 25 to 37 weeks, there was a linear response

to the dietary Val:Lys ratios as to egg production ($P < 0.002$) (%/bird/day Y = 31.445 + 62.135 Val; $R^2 = 0.99$) and egg mass ($P < 0.001$) (g egg/bird/day Y = 12.056 + 41.562 Val, $R^2 = 0.93$). Laying hens fed diets containing different Iso:Lys ratios presented quadratic response ($P < 0,05$) for the following parameters: egg production (%/bird/day) and egg mass (g egg/bird/day). Based on the evaluated parameters, the digestible Val:Lys and Iso:Lys ratios recommended for brown egg laying hens are 96% and 79%, respectively.

Key Words: valine, isoleucine, brown egg hens

M215 Influence of diet formulation technique on requirements of sulfur amino acids and lysine to brown egg laying hens. J. H. V. Da Silva*[1,2], P. B. Lacerda[1], D. V. Gonçalves Vieira[2], C. T. Silva[2], J. J. Filho[1], M. L. G. Ribeiro[1], J. M. B. De Souza[1], J. A. De Araújo[1], E. L. Da Silva[1], and F. G. Perazzo Costa[2], [1]*CCHSA-Universidade Federal da Paraíba*, *Bananeiras, Paraíba, Brazil*, [2]*CCA-Universidade Federal da Paraíba*, *Areia, Paraíba, Brazil*.

Three trials were carried out to evaluate the influence of 2 techniques of diet formulation on the requirements of amino acids and the relationship Met+Cys: Lys utilizing brown egg laying hens as biologic model. The first technique consisted of simultaneous supplementation of a reference diet (RD) deficient in Met+Cys and Lys with industrials sources of these amino acids, maintaining a constant relationship between these amino acids in 0,85 and the second technique consisted of RD deficient in one amino acid. Each trial was developed in a completely randomized design and involved 180 birds with 18 weeks of age and initial live weight of 1.64 kg. In trial one a RD deficient in Met+Cys and Lys was supplemented to provide levels of these amino acids of 0.55 and 0.64%; 0.62 and 0.72%; 0.69 and 0.81%; 0.76 and 0.88%; and 0.83 and 0.96%. In trial 2 the RD deficient only in Met+Cys was supplemented to provide 0.55; 0.62; 0.69; 0.76 and 0.83% Met+Cys, and in trial 3, the RD deficient only in Lys was supplemented to provide 0.64; 0.68; 0.72; 0.76; 0.80; 0.84 and 0.88 of Lys. All trials were divided into 6 periods of 28 d. In trial one the requirements of Met+Cys were 0.67% and Lys 0.79%. In trial 2 the requirement of Met+Cys was 0.65% and in trial 3 Lys was 0.76%. According the results Met+Cys and Lys requirements increased when the relationships between amino acids was maintained at 0.85. However, the relationship Met+Cys: Lys remained unchanged considering the estimates values from trials 2 and 3. These results suggest that the technique of formulating diets influences the amino acid requirements of birds but not the Met+Cys: Lys relationship.

Key Words: egg production, experimental method, nutritional interrelation

M216 Amino acid digestibility in corn, soybean meal, field peas, and corn co-products fed to weanling pigs. G. I. Petersen* and H. H. Stein, *University of Illinois*, *Urbana*.

Several alternative feedstuffs are available for use in weanling pig diets, but the standardized ileal digestibility (SID) of AA in most ingredients have not been measured in weanling pigs. The objective of the present experiment, therefore, was to measure the SID of AA in corn, soybean meal, corn gluten meal, high protein distillers dried grains, and field peas fed to weanling pigs. Twelve weanling barrows (initial BW: 10.3 ± 0.9 kg) were prepared with a cannula in the distal ileum and randomly allotted to a replicated 6 × 6 Latin square design with 6 diets and 6 periods in each square. Five diets were formulated using corn, soybean meal, corn gluten meal, high protein distillers dried grains, or field peas as the sole source of protein and AA. An N-free diet that was used to calculate basal endogenous losses of AA and protein was also formulated. Chromic oxide was included in all diets as an indigestible marker. All pigs were fed each diet for 7 d and ileal digesta were collected during the last 2 d of each period. Samples were lyophilized and analyzed for CP and AA and the SID of all AA were calculated according to standardized procedures (Table 1). It is concluded that the SID of all AA in corn gluten meal is similar to that in soybean meal, but high protein distillers dried grains have SID values for AA that are less than in both corn and soybean meal.

Table 1. Standardized ileal digestibility of AA in corn, soybean meal, corn gluten meal, high protein distillers dried grains, and field peas

	Corn	Soybean meal	Corn gluten meal	High protein distillers dried grains	Field peas
Ile	81.6^{b}	87.0^{ab}	88.2^{a}	72.0^{c}	82.2^{b}
Lys	75.9^{b}	86.6^{a}	84.5^{ab}	56.0^{c}	85.1^{a}
Met	86.4^{a}	88.2^{a}	90.4^{a}	80.9^{b}	79.7^{b}
Thr	75.7^{b}	83.7^{ab}	86.5^{a}	64.9^{c}	79.0^{ab}
Trp	85.0^{ab}	88.1^{a}	88.9^{a}	75.6^{c}	78.9^{bc}
Val	81.4^{b}	86.3^{ab}	88.0^{a}	70.8^{c}	81.2^{b}

^{abc}Means lacking common superscript in same row are different ($P < 0.05$).

Key Words: corn co-products, pigs, standardized ileal amino acid digestibility

M217 Pyrolic infusion of arginine increases portal vein blood flow in growing pigs. S. W. Kim*[1], M. I. Perret-Gentil[2], M. W. Hart[3], and R. D. Mateo[4], [1]*North Carolina State University*, *Raleigh*, [2]*The University of Texas at San Antonio*, [3]*Georgia State University*, *Atlanta*, [4]*Texas Tech University*, *Lubbock*.

This study was conducted to test if dietary arginine would affect portal vein blood flow (PVBF) in growing pigs. Two pigs (26.3 ± 0.6 kg BW), surgically fitted with catheters into the carotid artery (CA), portal vein (PV), mesenteric vein (MV), and pyloric region of the stomach (PL), were allotted to 2 × 2 Latin square design with 2 treatments: Injection of arginine-HCl (ARG); and injection of L-alanine (CON) through the PL catheter and with 2 periods (72-h intervals). Alanine was used as a non-specific nitrogen source in CON matching the contribution of nitrogen from arginine in ARG. Each period was composed of 48-h feeding (0.09 kg x $BW^{0.75}$), 19.5-h fasting, and 4.5-h infusion. A corn-soybean meal based diet with 18.2% CP and 3.35 Mcal ME/kg but without supplemental arginine was fed to pigs for 48 h before fasting. Para-aminohippuric acid (PAH) was infused (3.2 mg/min) into MV for a 4.5 h period. L-arginine-HCl (19 g) and L-alanine (32 g) was mixed with 100 mL distilled water and injected into the lumen of PL catheter 60 min after beginning the PAH infusion period. Blood samples (3 mL) were collected simultaneously from CA and PV catheters at −60, −30, 0, 15, 30, 45, 60, 90, 120, 150, and 210 min relative to injection to measure PAH concentration in the plasma. The PVBF rate (L/min) was calculated by PAH infusion rate (mg/min) / ($[PAH]_{PV}$–$[PAH]_{CA}$) (mg/L). Blood flow before the injection was averaged 1.85 ± 0.23 L/min. After injection, average increase in PVBF of ARG (1.66) tended to be greater ($P = 0.09$) than PVBF of CON (−0.14) during the entire 210 min. Increase in PVBF of ARG was greater ($P < 0.05$) than PVBF of CON at 60 (6.05 vs. −0.20) and 90 (3.40 vs. −0.77) min after the injection. Increase in PVBF occurred ($P < 0.05$) at 60 min and maintained until 90 min after injection of arginine whereas injection of alanine did not increase PVBF during the 210 min period. This study suggests that

one time dose of arginine can have a short-term increase in PVBF in growing pigs.

Key Words: arginine, blood flow, pigs

M218 Apparent and standardized ileal digestibilities of amino acids for pigs fed corn-soybean meal-based diets at varying crude protein levels. H. Zhai* and L. Adeola, *Purdue University*, *West Lafayette, IN*.

A study was conducted to determine the effect of CP level on apparent (AID) and standardized ileal digestibility (SID) of AA. Six pigs (initial BW 47.1 ± 0.97 kg) fitted with T-cannula at distal ileum were fed 6 diets for 6 periods in a 6 × 6 Latin square design. The 6 diets consisted of a nitrogen-free diet and 5 corn-soybean meal-based diets that contained 5 CP levels at 6.8, 10.5, 14.1, 17.7, and 21.4%. Each period consisted of a 5 d of adjustment period and 2 of ileal digesta collection for 10 h on each of d 6 and d 7. The ratio of corn:soybean meal was fixed at 3 to 2 by weight and cornstarch was added to dilute the CP concentration. Chromic oxide was included at 0.5% as an indigestible marker. The results showed basal endogenous loss ranged from 65 mg/kg DMI for Met to 3,104 mg/kg DMI for Pro. Proline and Gly (1,053 mg/kg DMI) were the 2 most abundant endogenous AA in endogenous flow and together accounted for approximately 43% of the total endogenous AA flow. The AID were 80.9 to 84.7%, 85.1 to 87.4%, 72.9 to 79.5%, and 86.5 to 87.9% for Lys, Met, Thr, and Trp individually with corresponding SID being 86.6 to 88.6%, 87.5 to 90.3%, 82.7 to 86.8%, and 90.2 to 93.6% as dietary CP increased from 6.8 to 21.4%. There were linear increases in AID of N, Arg, Ile,Val, Thr, Gly and Tyr ($P < 0.05$) as CP increased and linear decreases in SID of Leu, Trp, Asp, Cys, and Glu ($P < 0.05$). Both linear and quadratic effects were observed in AID and SID for Pro ($P < 0.05$). In conclusion, the protein levels in corn-soybean meal diets evaluated in the current study affected SID of the indispensable AA Leu, Phe, and Thr and the dispensable AA Gly, Pro, and Tyr.

Key Words: amino acid, apparent ileal digestibility, standardized ileal digestibility

M219 Influence of total lysine level provided during the finishing period on carcass, meat and fat characteristics of heavy barrows and gilts. M. A. Latorre*[1], J. A. Rodríguez-Sánchez[2], M. Blanco[2], M. A. Sanz[2], and M. Joy[2], [1]*Universidad de Zaragoza*, *Spain*, [2]*CITA de Aragón*, *Zaragoza, Spain*.

A total of 120 Duroc × (Landrace × Large White) pigs were used to study the influence of gender and lysine content during the finishing period on carcass, meat and fat characteristics. The experimental diets were based on corn, barley, wheat, and soybean meal diets, contained 2,280 Kcal NE/kg and 13.5% CP and were provided from 100 to 130 kg BW. There were 6 treatments with 2 genders (barrows and gilts) and 3 total lysine levels (0.70, 0.65 and 0.60%). Each treatment was replicated 4 times and the experimental unit was the pen constituted by 5 pigs allocated together. No significant interaction between gender and dietary treatment was detected. Carcasses from barrows had similar ($P > 0.05$) carcass yield but were ($P < 0.001$) heavier and fatter at the level of *gluteus medius* muscle (GM) than carcasses from gilts. The total weight of trimmed lean cuts (shoulder+ham+loin+sirloin) were heavier ($P < 0.01$) in barrows than in gilts but the yield was similar ($P > 0.05$). Meat from barrows had higher ($P < 0.05$) intramuscular fat content but lower ($P < 0.05$) protein content than meat from gilts. Subcutaneous fat from barrows had higher ($P < 0.05$) content in saturated fatty acids and lower ($P < 0.01$) in unsaturated fatty acids than that from gilts. The reduction in total lysine content in diet did not modify ($P > 0.05$) the weight and yield of carcass and main lean cuts but fat thickness at the GM muscle tended to increase ($P < 0.10$). Meat characteristics were not affected by dietary treatment but saturated fatty acids tended ($P < 0.10$) to increase and monounsaturated fatty acids tended ($P < 0.10$) to reduce as lysine content reduced. It is concluded that any effect of dietary treatment was independent of gender. The effect of reducing total lysine content provided during the finishing diet on carcass, meat and fat quality of pigs were scarce. However, a decrease of lysine levels from 0.70 to 0.60% could be interesting in the case of pigs intended for dry-cured products when a minimum carcass fat thickness is a criterion to choose the carcasses.

Key Words: lysine, carcass and meat quality, pigs

M220 Comparison of amino acid digestibility of corn, corn distillers dried grains with solubles (DDGS), meat and bone meal (MBM), and poultry-by-product meal (PBPM) determined with the precision-fed cecectomized rooster assay and the standardized ileal amino acid digestibility chick assay. E. J. Kim*[1], P. L. Utterback[1], T. J. Applegate[2], and C. M. Parsons[1], [1]*University of Illinois at Urbana-Champaign*, *Urbana,* [2]*Purdue University*, *West Lafayette, IN*.

The objective of this study was to evaluate and compare the standardized amino acid digestibility (SAAD) of several feedstuffs using 2 commonly accepted methods; the precision-fed cecectomized rooster assay (PFR) and the standardized ileal amino acid chick assay (SID). To carry out these objectives, 17 different feedstuffs were obtained. These samples included 6 corn, 6 corn distillers dried grains with or without solubles (DDGS/DDG), 2 meat and bone meal (MBM) and a poultry-by-product meal. The SAAD varied among the feed ingredients and among samples of the same ingredient. For corn, there were generally no differences in SAAD between the 2 bio-assay methods. When differences did occur, there was no consistent pattern among the individual amino acids due to bio-assay methods. The SAAD was not different between the 2 methods for the 4 DDGS samples; however, the PFR did yield greater SAAD for a high protein DDG and a conventionally processed DDGS. The PFR yielded greater SAAD values than the SID for several amino acids in one MBM and the poultry-by-product meal, but it yielded lower SAAD values for the other MBM. Overall, there were no consistent differences between methods for SAAD values.

Key Words: amino acid digestibility methods, roosters, chicks

M221 Feeding a diet containing specific excess amino acids minimizes the reduction in performance and carcass traits associated with an inflammatory response. A. Diaz[1], M. Raymond[1], R. Angel[2], and B. D. Humphrey*[1], [1]*California Polytechnic State University*, *San Luis Obispo,* [2]*University of Maryland*, *College Park.*

The objective of this experiment was to determine the effect of feeding specific amino acids in excess of their growth requirement on performance and carcass traits during an inflammatory response. Male Cobb 500 hatchlings were raised in pens (n = 15 chicks/pen) for 14 d and were fed a diet that met NRC requirements. On d 14, birds were fed 1 of 2 diets (n = 20/diet) that contained either adequate (A) or excess (E) amino acid levels. A and E diets were similar, except the E diet contained excess Phe (+0.43%), Trp (+0.14%), Thr (+0.30%) and Arg (+0.35%). On d 21 (0 h), half of the pens per dietary treatment (n = 10) were not injected or injected with 1 mg/kg BW of *E. coli* lipopolysaccharide (LPS). At 0, 3, 6, 9, 12, 15, 18, 21, 24, 48, 72, 96, 120, 144 and 168 h pen and feeder weights were measured and one bird per pen was sampled for determination of organ and carcass traits. LPS-injected chicks fed the E diet consumed 6.3% more feed from 0 to 168 h compared with chicks fed

the A diet ($P < 0.05$). LPS-injected chicks fed the E diet had 28% higher gain from 0 to 168 h compared with LPS-injected chicks fed the A diet ($P < 0.05$). LPS-injected chicks fed the E diet had lower feed conversion from 0 to 164 h compared with A chicks ($P < 0.05$). LPS-injected chicks fed the E diet had 7.4% higher body weights at 168 h compared with LPS-injected chicks fed the A diet ($P < 0.05$). Relative visceral weight was 12.2% higher in LPS-injected chicks fed the E diet compared with LPS-injected chicks fed the A diet ($P < 0.05$). At 168 h, absolute and relative pectoralis weight were higher in LPS-injected chicks fed the E diet compared with LPS-injected chicks fed the A diet ($P < 0.05$). These data indicate that feeding specific amino acids in excess of the growth requirement may help to mitigate the reductions in performance and carcass traits associated with an inflammatory response.

Key Words: amino acid, inflammation, pectoralis

M222 Amino acid digestibility of various feedstuffs of plant and animal origin using three different methods. E. J. Kim*, C. M. Jacobs, P. L. Utterback, and C. M. Parsons, *University of Illinois at Urbana-Champaign*, *Urbana*.

The objective of this study was to determine and compare amino acid (AA) digestibility of 3 distillers dried grains with soluble (DDGS), a corn gluten meal (CGM), canola meal, and a fish meal samples using the precision-fed cecectomized rooster assay (PFR), the standardized ileal assay (SID), and a newly developed precision-fed chick assay (PFC). For the PFR, after a 24 h feed withdrawal period, cecectomized roosters were precision-fed approximately 30 g of feed sample and excreta were collected for 48 h post-feeding. For the SID, 16 d-old broiler chicks were fed a semi-purified diet containing the feed samples from 17 to 21 d, with ileal digesta collected at 21 d. For the PFC, after a period overnight feed withdrawal, 22 d-old chicks were precision-fed 10 g of sample mixed with chromic oxide and ileal digesta were collected at 4 h post-feeding. Digestibility coefficients were standardized using a nitrogen-free diet (NFD) for the SID and PFC and using fasted roosters for the PFR. When 3 DDGS samples were evaluated, the PFR produced higher digestibilities than the PFC for all 3 DDGS samples for most of the amino acids. When comparing the PFR and the SID, the PFR yielded higher values than the SID for one DDGS, whereas there was no significant difference between the 2 methods for the other 2 DDGS samples. For the CGM, the PFR yielded significantly higher amino acid digestibilities than the SID and PFC for the majority of the amino acids. For canola meal, the PFR generally yielded greater amino acid digestibilities than the PFC with the SID yielding intermediary values. Differences did occur among methods for amino acid digestibility in fish meal; however, these differences were not consistent among methods or amino acids. The results of this study indicated there were differences among standardized amino acid digestibility values for the PFR, SID, and PFC in some instances but that the differences were not consistent among methods.

Key Words: amino acid digestibility methods, ileal digestibility, roosters and chicks

M223 Effect of the use of L-valine and metabolizable energy levels of diet on nitrogen intake, retention and apparent excretion in broilers. F. G. P. Costa*[1], C. C. Goulart[1], E. T. Nogueira[2], M. Kutschenko[2], J. H. V. Silva[1], V. P. Rodrigues[1], G. B. V. Lobato[1], and R. C. L. Neto[1], [1]*Federal University of Paraiba*, *Areia, PB, Brazil*, [2]*Ajinomoto Animal Nutrition*, *Sao Paulo, SP, Brazil*.

The experiment was conducted at the Agrarian Sciences Center of UFPB, Brazil. The aim was to evaluate the effect of the use of L-valine (VAL) and metabolizable energy (ME) levels of diet on nitrogen (N) intake, retention and apparent excretion in broilers from 1 to 42 d. Seven hundred and 20 male broiler chicks were distributed in completely randomized design, in factorial scheme 2 × 3 (without or with VAL × 3 ME levels). To the treatments 1, 2 and 3, only L-lysine, DL-methionine and L-threonine were added, which allowed CP to attend digestible amino acids ratio, and the ME varied −50, 0 and +50 kcal/kg, respectively, according to the requirements for each stage of creation. In treatments 4, 5 and 6 was also added VAL, resulting in a CP reduction, and ME was similar to that in the previous treatments. N retention was determined by the difference in body N content of the birds at 42 d (2 birds per pen, ground whole, with feathers) and an additional group with 15 chicks 1 d old, used to determine the initial N content. The apparent N excretion was determined by the difference between N intake (N content of diet x feed intake) and N retention. The N retention was always higher in birds fed diet with VAL (79.6 vs 75.2 g/bird). Assessing the levels of ME within each diet, it was found that for birds fed diets without VAL, the diet with −50 kcal/kg reduced N retention. However, when the VAL was used the greater N retention was observed with the highest ME level. The apparent N excretion was lower with the diet with VAL, for any ME levels evaluated (46.3 vs. 56.7 g/bird). For the VAL-free diet, the lowest N excretion was observed at the intermediate ME level and for the diet with VAL, the lowest N excretion was observed with the diet with +50 kcal. It is concluded that the use of VAL and increase of 50 kcal of ME/kg in diet improves N retention and reduces N excretion to the environment.

Key Words: amino acids, body protein, ideal protein

M224 Effect of the use of L-valine and metabolizable energy levels of diet on body composition of broilers. F. G. P. Costa*[1], C. C. Goulart[1], E. T. Nogueira[2], M. Kutschenko[2], J. H. V. Silva[1], V. P. Rodrigues[1], and R. C. L. Neto[1], [1]*Federal University of Paraiba*, *Areia, PB, Brazil*, [2]*Ajinomoto Animal Nutrition*, *Sao Paulo, SP, Brazil*.

The experiment was conducted at the Agrarian Sciences Center of UFPB, Brazil. The aim was to evaluate the effect of the use of L-valine (VAL) and metabolizable energy (ME) levels of diet on body composition of broilers at 42 d old. Seven hundred and 20 male broiler chicks were distributed in completely randomized design, in factorial scheme 2 × 3 (without or with VAL × 3 ME levels). To the treatments 1, 2 and 3, only L-Lysine, DL-Methionine and L-Threonine were added, which allowed CP to attend digestible amino acids ratio, and the ME varied −50, 0 and +50 kcal/kg, respectively, according to the requirements for each stage of creation. In treatments 4, 5 and 6 was also added VAL, resulting in a CP reduction, and ME was similar to that in the previous treatments. At 42 d 2 birds per pen were selected, killed by cervical dislocation after fasting for 24 h and ground whole (with feathers) to body composition analysis. There was an interaction between the use of VAL and ME levels for percentages of protein (%CP), fat (%EE) and water body, while the percentage of ash was not influenced by treatments (expressed in % as-fed). In diets without VAL the largest body %CP (17.1%) was found with the intermediate ME level and lower %CP (15.9%) with the lowest ME level. At the lowest ME level the body %CP was higher in birds fed diets with VAL in relation to those fed diets without VAL (17.5 vs. 15.9%), with no differences between the higher ME levels. This shows that in birds fed diets with VAL, the lowest level of CP and consequent reduction of excess amino acids to be excreted, resulting in less need of ME that diets without VAL. At the intermediate ME level, body %EE was higher when using a diet with VAL (12.8 vs. 10.3%). Using diets without VAL the lowest %EE (10.3%) was observed in intermediate ME level. It is concluded that

VAL can be used in diets with a reduction of 50 kcal in ME without harming the body composition of broiler chickens.

Key Words: body fat, body protein, ideal protein

M225 Different protein and conjugated linolenic acid levels on broilers diets. T. Previero[1], C. J. C. Castillo[2], N. B. Petroli[1], R. Albuquerque[3], C. S. S. Araujo*[4], and L. F. Araujo[1], [1]*Universtiy of Sao Paulo*, *Pirassununga, SP, Brazil*, [2]*University of Sao Paulo*, *Piracicaba, SP, Brazil*, [3]*University of Sao Paulo*, *Sao Paulo, SP, Brazil*, [4]*Poultry Nutritionist*, *Pirassununga, SP, Brazil*.

The objective of this research was to study the effects of the conjugated linoleic acid, known as CLA, associated with reduction of crude protein (CP) level in broiler diets. An experiment was conducted from 21 to 41 d, using 1440 male broilers Ross, with the same weight initial, which were allocated according to a completely randomized design, with factorial model 3x3, corresponding in 3 CLA inclusions levels (0%, 0,5% and 1,0%) and 3 CP levels (19%,17%,15%). Data were statistically evaluated by GLM. Weight gain reduction and increased feed conversion were only related to decrease of CP level. Carcass and breast meat yields decreased due to the reduction of CP addition in diets ($P < 0.05$). The interaction between CLA and CP factors modified liver size, and both elevated the abdominal fat ($P < 0.05$). In relation to parameters analyzed in breast samples, the pH elevated proportionally to CP inclusion, the redness and yellowness were modified by CP or CLA addition and interaction of both were detected to luminosity parameter ($P < 0.05$). About fatty acid composition, the addition of CP only elevated the stearic acid and CLA inclusion improved the saturated fatty acid levels and reduced the monounsaturated fatty acid levels ($P < 0.05$). An improvement on incorporation of CLA isomers was verified due to more inclusion of this product in 19% or 17% CP diets ($P < 0.05$). In the case of 15% CP diets, the incorporation of CLA isomers had a maxim limit. Reduction on CP can affect negatively and CLA can improve carcass parameters and carcass quality, respectively.

Acknowledgment: FAPESP (Financial Support: 2006/05128–1).

Key Words: carcass quality, fatty acids, performance

M226 Effect of dietary arginine, glutamine, and tryptophan on growth performance, gut morphology, and meat quality of broilers. S. J. Park*[1], C. Z. Alvarado[1], and S. W. Kim[2], [1]*Texas Tech University*, *Lubbock*, [2]*North Carolina State University*, *Raleigh*.

This study was conducted to evaluate the supplemental effects of Arg, Gln, and Trp on growth performance, gut morphology, metabolic response, and meat quality of broilers. Newly hatched birds were allotted to 4 dietary treatments (6 replicates per treatment and 6 birds per cage): C (Control); A (a diet with 0.5% L-Arg); G (a diet with 0.5% L-Gln); and T (a diet with 0.5% L-Trp). Corn and soybean meals were the major ingredients in the diets. All diets were isonitrogenous using L-Ala and isocaloric using corn oil. Birds were fed the diets for 6 wk based on a 3 phase feeding program (2 wk each). Body weight and feed intake were measured at the end of each phase. On d 11, 2 birds from each pen were killed to measure gut morphology and serum immunoglobulins (Ig). At 6 wk of age, 2 birds from each pen were killed to measure carcass characteristics. On d 11, serum IgA and IgG were not different among treatments. Heights of villus in jejunum of birds in C (65.9 μm), A (69.8 μm), and G (64.4 μm) were greater ($P < 0.05$) than birds in T (59.3 μm). Depths of crypts did not differ among treatments. At the end of wk 6, birds in A (2.55 kg), G (2.40 kg), and T (2.53 kg) were heavier ($P < 0.05$) than birds in C (2.14 kg). Feed intake and feed:gain ratio did not differ among treatments. Hot carcass weights of birds in A (1.89 kg), G (1.75 kg), and T (1.88 kg) were greater ($P < 0.05$) than birds in C (1.56 kg). Cold carcass weights of birds in A (1.97 kg) and T (1.98 kg) were greater ($P < 0.05$) than birds in C (1.64 kg). Weights of breast meat and thigh meat of birds in A (451 and 296 g, respectively), G (427 and 267 g), and T (451 and 277 g) were greater ($P < 0.05$) than birds in C (361 and 263 g). The pH of breast meat of birds in T (6.43) was higher ($P < 0.05$) than birds in C (5.94), G (6.02), and T (5.97). Collectively, dietary supplementation of L-Arg, L-Trp, and L-Gln at 0.5% improves growth and carcass gain of birds when fed for 6 wk period.

Key Words: amino acids, broilers, growth

M227 Dietary supplementation of L-glutamine and L-glutamate or sodium butyrate during early growth of female broilers. Y. Avellaneda*[1], J. Hernandez[1], C. Ariza-Nieto[2], and G. Afanador[1,2], [1]*Universidad Nacional de Colombia*, *Bogota, Colombia*, [2]*CORPOICA*, *Bogota, Colombia*.

This study determined the effects of dietary supplementation of a commercial mixture of L-glutamine and L-glutamate (GlnGlu) and sodium butyrate (SB) for female broiler on nutrients digestibility, intestinal morphometry and performance. Three hundred twenty-five 1-d COBB females broiler were randomly allocated to one of the 5 treatments: 0, 0.5, 1.0, 1.5% of GlnGlu and 0.07% of BS. In every treatment there were 5 replicate pens. Body weight and feed intake were record at 1, 8, 15 and 25 d of age. Three broilers from each treatment were randomly selected and sacrificed on d 8, 15 and 25 d. Intestinal tissues were collected at the middle part of duodenum, jejunum and ileum to measure crypt depth, villus height and width. During a 4-d balance period (21–24 d), the chicken received a diet with 0.5% chromium oxide and excreta were collected twice a day. Protein digestibility and apparent metabolize energy (AME) value were calculated. Data were analyzed as a completely randomized design. Dietary protein digestibility was higher ($P < 0.05$) in birds fed 1.5% of GlnGlu (64.2%) compared with control group (58.3%). AME was 3170 Kcal/Kg and 3161 Kcal/Kg for broilers fed with 1.0 and 1.5% Gln+Glu, respectively. These values were higher compared with the control group (2979 Kcal/Kg, $P < 0.05$). Digestibility of organic matter was directly related to EMA values. At d 25, broilers fed 1.5% of GlnGlu showed a villi of the duodenum larger compared with the control group (1347 vs 1080 um) and supplemented with GlnGlu (1127 and 1116 um, 0.5 and 1.0% of GlnGlu, respectively) ($P < 0.05$). Female broilers fed 1.5% of GlnGlu showed a higher body weight gain compared with both control and BS groups (36, 34.0 g and 32.3 g/d, respectively). BS group presented the lowest feed intake (42.4 g/d) compared with the other treatments (49.7 g/d, on average) ($P < 0.05$). Feed conversion ratio of BS and 1.5% GlnGlu groups were significantly lower compared with the control and 0.5% GlnGlu ($P < 0.05$). It can be concluded that the supplementation with biomolecules as L-glutamine and L-glutamate showed positive effects on female broiler performance.

Key Words: L-glutamine, L-glutamate, sodium butyrate, female broiler

M228 Evaluation of the fixed crude protein conversion factor (6.25) versus ingredient-specific conversion factors. N. Sriperm*[1], G. M. Pesti[1], and P. B. Tillman[2], [1]*University of Georgia*, *Athens,* [2]*Ajinomoto Heartland LLC*, *Chicago, IL*.

This study examines the validity of the historical nitrogen to crude protein conversion factor of 6.25 based upon assay values of commonly used feed ingredients, analyzed during 2009. A calculated protein level

for an ingredient should provide an indication of the amino acid content of that ingredient. Since laboratory methods for determining nitrogen content report both nitrogen from ammonia (NH_3) and from non-amino acid sources (nucleic acids, etc.), the determined crude protein value is typically over-estimated, relative to the nitrogen strictly from amino acids, the true protein. Amino acid values were collected from the Ajinomoto Heartland LLC laboratory analysis database. Ingredients evaluated included ground corn, soybean meal (dehulled, solvent extracted), corn distillers dried grains with solubles, poultry by-product meal and meat & bone meal. Data for ammonia (NH_3) and 18 individual amino acids were included in the determination of ingredient specific conversion factors. Using the nitrogen content for NH_3 and of each amino acid, along with the analyzed content of NH_3 and each amino acid within each ingredient, the average nitrogen content of each ingredient was calculated. Using these values, ingredient specific conversion factors: K_A, K_P and K (average of K_A and K_P) were determined as outlined by Mosse′ (1990). It should be noted that the determined ingredient specific conversion factors were not equal to the standard 6.25% factor. Plant protein sources had higher conversion factors than animal based protein sources. An ingredient specific true protein conversion factor is proposed as being more applicable than a standard fixed factor, especially when the determined true protein content is based upon nitrogen from amino acid analysis.

Table 1. Ingredient-specific nitrogen to crude protein conversion factors

Ingredient	n	K_A	K_P	K
Ground corn	75	5.65	5.02	5.33
Soybean meal	230	5.64	5.13	5.38
Corn DDGS	188	5.74	4.98	5.36
Poultry by-product meal	45	5.45	4.81	5.13
Meat and bone meal	156	5.37	4.77	5.07

Key Words: crude protein, amino acid, corn soybean meal

M229 Effect of dietary probiotic and prebiotic on ileal nutrient digestibility of Ross broiler chickens. H. Ziaie*[1], A. Zeinali[2], M. Bashtani[3], M. A. Karimi Torshizi[4], G. H. Hadarbadi[1], H. Farhangfar[3], and A. Nasr Abad[1], [1]*Agriculture and Natural Resources Research Center*, *Birjand, South Khorasan, Iran*, [2]*Ferdowsi University*, *Mashhad, Iran*, [3]*Birjand University*, *Birjand, Khorasan, Iran*, [4]*Tarbiat Moddares university*, *Tehran, Iran*.

An experiment was conducted using 240 one-day old male Ross broiler chickens to evaluate the effect of dietary probiotic and prebiotic on ileal nutrient digestibility of Ross broiler chickens. Chicks were allocated to a randomized complete block design with 4 replicate pens (15 birds per pen). The experimental treatments were: T1 = control, T2 = control + 15 ppm of Virginiamycin, T3 = control + 100 mg probiotic (Protexin) per kg diet and T4 = control diet + 100 mg prebiotic (Immnuwall) per kg diet. At age 21 and 42 d, ileal digestibility of nutrients was measured by Titanium oxide marker. Data was statistically analyzed using the GLM models of SAS. Duncan's multiple range test was used for pair-wise comparisons of treatment means. The results showed that supplemental diets significantly ($P < 0.05$) improved bioavailability of energy and ileal digestibility of protein. At 21 d of age, broiler fed with treatments 3 and 4 had lower bioavailability of energy and ileal digestibility of protein as compared with treatment 2, but their differences were not significant at 42 d of age. The experimental diets had no effect on ileal digestibility of fat. In conclusion, using probiotic and prebiotic in broiler diets could improve nutrient digestibility indicating that these compounds may be an alternative to antibiotics.

Key Words: broiler, antibiotic alternative, nutrient digestibility

M230 Tryptophan, niacin and insulin metabolism in weaned pigs? J. J. Matte*[1], Y. Primot[2], and N. LeFloc'h[3], [1]*Agriculture & Agri-Food Canada*, *Dairy & Swine R & D Centre, Sherbrooke, QC, Canada*, [2]*Ajinomoto-Eurolysine SAS*, *Paris, France*, [3]*Institut National de la Recherche Agronomique (INRA)*, *UMR-SENAH, St-Gilles, France*.

The present experiment aimed to better define the role of an active metabolite of tryptophan (Try) oxidation, niacin (vitamin B_3), on post-meal insulin response in weanling piglets. A group of 24 weaned piglets were distributed, at 4 wks of age, in 4 factorial dietary treatments: 2 additions of Try, 0 (-Try) vs. 0.10% (+Try) for Try/Lys ratios of 0.16 vs. 0.23, respectively, and 2 additions of dietary niacin, 15 mg/kg (LB_3) vs. LB_3 + 45 mg/kg (HB_3). Animals were fed ad libitum up to 10 wks of age and were trained to restricted feeding (1 kg/d) in one morning meal during one wk. At 11 wk of age, repeated blood samples were collected during 6 h following initiation of the meal (0.5 kg) to determine profiles of plasma C-peptide, insulin, glucose, Try, kynurenin (Kyn), an intermediate metabolite of Try oxidation and nicotinamide (Nam), an indicator of niacin status. There was no treatment effect on either the peak or the area under the curve of C-peptide or glucose after the meal ($P > 0.12$). However, for insulin, the postprandial peak was lower in +Try piglets especially within LB_3 piglets (Try effect and interaction Try*niacin, $P < 0.05$); values were 1.3, 1.0, 0.7 and 1.0 nM (SE: 0.1) in -Try LB_3, -Try HB_3, +Try LB_3 and +Try HB_3, respectively. The molar ratio insulin:C-peptide during the 0–90 postprandial period was lower ($P < 0.02$) in +Try vs -Try piglets (0.47 vs 0.57, SE:0.03). The post-meal plasma Try (96.2 vs. 72.3 μM, SE:0.1) and Kyn (1.7 vs. 1.3 μM, SE:0.1) were higher ($P < 0.01$) in +Try vs -Try piglets. Post-meal plasma Nam was higher in +Try vs -Try ($P < 0.01$) and in HB_3 vs LB_3 piglets ($P < 0.01$) with overall values of 1.0, 2.7, 2.7 and 4.0 μM (SE: 0.4) in -Try LB_3, -Try HB_3, +Try LB_3 and +Try HB_3, respectively. The present results on C-peptide, insulin and molar ratio insulin:C-peptide suggest that the Try action is exerted mainly on insulin clearance (catabolism and/or cellular uptake in target tissues) rather than on insulin secretion in piglets. However, the postprandial responses of the different plasma metabolites to dietary treatments suggest that the Try effect on insulinemia in piglets is unlikely modulated by either Nam or Kyn homeostasis after a meal.

Key Words: tryptophan, insulin, piglets

M231 Effect of glutamine and temperature on performance of broiler chickens. S. Cerrate*, R. Ekmay, C. Salas, and C. Coon, *University of Arkansas*, *Fayetteville*.

The effect of glutamine and 2 ambient temperatures were evaluated during the finisher period of broiler chickens, from 36 to 50 d of age. A corn-soy control and a corn-soy-glutamine diet (1% inclusion) were fed to broilers housed in one of 2 ambient temperatures: 21 ± 1°C (normal temperature) and 30 ± 0.6°C (heat stress). Data were analyzed as a 2 × 2 factorial design. Ten male birds housed individually were placed for each treatment. Broilers housed at 21°C showed greater BW gain and feed intake than did birds housed in 30°C. There were interactions between dietary treatments and temperature on BW gain ($P = 0.018$) and feed conversion ($P = 0.006$). Birds housed at 21°C showed similar BW gain, feed intake and feed conversion between the control and glutamine diets, whereas broilers fed the glutamine diet housed at 30°C had greater BW gain and a more efficient feed conversion than did birds fed the control diet. These data indicate that glutamine inclusion may be beneficial during heat stress.

Key Words: broiler, glutamine, housing temperature

M232 Effect of dietary protein content on cecal microbial ecosystem and mortality of young rabbits. S. Chamorro[1], R. Carabaño[2], J. García[2], I. Badiola[3], G. G. Mateos*[2], and C. de Blas[2], [1]*Instituto del Frío-ICTAN, CSIC*, *Madrid, Spain*, [2]*Universidad Politécnica de Madrid*, *Madrid, Spain*, [3]*CReSA (UAB-IRTA)*, *Bellaterra, Spain*.

The aim of this work was to study the effect of dietary CP content on cecal microbial ecosystem and mortality of young rabbits weaned at 25 d. Two (HP and LP) isoenergetic (3,200 kcal DE/kg DM) diets differing in the CP content (175 and 159 g/kg DM, respectively), were formulated. Rabbits (240/treatment) weaned at 25 d were fed experimental diets during 10 d, and mortality incidence from 25 to 35 d was recorded. At 35 d-old, 30 5 rabbits per treatment were slaughtered and cecal contents were taken to characterize the microbial population by restriction fragment length polymorphism (RFLP). The biodiversity degree (BD) defined as the number of fragments obtained by RFLP, and frequency of detection (FD) defined as the percentage of animals that had a fragment compatible with the presence of a certain bacteria, were recorded. Data were analyzed as a completely randomized design using type of diet as main effect. Mean comparisons of mortality and FD were made using a chi-squared test. A decrease of dietary CP content tended to reduce the mortality rate from 15 to 10% ($P = 0.09$). Animals fed LP diets showed a lower BD than those fed HP diets (1,905 vs. 2,561, $P = 0.04$). A reduction of dietary CP content led to a lower FD of several potential pathogens as *Helicobacter* spp. (from 80.0 to 57.1%, $P = 0.04$) and *Leptospira* spp. (from 77.1 to 57.1%, $P = 0.07$), and the FD of other intestinal bacteria as *Escherichia* spp. (from 45.7 to 20.0%, $P = 0.02$), and *Butyrivibrio fibrisolvens* (from 57.1 to 22.9%, $P = 0.003$). In conclusion, a reduction in dietary CP from 175 to 159 g/kg DM reduced the mortality rate, the biodiversity degree, the presence of several potential harmful bacteria at cecum, and should be contemplated as a strategy to increase the intestinal health in young rabbits.

Key Words: dietary protein, intestinal microbiota, rabbits

M233 Effect of lysine and leucine levels in wheat-based diets on the expression of two cationic amino acid-transporter proteins in growing pigs. M. A. Barrera, A. Morales*, M. Cervantes, A. B. Araiza, E. Avelar, and D. González, *ICA, Universidad Autónoma de Baja California, Mexicali.*

Dietary amino acid (AA) content may affect the AA absorption. Lysine is the first limiting AA in wheat for pigs, and leucine is recognized as an activator of mTOR, the protein synthesis regulator in muscle cells. An experiment was conducted to determine if adding lysine and leucine, above the NRC (1998) requirement level, to wheat-based diets affects the expression of b0,+ and CAT1 mRNA in 2 muscles (longissimus-LM and semitendinosus-SM), jejunum (J), and liver (L). Twenty crossbred pigs (Landrace-Ham-Duroc; BW of 16.4 ± 1.7 kg) were used. Treatments (T) were: T1, basal wheat-based diet fortified with crystalline lysine, threonine, and methionine; T2, basal plus 0.35% lysine; T3, basal plus 0.15% leucine; and T4, basal plus 0.35% lysine and 0.15% leucine. All diets were added with vitamins and trace minerals. At the end of a 28-d trial, 16 pigs were sacrificed and samples from LM, SM, L, and J were collected to analyze the expression of b0,+ and CAT1 mRNA. The effects of lysine, leucine, and their interaction were tested. Also, 3 contrasts were constructed to analyze the effect of the single or combined AA addition. The relative expression results (arbitrary units: ratios of b0,+ or CAT1 mRNA molecules:18S rRNA molecules) were: for b0,+; J, 1.84, 2.48, 0.43, 0.12; LM, 1.23, 3.71, 1.89, 1.50; SM, 0.80, 0.45, 0.81, 0.42; L, 1.41, 0.95, 4.26, 0.49; for CAT1; J, 0.10, 0.18, 0.13, 0.21; LM, 0.69, 1.38, 0.68, 1.08; SM, 0.33, 0.10, 0.54, 0.38; L, 0.92, 19.1, 0.36, 3.12, for T1 to T4, respectively. Leucine decreased b0,+ expression in J and LM ($P < 0.05$). Because of lysine addition the expression of b0,+ in LM increased ($P < 0.05$), but in SM decreased and tended to decrease in L ($P < 0.10$). Leucine increased but lysine decreased CAT1 expression in SM; in L there was an opposite response ($P < 0.05$). These data indicate that dietary AA levels affect the expression of their transporter proteins, and their effects are variable, depending on the AA and the animal tissue studied.

Key Words: swine, amino acids, transporters

M234 Effect of high lysine and leucine levels in wheat-based diets on performance and muscle expression of myosin mRNA in growing pigs. M. A. Barrera[1], M. Cervantes*[1], A. Morales[1], A. Araiza[1], D. Cervantes[1], V. Méndez[1], and H. Bernal[1], [1]*ICA, Universidad Autónoma de Baja California*, *Mexicali, BC, México*, [2]*Universidad Autónoma de Nuevo León*, *Monterrey, NL, México*.

Lysine is the first limiting amino acid (AA) in wheat-based diets for pigs; leucine is recognized as an activator of mTOR, which regulates protein synthesis in muscle cells. An experiment was conducted to evaluate the effect of adding lysine and leucine, above the NRC (1998) requirement levels, to wheat-based diets on the performance of growing pigs and the expression of myosin mRNA in the longissimus (LM) and semitendinosus (SM) muscles. Twenty crossbred pigs (Landrace-Ham-Duroc; BW of 16.4 ± 1.7 kg) were used in a Randomized Complete Block design. Treatments (T) were: T1, basal wheat-based diet fortified with crystalline lysine, threonine, and methionine; T2, basal plus 0.35% lysine; T3, basal plus 0.15% leucine; and T4, basal plus 0.35% lysine and 0.15% leucine. All diets were added with vitamins and trace minerals. At the end of the 28-d trial, 16 pigs were sacrificed and samples from LM and SM were collected to analyze the expression of myosin mRNA. The effects of lysine, leucine and their interaction were tested. Also, 3 contrasts were constructed to analyze the effect of the single or combined AA addition. The pig performance results were: weight gain, 0.607, 0.560, 0.492, 0.573 kg/d; feed intake, 1.24, 1.18, 1.11, 1.20 kg/d; feed conversion, 2.05, 2.14, 2.27, 2.11, for T1 to T4, respectively. There was a lysine x leucine interaction for weight gain and feed conversion ($P < 0.05$). Adding leucine alone decreased weight gain and depressed feed conversion ($P < 0.05$). Lysine addition to the leucine added diet tended to restore the daily gain ($P < 0.10$) and feed conversion ($P < 0.05$). The results of myosin mRNA relative expression (arbitrary units: ratios of myosin mRNA molecules:18S rRNA molecules) were: LM, 3.6, 3.3, 1.7, 0.12; SM, 1.46, 1.46, 0.59, 1.15, for T1 to T4, respectively. Leucine alone decreased myosin mRNA in both muscles ($P < 0.01$) and, combined with lysine, leucine further reduced myosin mRNA in LM ($P < 0.01$). These data indicate that excess of leucine negatively affects the expression of myosin mRNA, which was associated with a growth depression in pigs.

Key Words: swine, myosin, amino acids

M235 The effect of different animal and vegetable protein sources on the feed intake and weight gain of piglets. D. Solà-Oriol[1], J. Figueroa[1], E. Borda*[2], C. Chetrit[2], and J. F. Pérez[1], [1]*Universitat Autònoma de Barcelona*, *Bellaterra, Spain*, [2]*Bioiberica*, *Palafolls, Spain*.

Porcine Digestible Peptides (PDP; Palbio 50RD) is a highly digestible and economic protein source for weanling diets. The aim of the present work was to study the effect of PDP (52.8%CP) in the diet as compared with Peruvian fish meal (FM; 68.5%CP), spray dried animal plasma (SDAP; 75.0%CP), potato protein (PP; 79.5%CP) and soybean protein concentrate (SBP; 56.0%CP) on the early performance of weaned piglets. A total of 1540 26-d-old piglets (mixed sexes) were used in 4

consecutive trials conducted in the same commercial facility. Animals were distributed into 20 pens (18–20 piglets/ pen) according to the initial BW. Experimental treatments were formulated to meet or exceed piglet requirements with the same energy, protein, Lys, Met+Cys, Thr and Trp content. Control diet was formulated to contain 5% of PDP; and Test diet was obtained by replacing PDP by celite plus either FM (3.82%), SDAP (3.52%), PP (3.32%) or SBP (4.72%) according to their protein content. Feed was offered ad libitum in mash form. Individual animal weight and feed disappearance were recorded at 0, 7 and 14d post-weaning (PW) to calculate the average daily feed intake (ADFI) and average daily gain (ADG). Feed intake was not different ($P > 0.10$) between PDP, FM, SDAP or PP, but tended to be higher for PDP than SBP from 7 to 14d PW (324.8 vs 297.9 g/d; $P = 0.066$). The ADG of piglets fed on PDP tended to be higher ($P < 0.10$) than those fed FM or PP from 0 to 7d post-weaning, and was higher than those fed FM and SBP from 7 to 14d post-weaning (160.6 vs 128.0 g/d; and 200.0 vs 183.0 g/d; $P < 0.01$). However, no differences were observed on body weight at 14 d PW ($P > 0.10$). Lower feed conversion ratio (FCR) was observed for PDP compared with FM from 7 to 14d PW (1.714 vs 2.044; $P < 0.05$) but, higher compared with SDAP for the same period (2.272 vs 1.909; $P < 0.05$). Moreover, better FCR was also observed for PDP than FM during the entire starter phase (0 to 14dPW). Compared with the common protein sources, PDP may be considered as suitable source of protein for piglet diets improving the economic balance of the post-weaning phase.

Key Words: porcine digestible peptides, protein sources, piglets

M236 Aflatoxins and productive performance of two broiler breeder genotypes. A. Scher*[1], A. P. Rosa[1], J. M. Santurio[2], A. Londero[1], T. N. N. Vieira[1], and J. A. G. Ferreira Jr.[1], [1]*Poultry Laboratory – Universidade Federal de Santa Maria*, *RS, Brazil*, [2]*Lapemi– Universidade Federal de Santa Maria*, *RS, Brazil*.

The objective of this study was to determine the effect of aflatoxins (AFL) exposure on productive aspects of 2 broiler breeder genotypes. The experiment was carried out at The Federal University of Santa Maria – Brazil. 660 broiler breeder females and 60 males were submitted to intoxication with AFL (AFB1:86%, AFB2: 8.5%, AFG1:3.8%, AFG2: 1.7%) from the 24th to 64th week. From 65th to 68th week, all birds were fed with AFL free diets to evaluate residual effects. The estimated parameters were egg production and egg weight. The experimental design was in a CRD in factorial arrangement with 3 levels of AFL (0.0, 0.50 and 1.0 mg/kg diet) and 2 breeders' strains (A and B), totaling 6 treatments with 5 replicate pens of 22 females and 2 males each. The laying rate was depreciated by the addition AFL in the diet. The addition of 1.0mg AFL/kg of diet was more harmful than 0.5mg AFL/kg, indicating a dose dependent effect. Breeders fed diets containing 0.0; 0.5 and 1.0mg AFL/ kg had average laying rates of 63.93; 61.54 and 58.53% respectively ($P \leq 0.0001$) during the intoxication period. It was observed that strain B breeders had a laying rate of 61.72%, and strain A laying rate that was 60.94% ($P = 0.0018$). There was interaction among the levels of AFL and the strains ($P = 0.0779$). Birds of genotype B, when subjected to 0.5 and 1.0mg AFL/ kg diet, showed eggs productions 3.03 and 8.73% lower than not intoxicated. In strain A, the reduction in egg production was 4.45 and 8.16% when the birds were intoxicated with 0.5 and 1.0mg AFL/kg diet, respectively. There was no recovery in the laying rate of birds intoxicated after withdrawal of the AFL. The eggs weight was not influenced by levels of AFL; however, strain A breeders produced the heaviest eggs during the study period. The productive performance of broiler breeders was depressed by AFL. Strain A breeders were more susceptible to 0.5 mg AFL/kg diet than those of strain B.

Key Words: egg production, breeders, strains

M237 Progeny of broiler breeders from two genotypes intoxicated with aflatoxins. A. Scher*[1], A. P. Rosa[1], J. M. Santurio[2], A. Londero[1], G. Farina[1], and J. A. G. Ferreira Jr.[1], [1]*Poultry Science Lab – Universidade Federal de Santa Maria*, *Santa Maria, RS, Brazil*, [2]*Lapemi– Universidade Federal de Santa Maria*, *Santa Maria, RS, Brazil*.

The objective of this study was to evaluate the performance of the progenies of 2 broiler breeder genotypes intoxicated with aflatoxins (AFL). This study was carried out at Poultry Laboratory at The Federal University of Santa Maria – Brazil. Were performed 3 experiments, from 1 to 21 d, each using 600 chicks. In the first (Experiment 1), were used chicks from eggs produced by hens with 32 wk of age, the second and third evaluations were carried out with chicks produced by breeders with 48 (Exp.2) and 64 wk of age (Exp.3), respectively. The progenies were housed in batteries, located in an environment controlled room. For each experiment was used a CRD factorial arrangement 3x2 (0.0, 0.5 and 1.0mg of AFL/kg in breeders diets and 2 genotypes: A and B), totalizing 6 treatments with 10 repetitions of 10 males each. The feed and water were provided ad libitum. In the Experiment 1, hens fed diets containing AFL produced chicks with lower body weight (BW) ($P \leq 0.0001$). The addition of 0, 0.5 and 1.0mg AFL/kg resulted in chicks with 41.83g, 41.48 and 41.09g of BW, respectively. In Experiments 2 and 3, only the addition of 1.0mg/kg AFL in breeders diets depressed chicks' BW ($P = 0.0704$ and $P = 0.0341$). In all experiments, chicks produced by breeders submitted to diets containing 1mg AFL/kg had lower body weight at 21 d. Progeny from genotype A breeders had higher BW, at 1 and 21d, than genotype B progeny. Studying the interaction among the AFL levels and the genotypes, it was observed that genotype B breeder's exposure to AFL did not affect the progeny's initial weight, however, in genotype A, there was a decreased progeny initial weight from breeders exposed to AFL. The addition of 1 mg AFL/kg in broiler breeder's diets resulted in negative effect on the progenies weights.

Key Words: progeny, breeders, strains

M238 The effects of the dietary supplementation with essential oils from selected species of the Lamiaceae family on the performance of growing broilers chickens. L. Roldan*[1], C. Ariza-Nieto[2], G. Diaz[1], and G. Afanador[1,2], [1]*Universidad Nacional de Colombia*, *Bogota, Colombia*, [2]*CORPOICA*, *Bogota, Colombia*.

The effects of essential oils (EO) obtained from 3 Lamiaceae plants (*Thymus vulgaris*, *Rosmarinus officinalis* and *Ocimum basilicum*) on the performance of growing broilers were investigated. A total of 210 one-day-old Ross male broiler chicks were placed in 30 brooder cages and were randomly assigned to the 5 experimental groups: 1) control; 2) growth promoter antibiotic, 500 ppm Bacitracin; 3) 600 ppm of thyme EO; 4) 600 ppm of rosemary EO, and 5) 600 ppm of basil EO. Throughout the experimental period of 21 d, body weight gain and feed intake were recorded at 7, 14, and 21 d of age, and feed conversion ratios were calculated. Data were analyzed as repeated measures under a completely randomized design using the MIXED procedure of SAS (Ver. 9.0, SAS Institute, Cary, NC).The statistical model included the fixed effects of EO supplementation, age and the interaction. Random intercepts and slopes were included to account for within pen effect. A likelihood ratio test (LRT) was used to test which variance/covariance (compound symmetry, unstructured) structure fit better to the data using the residual maximum likelihood (REML) algorithm. Additionally, LRT was performed using the maximum likelihood (ML) estimating method to eliminate nonsignificant factors from the model. The final model was run using REML. Least squares means adjusted by Tukey method were used to compare means. Body weight gain and feed consumption were not significantly affected ($P > 0.05$) by EO supplementation. The supplementation of dietary basil EO resulted in a significantly ($P < 0.05$) lower feed conversion ratio (1.18) compared with the other groups; growth promoter antibiotic (1.26), control (1.25), rosemary EO (1.24) and thyme EO (1.28). This parameter indicated that basil EO exerted a growth promoter effect in broiler chickens.

Key Words: essential oils, Lamiaceae, broilers

M239 Effect of crude glycerin on the performance of female broilers chickens at high altitude. C. Ariza-Nieto*[1], Y. Avellaneda[1], and G. Afanador[1,2], [1]*CORPOICA*, *Bogota, Colombia*, [2]*Universidad Nacional de Colombia*, *Bogota, Colombia*.

This study evaluated the use of crude glycerin, a co-product of biodiesel production, in a feeding program for female broilers chickens maintained at high altitude. Six hundred forty 24-d-old Ross female broilers were randomly assigned to 1 of 4 glycerin levels (0, 3, 6, and 9% of the diet). The birds were placed in 16 pens during growth-finishing phase and their performance was determined every other week until slaughter. Data were analyzed under a completely randomized design as repeated measures on time using the MIXED procedure of SAS (Ver. 9.0, SAS Institute, Cary, NC, USA). The shadow price of crude glycerin was established using linear programming. Glycerin levels did not affect feed intake (average during the 18 d period female broilers was 135.6 ± 16.6 g/bird). Body weight gain was lower ($P = 0.0799$) in female broilers chickens fed 9% glycerin (64.9 g), compared those receiving 3% (68.3 g) or 6% (69.4 g), respectively. The level of inclusion of glycerin showed a quadratic effect ($P = 0.0177$), an inclusion level of 4.2% of crude glycerin maximizes body weight gain. Feed conversion of birds fed glycerin at 3% and 6% of inclusion were significantly lower ($P < 0.05$) compared with the control and 9% group. This ratio showed a quadratic effect and 3.88% of crude glycerin was the optimum. No significant effects on mortality were shown due to the inclusion of crude glycerin. Diets containing up to 4% of crude glycerin maximizes performance of female broilers at high altitude during growing-finishing phase.

Key Words: glycerin, female broilers, high altitude

M240 Vitamin E, herbs and spices in broilers diets: Evaluation of oxidative stability of pre-cooked meat balls. A. M. C. Racanicci*[1], J. F. M. Menten[2], and M. Nascente[1], [1]*University of Brasília (UnB)*, *Brasília, DF, Brazil*, [2]*University of São Paulo (ESALQ)*, *Piracicaba, SP, Brazil*.

The dietary utilization of natural antioxidants has been reported to improve oxidative stability of chicken meat and meat products. The objective of this study was to evaluate the dietary supplementation of resin oils from previously selected herbs and spices on oxidative stability of stored pre-cooked meat. Resin oil from 6 herbs (H: rosemary, thyme, oregano, sage, bay, and basil) and 3 spices (S: cinnamon, clove, and ginger) were microencapsulated (20% of resin oil) and fed to 80 male one-day-old Cobb chicks raised in 20 cages, randomly assigned to 8 treatments with 2 replications of 5 birds. Experimental treatments were CONT (basal diet with tocopherol from premix and feed ingredients); VITE (basal diet + 200 mg α-tocopheryl acetate/kg); H500 (basal diet + 100 mg of herbs/kg); H250 (basal diet + 50 mg of herbs/kg); S500 (basal diet + 100 mg of spices/kg); S250 (basal diet + 50 mg of spices/kg); HS500 (basal diet + 100 mg of herbs and spices/kg) and HS250 (basal diet + 50 mg of herbs and spices/kg). At 41 d of age, 5 birds of each treatment were slaughtered and breast meat collected, minced, pooled, and mixed to 0.1% of salt to produce meat balls (±30g). After vacuum-packaging, the balls were cooked, re-packed and stored in a cold and dark room for up to 8 d. TBARS were determined in duplicate in 3 samples per treatment on d 0, 1, 3, 6 and 8 to assess the degree of lipid oxidation during chilled storage. The supplementation of α-tocopherol (VITE) protected meat balls against lipid oxidation as shown by statistically lower ($P < 0.0001$) TBARS values at d 8 (30.3 μmol MDA/kg of meat) compared with all treatments (CONT 56.7, H500 70.0, S500 56.3, HS500 65.0, H250 61.1, S250 62.7 and HS250 71.4 μmol MDA/kg of meat). However, the supplementation of natural antioxidants (H, S or HS) showed an unpredicted prooxidant effect demonstrated by the increase ($P < 0.0001$) in TBARS values compared with CONT for both concentrations, except S500.

Key Words: natural antioxidants, tocopherol, TBARS

M241 Effect of technical grade glycerin on the performance of brown laying hens at high altitude. Y. Avellaneda*[1], D. Cifuentes[1], G Afanador[1,2], and C. Ariza-Nieto[1], [1]*CORPOICA*, *Bogota, Colombia*, [2]*Universidad Nacional de Colombia*, *Bogota, Colombia*.

Biodiesel production processes generate about 10% glycerin by volume as a waste co-product. In recent years production has increased exponentially, which have led to a reduction of its price, making this co-product an opportunity to reduce production costs of feed in the poultry industry. The aim of this study was to evaluate the use of technical grade glycerin (99.5% purity) in brown layer hens at high altitude. Eighty 24-wk-old Babcock Brown laying hens were randomly assigned to one of the 4 glycerin levels (0, 2.5, 5.0, and 7.5%). Hens were placed in 40 cages during 20 weeks and their performance was record every other week and during the study, they were fed ad libitum with a feed meal (2800 kcal AMEn/ kg, 19% CP, 0.86% digestible lysine, 4.0% Ca and 0.42%

P available) and drinking water was also available ad libitum. Data were analyzed under a completely randomized design as repeated measures on time using the MIXED procedure of SAS (Ver. 9.0, SAS Institute, Cary, NC). Feed intake, egg production, egg mass, feed conversion per dozen and feed conversion on an egg mass were not affected ($P > 0.05$) due to the inclusion of technical grade glycerin. On average feed intake, egg production, egg weight, feed conversion per dozen, and feed conversion on an egg mass basis were 111.5 g/d, 93.2%, 58.9 g, 2.4, and 1.5, respectively. In terms of quality of the eggs, the albumen height was not affected due to the inclusion of glycerin (6.21 ± 1.08 mm), but the eggs of hens 2.5% group showed a thicker eggshell compared with the 5 and 7.5% ($P < 0.05$). Pale-yolks were observed in eggs from hens fed 5.0 or 7.5% glycerin compared with the control. It is concluded that technical grade glycerin in diets for brown laying hens up to 7.5% did not affect productive performance, but egg quality related to the color of the yolk can adversely be affected when the inclusion level of glycerin increases from 5.0 to 7.5%.

Key Words: technical glycerin, performance, laying hen

M242 Effects of Korean herb supplementation (*Paeniae radix*, *Angelicae gigantis radix*, *Cnidium rhizome*, and *Polygoni multiflori radix*) on growth performance, nutrient digestibility, blood characteristics, meat quality and fatty acid content of meat of growing pigs. Q. W. Meng*, J. S. Yoo, H. J. Kim, J. P. Wang, J. H. Jung, and I. H. Kim, *Department of Animal Resource and Science, Dankook University*, *Cheonan, Choongnam, Korea*.

This study was conducted to investigate the effects of Korean herb mixture supplementation (*Paeniae radix*, *Angelicae gigantis radix*, *Cnidium rhizome*, and *Polygoni multiflori radix*) on growth performance, nutrient digestibility, meat quality and fatty acid content of meat produced by growing pigs. A total of 64 pigs (40.19 ± 1.42kg) were evaluated over 84 d. Dietary treatments included: 1) CON (basal diet), 2) KH (basal diet + 1% Korean herb mixture), 3) HKH (basal diet + 1% Korean herb mixture with heat treatment), and 4) HKHE (HKH + 0.2% β-mannanase). Each treatment consisted of 4 replicates with 4 pigs per pen in a randomized complete block design. The highest ADG, digestibility of dry matter (DM), nitrogen (N) and energy ($P < 0.05$) was observed in the HKHE group during wk 0–6. A decreased DM, N and energy digestibility were observed in the KH group when compared with other groups during wk 0–6. Moreover, dietary HKHE resulted in a higher HDL-cholesterol ($P < 0.05$) and lower LDL-cholesterol than the CON treatment at the end of the experiment. The meat pH was highest in the HKHE group and lowest in the KH group ($P < 0.05$). Pigs fed the KH diet showed the lowest marbling ($P < 0.05$) among treatments. The drip loss on the fifth day was higher ($P < 0.05$) in the CON group than the KH group. Of the fatty acids, the saturated fatty acid (SFA) levels were higher in the CON group ($P < 0.05$) than in the HKHE group. Polyunsaturated fatty acid (PUFA) was shown to be higher in the HKHE group ($P < 0.05$) than in the CON group. In conclusion, supplementation of the diet with Korean herb mixture improved growth performance, nutrient digestibility and meat quality.

Key Words: Korean herb mixture, meat quality, growing pigs

M243 Effects of dietary bamboo vinegar supplementation on growth performance, blood characteristics, meat quality, fatty acid content and fecal malodor emission in finishing pigs. Q. W. Meng*, J. H. Lee, H. D. Jang, T. X. Zhou, L. Yan, and I. H. Kim, *Department of Animal Resource and Science, Dankook University*, *Choenan, Choongnam, Korea*.

A 42 d trail with 60 [(Landrace × Yorkshire) × Duroc] pigs (79.66 ± 1.42 kg) was conducted to investigate the effects of bamboo vinegar (Bio-BV) supplementation in diets on growth performance, blood characteristics, meat quality, fatty acid and fecal malodor emission in finishing pigs. Pigs were randomly allotted to 1 of 3 dietary treatments in a randomized complete block design according to their sex and body weight (BW) (5 replicates with 4 pigs per pen). The experimental treatments included: 1) CON (basal diet), 2) BV1 (CON + 0.1% Bio–BV), and 3) BV2 (CON + 0.2% Bio-BV). BV1 and BV2 supplementation had higher ADG ($P < 0.05$) than CON group during 0–3 weeks as well as the overall period. Pigs fed diets with BV2 increased pH and sensory score (firmness) ($P < 0.05$) compared with the other groups. Moreover, the BV2 treatment improved sensory color and a* value ($P < 0.05$) compared with the control group. L* value was significantly improved ($P < 0.05$) when pig received control diet compared with BV2 treatment. In term of fatty acid, the total SFA level and stearic acid (C18:0) were improved ($P < 0.05$) in BV groups compared with CON group. Bio-BV supplementation decreased the total UFA and UFA/SFA ratio ($P < 0.05$) when compared with those fed CON diet. Pigs fed Bio-BV supplementation improved ($P < 0.05$) linoleic acid (C18:2n–6) concentration compared with CON. In fecal malodor emission, NH_3 emission was significantly reduced ($P < 0.05$) in BV2 group compared with CON and BV1 groups on the first and 5th day. On 10th day, CON treatment showed greater NH_3 emission ($P < 0.05$) than BV1 treatment. BV1 group had higher ($P < 0.05$) NH3 emission than BV2 group. Pigs fed control diet had higher ($P < 0.05$) H_2S and total mercaptan concentration than those fed BV2 diet. In conclusion, Bio-BV supplementation can exhibit beneficial effects on growth performance and meat quality, and concomitantly decreases NH_3, H_2S and Total mercaptan emission. Besides, Bio-BV administration increased certain unsaturated fatty acids while decreasing some saturated fatty acids.

Key Words: bamboo vinegar, meat quality, finishing pigs

M244 The effects of caper (*Capparis ovata* Desf.) on some hematological parameters and organs of Lohmann roosters. O. Yildiz-Gulay*[1], M. S. Gulay[1], A. Balic[2], and A. Ata[1], [1]*Mehmet Akif Ersoy University, Faculty of Veterinary Medicine*, *Burdur, Turkey*, [2]*Sakarya Toyota Hospital*, *Sakarya, Turkey*.

Caper (*Capparis* genus in the Capparaceae family) is a plant found in tropical/subtropical areas. Caper is consumed widely in most Mediterranean countries and can be consumed for long time periods. However, no detailed study has been performed concerning consumption of capers. Thus, the purpose of this study was to determine the effects of caper (*Capparis ovata* Desf.) on blood parameters, body weight (BW) changes, and organs of Lohmann roosters. Twenty-four week-old roosters were randomly assigned to control (C) and caper treatment (TR) groups (8 per group) and fed a standard diet (14% crude protein and 3000 kcal/kg metabolizable energy). Roosters in C received 10 mL of tap water, whereas roosters in TR received 1 g of caper per 1 kg of BW suspended in 10 mL of tap water. Experiment was lasted for 39 d and treatments were given by oral gavages. Roosters were weighed at the end of caper treatments and blood was taken from the vena brachialis. Organ weights were recorded after sacrifice. No negative effect of caper treatment was observed on hemoglobin (C = 15.6 ± 0.58 vs. TR = 15.2 ± 0.35 g/dL), hematocrit (C = 38.3 ± 1.13 vs. TR = 37.1 ± 1.21%), plasma protein (C = 5.3 ± 0.21 vs. TR = 5.6 ± 0.39 g/dL), red blood cell count (C = 2.97 ± 0.14 vs. TR = 3.18 ± 0.11 × 10^6/μL), white blood cell count (C = 27.1 ± 0.98 vs. TR = 25.6 ± 0.89 × 10^3/μL), BW (C = 2070.6 ± 35.8 vs. TR = 2022.8 ± 56.4 g), liver weight (C = 25.8 ± 0.88 vs. TR = 26.5 ± 1.63 g), kidney weight (C = 5.12 ± 0.24 vs TR = 5.14 ±

0.24 g), testis weight (C = 10.4 ± 1.33 vs TR = 10.9 ± 1.08g), pancreas weight (C = 3.83 ± 0.13 vs. TR = 3.91 ± 0.21 g) or heart weight (C = 9.65 ± 0.60 vs. TR = 9.45 ± 0.52 g). In addition, no apparent changes in liver, kidney, testis, pancreas and heart were detected by gross post mortem and histopathological examination to suggest toxic effects of oral use of caper for 39 d. Interestingly, Caper treatment increased the thrombocyte levels in treated roosters (C = 0.244 ± 0.26 vs TR = 0.377 ± 0.21× 10^5/μL; $P < 0.01$). In conclusion, the results suggest no toxic effect of capers in roosters. Moreover, high thrombocyte count due to caper treatment should be evaluated further for use in diseases causing low thrombocyte counts.

Key Words: rooster, hematological parameters, histopathology

M245 Safety evaluation of Event 5307 transgenic corn in broiler chickens. A. Sauvé[2] and J. T. Brake*[1], [1]*North Carolina State University, Department of Poultry Science, Scott Hall*, *Raleigh,* [2]*Syngenta Biotechnology, RTP*, *Raleigh, NC*.

A 49-d feeding study evaluated whether broiler diets prepared with Event 5307 transgenic maize (corn) had an effect on broiler livability, BW, feed conversion ratio (FCR), feed consumption, or carcass yield when compared with diets prepared with either non-transgenic, near-isogenic control corn or commercially available control corn (NC2007). The 5307 corn contained eCry3.1Ab and phosphomannose isomerase (PMI) transgenic proteins. The eCry3.1Ab protein is a chimera of modified Cry3A and Cry1Ab proteins and has insecticidal activity against certain corn rootworm species. The PMI protein acts as a selectable marker enabling the selection of positive transformants. Broiler males had a 49-d BW of 3,543 g while females weighed 2,898 g. Overall livability was 98%. Final 49-d BW, adjusted FCR, feed consumption, and livability of the 5307 transgenic, non-transgenic, and NC2007 groups did not differ. There were no statistically significant differences other than during the grower diet period, when the 5307 transgenic group had a lower FCR compared with the NC2007 group, with the non-transgenic group being intermediate. This difference was small in magnitude, resolved by the finisher diet period and was not considered adverse. There were no differences in carcass yield between groups on a gross BW basis. When compared on a percentage BW basis, the thighs of males in the non-transgenic group weighed more than those in the 5307 transgenic and NC2007 groups and the thighs and Pectoralis minor of females in the non-transgenic and NC2007 groups weighed more than those in the 5307 transgenic group. However, due to the lack of differences in other carcass parts these were considered incidental. Diets prepared with 5307 transgenic corn supported rapid broiler growth and excellent FCR without a significant impact on overall carcass yield. The results clearly indicate that the transgenic corn had no deleterious effects on bird health in this study.

Key Words: transgenic corn, transgenic maize, 6307 corn

M246 Effect of garlic extract (Garlicon) on piglet productive performance in the nursery period. J. Morales[1], R. López[2], P. Coscojuela[2], and C. Piñeiro*[1], [1]*PigCHAMP Pro Europa*, *Segovia, Spain*, [2]*Prebia Feed Extracts*, *Toledo, Spain*.

Intensive research has focused on the potential of phytogenic feed additives to replace antibiotics in piglet diets, mainly based on their potential to promote a beneficial gut microflora which protects the host against pathogens and helps to alleviate periods of stress. In vitro, the antimicrobial effect of some plant extracts, as in the case of garlic, is as consistent as the effect of antibiotics. However, their effect in vivo is not consistent compared with antibiotics. The aim of this study was to assess the effect of a plant extract based on garlic (GAR) in weaned piglets. Three different dietary doses of GAR were assessed (50, 100, and 150 ppm) in a 3-wk period, and compared with a negative control group and with a positive control group supplemented with gentamycin (20 ppm). For the experiment, 280 piglets were used (10.3 ± 1.81 kg BW) and allotted in 40 pens (8 per treatment). Average daily gain (ADG), feed intake (FI) and feed efficiency were controlled in the starter phase (42 to 70 d of age). A linear and quadratic effects were observed with GAR supplementation and groups supplemented with 50 and 100 ppm of GAR showed higher average daily gain (ADG) and final BW than the negative control and 150 ppm groups (532, 592, 592, 559 g/d ADG; $P < 0.01$ in control, 50, 100 and 150 ppm groups, respectively). Feed intake tended to be higher in GAR groups than in the control group ($P < 0.10$), while feed efficiency did not differ among groups. In comparison with gentamycin, productive performance was not different in the GAR supplemented piglets, being numerically higher performance in 50- and 100-ppm GAR than in gentamycin-supplemented piglets. No differences were found in feed efficiency between antibiotic and GAR groups. We conclude that GAR supplementation improved ADG, FI and, consequently, final BW in the nursery period, especially supplemented at 50- and 100-ppm. Furthermore, productive performance obtained by the GAR supplementation was as consistent as the one obtained by the dietary gentamycin.

Key Words: plant extracts, phytogenic additives, pigs

M247 Effect of different levels of substitution of maniçoba hay on the performance of free-range birds in the semi-arid region. P. E. N. Givisiez*[1], M. A. S. F. Campos[2], C. C. Goulart[1], F. G. P. Costa[1], and J. H. V. Silva[1], [1]*Universidade Federal da Paraiba*, *Areia, PB, Brazil*, [2]*Universidade Federal do Rio Grande do Norte*, *Natal, RN, Brazil*.

Local resources should be evaluated as potential ingredients to be used in poultry feeding in alternative or organic systems. This study evaluated the effect of partial substitution of conventional corn-soybean meal diet by maniçoba hay (*Manihot pseudoglaziovii*) on the performance and cut yields of free-range birds in the semi-arid region of Brazil. Eighty-four Paraiso Pedres birds were randomly distributed into 3 treatments and 4 repetitions of 7 birds (4 males and 3 females). Diets for the growing (30 to 42 d) and final (43 to 73 d) phases were partially substituted by 0, 10 and 20% of maniçoba hay. Body weight (BW), weight gain (WG) and feed:gain ratio (F:G) were determined for each phase. Two birds per repetition were killed at 73 d to determine carcass weight, absolute (g) and relative weight (%) of cuts and abdominal fat. Data were submitted to ANOVA in a completely randomized design, with 3 treatments and 4 repetitions for performance parameters and 8 repetitions for carcass and cuts analyses. Means were compared by Tukey's test at 5% probability. BW, FI and WG were not affected by the use of maniçoba hay until 42 d. Conversely, weight gain (42 to 73 and 30 to 73 d), body weight at 73 d and FC were negatively affected by increasing maniçoba levels, probably as a result of higher crude fiber levels in the diet and lower AME and AMEn. Carcass, breast and drumstick weights (g) were decreased ($P < 0.05$) by increasing levels of maniçoba, as well as breast yield (%). Therefore, maniçoba hay should not be used if cuts are to be commercialized. On the other hand, the majority of free-range birds are commercialized as live birds or whole carcasses, and levels up to 10% would not impair gain. In conclusion, maniçoba hay may be used up to 10% for free-range birds reared in the semi-arid region without affecting profit.

Key Words: dietary fiber, free-range birds, performance

M248 Performance of broilers fed mash or pellet diets containing whole or ground pearl millet. T. R. Torres[1], M. C. M. M. Ludke*[1], J. V. Ludke[2], C. B. V. RAbello[1], M. A. M. Faria[1], E. M. S. R. Andrade[1], E. J. O. Souza[1], and M. R. Lima[1], [1]*Universidade Federal Rural de Pernambuco*, *Recife, Pernambuco, Brasil*, [2]*Embrapa Suínos e Aves*, *Concordia, Santa Catarina, Brasil*.

The effect of whole or ground millet grain inclusion at level of 20% into mash or pellet diets on performance of male broilers reared during 21 d was evaluated. The trial was established in 2 nutritional phases: from 1 to 7 and 8 to 21 d of age. A randomized block design in a factorial 3 × 2 with 3 diets (without millet -CSBM, with whole -WMG or ground millet grain -GMG) and 2 physical forms (mash, m, or pellet, p) were established containing 5 replicates per treatment and 10 birds per experimental unit. Parameters evaluated were feed intake, weight gain -WG, feed to gain ratio -F:G and feed efficiency (energetic - FE and proteic - EP) in both phases and during entire trial. Broilers fed mash diets had higher feed consumption than those fed pellet diets: 153 g x 144 g in period 1 to 7 d ($P < 0.05$, CV = 4.46%), 986 g x 944 g in period 8 to 21 d ($P < 0.05$, CV = 3.57%), 1170 g x 1117 g in total period ($P < 0.05$, CV = 3.18%). Feed to gain ratios were better for pellet diets than for mash diets: 1.24 × 1.33 in period 8 to 21 d ($P < 0.05$, CV = 2.62) and 1.27 × 1.18 in total period ($P < 0.05$, CV = 2.13). The proteic efficiency was higher for pellet diets than for mash diets in period 8 to 21 d: 3.82 × 3.57 g/g ($P < 0.05$, CV = 2.64%). In Table 1 were presented the mean values of parameters whose interactions between factors were significant ($P < 0.05$). Pearl millet may be used either in whole grain or ground when fed in pellet diets.

Table 1. Mean values of the evaluated parameters with significant interaction between physical form of diets and diet type

From 1 to 7 days	Physical form	WMG	GMG	CSBM
F:G g/g	mash	1.07^{a}	1.03^{a}	1.03^{a}
	pellet	0.94^{b}	0.98^{b}	0.94^{b}
WG, g	mash	141.5^{b}	151.1	147.8
	pellet	154.5^{a}	148.9	150.8
EE, g/g	mash	0.314^{b}	0.322^{b}	0.323^{b}
	pellet	0.356^{a}	0.340^{a}	0.359^{a}
PE, g/g	mash	4.24^{b}	4.40^{b}	4.40^{b}
	pellet	4.80^{AB,a}	4.62^{B,a}	4.86^{A,a}

^{a,b}Different lowercase letters within a column were different ($P < 0.05$).

^{A,B}Different uppercase letters within a row were different ($P < 0.05$).

Key Words: diet physical form, feed efficiency, poultry

M249 Using marine algae *Chlorella vulgaris* as a prebiotic alternative on broiler chicks. M. Rezvani*, M. Zaghari, M. Shivazad, and H. Moravej, *University of Tehran*, *Karaj, Tehran, Iran*.

To evaluate the effects of chlorella on broiler chick performance, an experiment was conducted by using 80 Ross 308 male broiler chicks. The experiment was accomplished in completely randomized design including 5 treatments with 4 replication and 4 mail chicks in each. The basal diet based on corn-soybean meal and without any additives was formulated. A graded level of chlorella (0.07, 0.14, and 0.21%) was added to basal diet to formulating diets 2, 3 and 4 respectively. To comparing the effects of chlorella with commercial prebiotics an extra diet (diet 5) was formulate by adding a commercial prebiotic to the basal diet. Data was analyzed by using GLM procedure of SAS software means were compared by Duncan multiple range test. Results showed that there were no significant differences in weight gain between the treatments in all ages. While the chlorella treatments in compare with the control treatment had numeral increasing in this trait. Feed conversion ratio significantly decreased by adding the chlorella and commercial prebiotic to the basal diet at 42 d of age ($P < 0.05$). Evaluation of ceca content showed an increasing in lactobacillus population and improving the ratio of lactobacillus to coliform population by increasing the chlorella in the basal diet. The results of this experiment indicated that chlorella have prebiotic properties and even have better performance in some quality to compare the commercial prebiotics.

Key Words: broiler, chlorella, prebiotic

M250 Effects of mung bean waste on pelleting characteristics, growth performance, nutrient digestibility and carcass quality in broilers. N. Amornthewaphat*, P. Rungcharoen, Y. Ruangpanit, S. Rattanatabtimthong, and S. Attamangkune, *Kasetsart University*, *Bangkok, Thailand*.

Series of experiments were conducted to determine the apparent metabolizable energy of mung bean waste in broilers and effects of mung bean waste inclusion in broiler diets on growth performance and nutrient digestibility. In Exp. 1, 120 male broilers (28-d of age; 10 chicks per metabolic cage; 6 cages per treatment) were randomly fed 2 experimental diets consisting of corn soybean basal diet and 20% mung bean waste substituted basal diet. The apparent metabolizable energy of mung bean waste for broilers was 1,844.71 ± 130.71 kcal/kg. In Exp. 2, a total of 1,200 broilers were used in a 42-d growth assay with 3 phase-feeding programs (50 chicks per pen; 6 pens per treatment). Treatments were mung bean waste inclusion of 0%, 5%, 10% and 15% in the experimental pelleted diets and arranged in a randomized completely block design. Sex was a block factor. Increasing mung bean waste resulted in increased palm oil inclusion in the diets. These resulted in linearly decreased pelleting energy consumption and pellet durability index ($P \leq 0.001$). Increasing mung bean waste in the diets decreased ($P \leq 0.05$) body weight gain of starter chicks from 612 to 583 g and linearly suppressed ($P \leq 0.001$) feed conversion from 2.25 to 2.35. There was no difference in growth performance for a grower and a finisher period. For the carcass quality, decreased abdominal fat ($P \leq 0.001$) and increased gizzard weight ($P \leq 0.05$) were observed in chicks fed mung bean waste diets. In Exp. 3, 96 male broilers were used in a 10-d total excreta collection assay (6 broilers per metabolic cage; 4 cages per treatment). Treatments used were the same as in Exp. 2. There was linear decrease ($P \leq 0.05$) dry matter from 80.07 to 77.41% and fiber utilization from 26.83 to 13.59% with increasing mung bean waste. In conclusion, the recommendation of mung bean waste inclusion in the broiler diets should less than 5% to achieve optimum growth performance and nutrient digestibility of broilers.

Key Words: mung bean waste, broilers, growth performance

M251 Effects of dietary grape seed polyphenols on plasma lipid and mineral contents, and intestinal microflora in broiler chicks. A. Viveros*[1], S. Chamorro[2], A. Brenes[2], C. Romero[3], I. Arija[1], and C. Centeno[2], [1]*Facultad de Veterinaria, UCM, Madrid, Spain*, [2]*Instituto del Frio-ICTAN, CSIC, Madrid, Spain*, [3]*Escuela Tecnica Superior de Ingenieros Agronomos, UPM, Madrid, Spain*.

Grapes contain a large array of phenolic compounds which have been showed to have hypolipidemic and anti-microbial effects as well as to act as antioxidant by scavenging reactive oxygen species (ROS) and chelating metal ions which promote the generation of ROS. An experiment was conducted to study the effect of the inclusion of grape seed extract (GSE) and vitamin E in broiler chicks diets on performance,

plasma lipid and mineral contents, and ileal and cecal microflora at 21 d of age. Experimental diets were as follows: 1) Control wheat-soybean diet (WS); 2) WS + vitamin E (200 mg/kg); 3) WS + 50 mg/kg tetracycline; 4, 5, 6 and 7) WS + 0.025, 0.25, 2.5 and 5.0 g/kg GSE, respectively. Each treatment was randomly assigned to 7 pen replicates (5 birds each). Performance was not affected by dietary treatments except in the case of birds fed the highest GSE diet which showed a decrease of body weight. The inclusion of graded concentrations of GSE in the chicken diets lowered the concentration of plasma cholesterol and LDL-cholesterol and increased the content of plasma triglycerides and HDL-cholesterol in a dose-dependent manner. Plasma VLDL-cholesterol was not affected by dietary treatment. Compared with the vitamin E diet, the GSE diet increased the concentration of plasma triglycerides and reduced the contents of plasma HDL and LDL-cholesterol. Regarding plasma mineral contents, the addition of increasing concentrations of GSE in the chicken diets reduced the concentrations of copper, iron and zinc compared with those fed the control and vitamin E diets. In the ileal content, birds fed the lowest concentration of GSE had a lower population of *E. coli* than in any other treatment group. Compared with the control diet, the GSE diet reduced the populations of *E. coli* and coliformes in the cecal digesta. In conclusion, dietary GSE reduced the iron and copper status of broiler chick which could play an important role in the antioxidant processes. GSE has showed to have hypocholesterolemic effect and caused a decrease in the populations of *E. coli* in the intestinal microflora.

Key Words: chicks, grape polyphenols, blood parameters and intestinal microflora.

M252 Comparison of dietary supplementation of cumin essential oil and prebiotic on humoral immune response, blood metabolites and performance of broiler chickens. M. Aami-Azghadi, A. Golian*, H. Kermanshahi, and M. Sedghi, *Ferdowsi University of Mashhad*, *Mashhad, Khorasan Razavi, Iran*.

Five hundred day-old male Ross broiler chicks were divided into 50 groups of 10 birds each and randomly assigned to 10 dietary treatments with 5 replicates each. Two corn-soybean meal-based diets were first provided to meet 100% and 95% of recommended digestible amino acids (RDAA) for starter (1–14 d), grower (15–35 d) and/or finisher (36–49 d) periods. Each starter diet was subdivided into 5 parts and supplemented with 0 and 2 g/kg Fermacto and 0.2, 0.4 and 0.8 g/kg cumin essential oil (CEO). The grower diets contained half of the same supplementation in the starter diets and each of the un-supplemented finisher diet was fed to the corresponding birds. The performance parameters were determined during all periods and carcass yields and relative organ weights measured on d 28 and 49. The blood metabolites, cell differentiation and total anti-SRBC, IgG and IgM titers measured on d 26 in birds fed 100% RDAA diets. The CEO and Fermacto did not have a significant effect ($P > 0.05$) on performance in the starter and finisher periods but higher BWG was observed in birds fed diet with the lowest level of CEO in the grower period. Birds fed diet with 100% RDAA and Fermacto had higher feed: gain ratio in the growing period compared with those fed diet of similar AA and 0.2 g/kg of CEO. A 5% decrease in the RDAA had no adverse effect ($P > 0.05$) on the overall FI and BWG, but FCR was increased ($P > 0.05$). Carcass yields and cuts were not influenced ($P > 0.05$) by CEO, Fermacto or DAA levels. There was not a significant difference ($P > 0.05$) in total anti SRBC, IgG and IgM titers The inclusion of Fermacto or various levels of CEO in diets did not affect ($P > 0.05$) serum metabolite (mg/dL) at d 28, although triglyceride and VLDL concentrations was lower ($P < 0.05$) in chicks fed starter diet contained 0.4 g/kg CEO.

Key Words: cumin essential oil, humoral immune response, chickens performance

M253 Effect of ginger root and ginger oil on antioxidant status and meat quality of broilers. G. F. Zhang[1], Z. B. Yang*[1], Y. Wang[2], W. R. Yang[1], and S. Z. Jiang[1], [1]*Shandong Agricultural University*, *Tai-an, Shandong, China*, [2]*Agriculture and Agri-Food Canada, Lethbridge Research Centre*, *Lethbridge, AB, Canada T1J 4B1*.

A total of 720 broilers were used to investigate the effects of ginger root and ginger oil on antioxidant status and meat quality of broilers. The birds were randomly distributed into 6 treatments with 3 pens of 40 each. Dietary treatment included 1) BD(basal diet), 2) BD+ antibiotics (40 mg/kg bacitracin zinc and 8 mg/kg colistin sulfate), 3) BD+5 g/kg ginger root, 4) BD+10 g/kg ginger powder, 5)BD+20 g/kg ginger powder, 6) BD+100 mg/kg ginger oil (essential oil from ginger). Broilers were fed starter rations from d1 to 21 and finisher rations from d22 to 42. Blood and liver samples were obtained to determine the antioxidant status. Breast muscle samples were collected to determine meat quality of broilers. Supplementation of ginger powder or ginger oil all increased ($P < 0.05$) the activities of total superoxide dismutase (TSOD), glutathione peroxidase (GSH-Px), as well as total antioxidant capability (TAOC), and decreased ($P < 0.05$) the MDA content in serum of chickens compared with the control group at 21 and 42 d of age. Broilers addition of 10 or 20 g/kg of ginger had higher ($P < 0.05$) serum TSOD (145.37, 141.73 vs. 129.10 U/mL at 42d) and GSH-Px activities and lower MDA content (6.25, 6.17 vs. 8.86 nmol/mL at 21d) than the antibiotics group. In liver, addition of ginger significantly elevated ($P < 0.05$) TSOD (21d) and GSH-Px (21d) activities and improved the TAOC (21d and 42d) in contrast to the control. Significant increases ($P < 0.05$) of Hunter a* values and decreases ($P < 0.05$) of drip loss and water loss rate of breast muscle were observed in broilers supplemented with ginger powder and ginger oil in contrast to the control or the antibiotics group. There was no effect on pH value. It was concluded that diets supplemented with ginger could improve meat quality by increasing the antioxidant status of broilers. Ginger powder and ginger oil can be used as a potential additive substituted for antibiotics.

Key Words: ginger, broilers, antioxidant status

M254 Utilization of Mexican sunflower (*Tithonia diversifolia*, Hemsley A gray) leaf meal on the average production cost and returns of broiler chicks. A. H. Ekeocha*[1], A. Akinfemi[1], O. A. Adu[1], and O. A. Adebiyi[1], [1]*Department of Animal Science University of Ibadan*, *Ibadan, Oyo State, Nigeria*, [2]*Faculty of Agriculture P.M.B.135, Nasarawa State University*, *Shabu - Lafia Campus, Nasarawa State, Nigeria*, [3]*Department of Animal Production and Health, Federal University of Technology*, *Akure, Ondo State, Nigeria*, [4]*Department of Animal Science, University of Ibadan*, *Ibadan, Oyo State, Nigeria*.

One hundred and fifty, white, day old Arbor Acre broiler chicks were used in evaluating the utilization of Mexican sunflower meal on the economics of broiler chicks. The broiler chicks were randomly assigned to 5 treatments A, B, C, D, and E. Treatment A served as the control and treatments B, C, D, and E received Mexican sunflower leaf meal at 2.5, 5.0, 7.5, and 10.0% levels replacing maize and soymeal respectively. Feed and water were provided ad-libitum and routine vaccinations and medications administered. Performance characteristics measured were feed intake and net profit. The results of the experiment showed that there were significant differences ($P < 0.05$) in the live weight and feed intake. However, birds on treatment A performed best by attaining a live weight of 2610.30 g in 8 weeks with feed intake of 4,680.56g per bird.

The same birds yielded the highest net profit of N182.42 or $1.586 per bird on dressed weight unlike a deficit of N63.29 or $0.55 per bird on birds in treatment E (10% MSLM) and N306.75 or $2.667 per bird on live weight and a profit of N18.74 or $0.163 per bird in treatment E (10%MSLM). Birds in treatments B(2.5% MSLM), C (5.0% MSLM) and D(7.5% MSLM) have appreciable level of profits which suggest that in the absence of conventional feed stuff, nonconventional feeds such as MSLM at 2.5% to 7.5% can be optimized in the diets of broilers.

Key Words: lesser known sunflower, production cost, broiler chicks

M255 Dietary supplementation of medicinal plants and organic acid on serum lipid profile in Ross broilers. H. Ziaie*[1], A. Zeinali[2], G. H. Hadarbadi[1], M. A. Karimi Torshizi[4], M. Bashtani[3], and H. Farhangfar[3], [1]*Agriculture and Natural Resources Research Center*, *Birjand, South Khorasan, Iran*, [2]*Ferdowsi University*, *Mashhad, Iran*, [3]*Birjand University*, *Birjand, Khorasan, Iran*, [4]*Tarbiat Moddares University*, *Tehran, Iran*.

This study evaluated the supplementation of medicinal plants and organic acid on the serum lipid profile in a feeding program for broilers maintained at commercial condition. Two hundred and 40 1-d old Ross male broiler chicks were placed in 16 cages under a completely randomized design. Cages were randomly assigned to 4 treatments: 1) control diet based corn and soybean meal without supplementation; 2) control + antibiotic, 150 ppm of Virginiamycin; 3) control + 450 mg medicinal plants Digestrom /kg diet; and T4) control diet + 400 mg organic acid Formycine /kg diet). At d 28 and 42 of the experiment, 4 birds from each replicate were randomly selected and blood samples taken from the wing vein into syringes. The blood samples were then centrifuged at 2,000 × *g* for 10 min and the serums were transported into aseptically treated vials then at 20°C for further analysis. Serum samples were analyzed for determining the total cholesterol, triglyceride, HDL cholesterol, and LDL cholesterol by enzymatic diagnostic kit (Sigma kit). Experimental units were treated under T3, which was found to have the lowest cholesterol, triglyceride, and LDL cholesterol concentrations. This treatment also resulted in an increased HDL/LDL ratio compared with T1 and T2. Supplementation diets with medicinal plants and organic acid had no significant effect on HDL cholesterol. In addition, treatment 4 reduced serum total cholesterol and LDL cholesterol concentrations in broilers during 42 d. Generally, the results indicated that the medicinal plants and organic acid as an alternative antibiotic have a hypolipidemic effect in broilers.

Key Words: hypolipidemic, probiotic, prebiotic

M256 Changes of internal egg quality during cold storage when hens fed diets containing cottonseed meal treated with sodium bentonite. A. Gilani, H. Kermanshahi, A. Golian*, and A. Tahmasbi, *Ferdowsi University of Mashhad*, *Mashhad, Iran.*

This experiment was designed to determine interactive effects between dietary sodium bentonite (SB) containing ferric oxide and free gossypol (FG) on internal egg quality during cold storage. In a 3 × 3 factorial arrangement in a CRD with 9 dietary treatments in 4 replicates consisting of 3 levels of SB (0, 1, and 2%) and 3 levels of CSM (0, 10, and 20%) were tested. Nine mash diets were fed to 288 commercial Hy-Line W-36 hens from 51 to 62 wk of age after 1 wk of acclimatization. Each experimental unit consisted of 2 cages with 4 birds per cage. The 4 eggs were randomly chosen in each experimental unit from the eggs laid during the 4 consecutive days at every 28-d period (total 3 periods) and then were stored at 4°C for 1, 2, 3, and 4 wk to enhance yolk discoloration, respectively. After storage, eggs were individually opened, and the degree of yolk discoloration was scored based on egg yolk scoring protocol. After determination of albumen spread, the yolk was separated from the albumen and the pH of yolk and albumen was measured. Data were analyzed using the GLM procedure of SAS 9.1. Tukey's Studentized Range (HSD) test was used to compare means ($P < 0.05$).Yolk score significantly ($P < 0.01$) increased with increasing of CSM and significantly ($P < 0.01$) diminished with increasing of SB in the diet during cold storage. There was no significant effect of dietary treatments on spread of albumen, but albumen quality gradually decreased during 4 weeks. Generally, pH of yolk and albumen increased after cold storage. There was no significant effect of dietary treatments on pH of yolk or albumen. Egg discoloration in the current research was limited to that associated with gossypol. No eggs were observed to have developed pink albumen. In this study, cloudy white was sometimes observed after cold storage in all treatments. The yolks of eggs laid by hens consuming CSM became rubbery, viscous, and pasty in appearance after cold storage. Under the conditions of this experiment, SB in the diet was useful for reduction of yolk discoloration.

Key Words: cottonseed meal, sodium bentonite, internal egg quality

M257 Sensory characteristics of table eggs from laying hens fed diets containing hemp oil or hemp seed. E. Goldberg*, D. Ryland, N. Gakhar, J. D. House, and M. Aliani, *University of Manitoba*, *Winnipeg, MB, Canada*.

Hemp seed contains approximately 30% oil, and this oil is rich in α-linolenic acid (17% of total fatty acids). As such, hemp seed and its' oil can be used in poultry diet formulations to produce eggs enriched with these essential fatty acids. Ideally, enriched eggs should maintain the characteristic sensory attributes of non-enriched eggs to remain acceptable to consumers. The concern with omega-3 eggs in the past has been the potentially deleterious effects on sensory attributes including off-flavor and off-odor, and altered texture. The current study was designed to assess the sensory attributes of eggs procured from hens consuming diets containing hemp seed products. Forty-eight individually caged Bovan hens received 1 of 6 isonitrogenous and isoenergetic diets containing 0, 4, 8, 12% hemp oil or 10, 20% hemp seed for a 12 week period. Trained panelists (n = 8) evaluated 6 aroma and 7 flavor attributes of cooked eggs. Attributes that were measured included "egg," "salty," "sour," "milky," "creamy" and "buttery," with "sweet" as the additional flavor attribute. No significant differences in aroma or flavor ($P > 0.05$) were found between eggs from different dietary treatments. For yolk color, L*, a* and b* values (mean ± SD) for control (0%) eggs were 61.0 ± 0.3, 1.0 ± 0.1, and 43.2 ± 0.4, respectively. Addition of either hemp seed or hemp oil led to significant ($P < 0.05$) reductions in L*, and significant ($P < 0.05$) increases in a* and b*, with the largest changes observed in the 20% hemp seed treatment (L* = 58.7 ± 0.1; a* = 5.3 ± 0.1; b* = 60.0 ± 0.3). The results provide evidence that hemp oil or seed use in poultry diet formulations leads to increased yolk color intensity, but does not have adverse effects on flavor and aroma profiles of the cooked eggs.

Key Words: sensory, egg, hemp

M258 Effect of guar meal as a source of protein on laying hens performance. P. Soleimani, A. Golian*, H. Kermanshahi, and M. Sedghi, *Ferdowsi University of Mashhad*, *Mashhad, Khorasan Razavi, Iran*.

An experiment was conducted to evaluate guar meal (GM) as a source of protein on laying (58 weeks of age) performance and egg quality. Two hundred 20 8 laying hens (58 weeks of age) were fed diets containing

0, 3, 6 and 9% guar meal with/without β-mannanase (Hemicell) for 12 weeks. A complete block randomized design with 4 × 2 factorial arrangement were used to have 8 diets of each fed to 4 replicate hens of 9 each. Daily egg production and weekly egg weight and feed consumption were recorded. Three eggs from each replicate were used to measured egg components each other week. Hen-day egg production was significantly decreased when hens fed diets contained 6 and 9% GM in first week and only 9% GM at second week of experiment as compared with 0 and 3% GM fed birds. Whereas hen-day egg production was not influenced when hens fed up to 9% GM after third week. Egg mass was significantly lower when hens fed 9% GM during the experimental periods compared with control and 3% GM fed birds (46.8 vs. 50.8 or 52.4, respectively). Feed conversion ratio (FCR) in 3 initial weeks of experiment was significantly higher in 9% GM fed birds. Feeding of GM did not affect specific gravity, percentage wet albumen and wet yolk based on percentage of whole egg weight and shell weight and thickness. Feed consumption, hen-day egg production, egg mass, FCR and egg quality were not affected by Supplementation of β-mannanase during the experimental periods. The results of this study showed that 6% GM may be added to the diet of laying hens with no adverse effects on performance.

Key Words: guar meal, egg production, laying hen

M259 Effect of dietary supplementation of licorice extract on egg quality and performance of hens. M. Sedghi, A. Golian*, and P. Soleimani, *Ferdowsi University of Mashhad*, *Mashhad, Khorasan Razavi, Iran*.

The objective of this study was to determine the effects of various levels of dietary licorice extract on egg production, egg weight, specific gravity, feed conversion ratio, egg shell quality and egg yolk color. One hundred 20 8 laying hens (58 weeks age) were divided to 4 groups with 4 replicates (8 hens each) in a complete block randomized design. Data were analyzed using ANOVA and means were separated using Tukey's HSD ($P < 0.05$). The experimental diets were supplemented with 0, 2, 4 or 6 g/kg of diets licorice extract. Daily egg production, weekly egg weight and feed consumption were recorded. Three eggs in each replicate were used to measured egg components each other week. Daily egg production in hens fed diet supplemented with 4 g/kg of licorice extract numerically increased ($P = 0.06$) when compared with the control diet in the entire experiment. Hens fed diet 4 g/kg licorice extract had significantly increased ($P < 0.05$) shell thickness compared with those fed diets supplemented with 6 g/kg (389 vs. 374 mm). Percentage of abdominal fat pad was significantly decreased ($P < 0.05$) in birds fed diet containing 6 g/kg licorice extract compared with control diet (0.83 vs. 1.49%). Performance parameters (feed consumption, feed conversion ratio), egg parameters (egg weight, dry shell weight, egg-specific gravity, percentage of wet albumen and wet yolk based on percentage of whole egg weight) and organ weights were not influenced ($P > 0.05$) by licorice supplementation. It seems that licorice extract at the level of 4 g/kg may have positive effects on egg production, shell quality and decreases abdominal fat pad at 6 g/kg level.

Key Words: licorice extract, egg production, laying hen

M260 Effects of fermented garlic powder supplementation on production performance, egg quality and blood characteristics of laying hens. J. S. Yoo*, H. J. Kim, J. P. Wang, X. Ao, J. H. Jung, and I. H. Kim, *Department of Animal Resource and Science, Dankook University*, *Cheonan, Choongnam, Korea*.

The effects of fermented garlic powder on the production performance, egg quality and blood characteristics of laying hens were studied in a 35–d experiment. A total of 240 (ISA brown) 41-wk-old layers were allocated into the following 4 treatments: 1) CON (basal diet), 2) G1 (CON + 0.005% fermented garlic powder), 3) G2 (CON + 0.01% fermented garlic powder), and 4) G3 (CON + 0.02% fermented garlic powder). There were no differences ($P > 0.05$) in the egg production, egg weight, eggshell breaking strength and eggshell thickness among groups throughout the entire experimental period. However, the yolk height increased significantly ($P < 0.05$) in response to the addition of fermented garlic powder during the 5th week. Additionally, the yolk color was greater ($P < 0.05$) in the CON and G3 groups than in the G1 and G2 groups during the 5th week. The Haugh unit value was higher ($P < 0.05$) in groups that received the fermented garlic powder treatments during the 5th week than in the CON group. None of the treatments had a significant effect on the total protein, albumin, and IgG levels in blood throughout the experimental period ($P > 0.05$). There was a significant ($P < 0.05$) reduction in the serum cholesterol concentration when the dietary level of fermented garlic powder was increased from 0.005 to 0.02%. Overall, this study demonstrated that the addition of fermented garlic powder to the diets of laying hens reduced the serum cholesterol concentration without any adverse effects on production performance. In conclusion, dietary fermented garlic powder supplementation improved yolk height and Haugh unit, and reduced serum cholesterol concentration laying hens.

Key Words: fermented garlic powder, egg quality, laying hens

M261 Effects of marine algae (*Spirulina platensis*) on egg yolk color and laying hens performance. N. Zahroojian, H. Moravej*, and M. Shivazd, *University of Tehran*, *Karaj, Tehran, Iran*.

Egg yolk color has always been regarded as an important egg quality characteristic. There are some synthetic pigments for produce an aesthetically pleasing yolk color of egg, but consumers often prefer eggs that were enriched by natural materials. It seems that the algae as a natural pigment can be useful for produce an aesthetically pleasing yolk color. Therefore, in this experiment, a total of 128 Hy-line W36 hens, 63 weeks of age were used. Hens were put at random into 4 treatment groups (4 replicates and 32 hens per treatment). The hens were fed 4 diets; 3 diets with different levels of spirulina (1.5%, 2% and 2.5%) and one control group based on wheat and soybean meal that received no spirulina in the ration. Egg production, feed conversion ratio, feed intake, egg weight and yolk color were compared with control group. Egg yolk color was measured by the BASF *Ovo-color* fan. Our Results indicated that egg production, feed conversion ratio, feed intake and egg weight did not show any changes with the spirulina addition ($P < 0.05$), while a significant increase in egg yolk color was observed in the treatments that received the spirulina comparing to control diet ($P < 0.0001$). Yolk color scores of control group and different levels of spirulina (1.5, 2, and 2.5%) were 1.5, 10.5, 11.4, and 11.6 in BASF color fan, respectively. There were no significant differences between the treatments with 2% and 2.5% of spirulina, so we can suggest using 2% spirulina in the egg industry to produce an aesthetically pleasing yolk color.

Table 1. Effect of treatments on egg production, feed conversion ratio, feed intake, egg weight and yolk color

Spirulina level (%)	Egg production, n	Feed conversion ratio	Feed intake	Egg weight	Yolk color
0 (control group)	74.168[a]	1.562[a]	100.275[a]	63.923[a]	1.55[c]
1.5	78.333[a]	1.550[a]	97.803[a]	63.198[a]	10.55[b]
2	82.083[a]	1.520[a]	96.495[a]	63.598[a]	11.43[a]
2.5	73.645[a]	1.532[a]	97.393[a]	63.473[a]	11.66[a]
P-value	0.2083	0.7552	0.4059	0.8403	<0.0001
SEM	2.7	0.03	1.36	0.8	0.11
CV%	6.98	3.77	2.76	2.53	2.35

[a–c]Means in a column with different superscripts differ significantly.

Key Words: egg yolk color, marine algae (*Spirulina platensis*), laying hen performance

M262 Use of salvage pet food in diets of weaned pigs. J. P. Holt and S. J. Gasca*, *Illinois State University*, *Normal*.

The United States pet food industry produced over 8 million tonnes of pet food in 2008 and continues to grow. A by-product of this industry, salvage pet food (SPF), is often available to swine producers. Two experiments were conducted to determine the effects of adding SPF as an alternative ingredient in weaned pig diets. SPF, an expired, extruded dog food product, was ground and added to conventional weaned pig diets at 0 (CON), 10, 25, or 40%, substituting corn and soybean meal. SPF had the following nutrient composition: 22.7% CP, 3.7% CF, 8.9% crude fat, and 7.2% ash. Two dietary phases were mixed. Barrows (n = 24) were placed into metabolism crates and fed phase 2 experimental diets for 10 d, with 3 d of total feces collection. Feed and fecal samples were analyzed for GE using bomb calorimetry and nitrogen using the combustion method. For a growth assay, 348 pigs, blocked by weight and sex, were placed into 48 nursery pens. Pigs were fed a common pre-starter for 4 d followed by their respective experimental diets for 28 d (14 d per phase). Pig weight and feed disappearance were measured weekly and used to calculate ADG, ADFI, and G:F. Blood samples were collected weekly, from one pig per pen, for analysis of blood urea nitrogen (BUN). Diets containing 40% SPF were found to have a greater energy density than anticipated. However, GE intake of pigs was not different ($P > 0.05$) between treatments during the metabolism trial. There was no effect ($P > 0.05$) of SPF inclusion on energy and nitrogen digestibility of pigs fed experimental diets. Analysis of growth data revealed that pigs fed diets containing 25 and 40% SPF had an increased ($P < 0.05$) G:F compared with pigs fed the CON diet. Pigs fed diets containing 40% SPF tended ($P = 0.07$) to have increased BUN in comparison to pigs fed either 0 or 10% SPF. Results of these experiments show that SPF is a quality ingredient for use in weaned pig diets; when included at high levels, pigs displayed a greater efficiency of feed utilization.

Key Words: pet food, swine

M263 Effect of meat powder supplementation on growth performance, nutrient digestibility and blood characteristics of growing pigs. S. M. Hong*, J. H. Lee, J. P. Wang, Q. W. Meng, B. W. Yang, and I. H. Kim, *Department of Animal Resource and Science, Dankook University*, *Cheonan, Choongnam, Korea*.

A total of 48 [(Duroc × Yorkshire) × Landrace] pigs (25.67 ± 1.13 kg) were used in a 42–day trail to investigate the effects of dietary meat powder on growth performance, nutrient digestibility and blood characteristic in growing pigs. Pigs were allotted into 3 dietary treatments in a randomized complete block design according to sex and initial BW. Dietary treatments included: 1) CON [basal diet], 2) M2 [basal diet + 0.2% meat powder] and 3) M4 [basal diet + 0.4% meat powder]. Each treatment had 8 replicates with 2 pigs per pen. Pigs were housed in an environmental controlled, slatted-floor facility in 24 adjacent pens (1.80 × 1.80 m2) and were allowed ad libitum access to feed and water through a self-feeder and nipple waterer throughout the experimental period. In the current study, dietary meat powder did not affect the growth performance (ADG, ADFI and G/F ratio). Nutrient digestibility (DM, N and energy) were not affect by the inclusion of the meat powder, although a numerically increase was observed on the N digestibility in the M2 treatment compared with the CON treatment. In addition, pig fed the dietary meat powder diets had a decreased (Linear $P = 0.006$) BUN concentration in serum with the increasing meat powder level, which suggested that the meat powder could exert positive to the protein utilization. However, no effect was observed on the creatinine concentration among the treatments. In conclusion, dietary meat powder could improve the protein utilization and have a tendency to increase the nutrients digestibility.

Key Words: meat powder, growth performance, growing pigs

M264 Effects of fermented garlic powder on growth performance and blood profiles of weanling pigs. J. P. Wang*, J. H. Lee, H. J. Kim, L. Yan, S. M. Hong, and I. H. Kim, *Department of Animal Resource and Science, Dankook University*, *Cheonan, Choongnam, Korea*.

The overall objective of this study was to evaluate the growth performance and blood profile responses of pigs fed diets supplemented with fermented garlic powder. Garlic (*Allium sativum*) has several beneficial effects for either human or animals having antimicrobial, antioxidant, as well as antihypertensive properties. The growth performance and blood profile responses of 144 weanling pigs (5.5 ± 0.4 kg) fed dietary supplementation of fermented garlic powder were evaluated in a 5-wk trial. Pigs were randomly allocated to the following 4 dietary treatments: CON (basal diet) and CON with fermented garlic powder added at 0.05% (G0.05), 0.10% (G0.1) or 0.20% (G0.2). There were 6 replications with 6 pigs per pen. Throughout the experimental period, no effect on G:F was observed ($P > 0.05$). However, during wk 1–3, the ADFI was higher ($P < 0.05$) in the G0.05 group than the other treatment groups. In addition, the ADG was improved during wk 3–5 ($P < 0.05$) in response to fermented garlic powder treatments, while only the ADFI in the G0.05 group was increased ($P < 0.05$). Overall (0–5 wk), G0.05 treatment increased the ADG by 10% and the ADFI by 12% ($P < 0.05$) when compared with the CON group. Furthermore, the IgG, RBC and lymphocyte levels were greater ($P < 0.05$) in the G0.1 and G0.2 treatment groups at the end of the trial. In conclusion, the addition of fermented garlic powder improved the ADG in weanling pigs and partially benefited the immunity.

Key Words: fermented garlic powder, growth performance, weanling pigs

M265 Evaluation of algae meal from *Nannochloropsis oculata* as a protein source for non-ruminant animals. B. A. Howe*[1], I. N. Roman-Muniz[1], B. D. Willson[2], and S. L. Archibeque[1], [1]*Colorado State University, Department of Animal Sciences*, *Fort Collins*, [2]*Colorado State University, Department of Mechanical Engineering*, *Fort Collins*.

A study was developed to explore the safety and potential use of algae meal that remained after the oil was extracted from the algae species

Nannochloropsis oculata for biodiesel production. This algae meal was included at 10% (DM basis) to a test diet that was isocaloric and isonitrogenous to the control diet (as analyzed by proximate analysis). Twenty-four adolescent male Sprague-Dawley rats were used (n = 12/treatment). The rats were fed ad-libitum for 36 d and body weights were recorded every 7 d. Blood was drawn via a lateral venous tail puncture, and analyzed for metabolites on d 0, and 21 of the study. A nutrient balance trial was conducted from d 21 through d 28, measuring all food and water consumed, as well as all feces and urine produced. On d 36 of the study, the rats were killed, blood was collected via a heart puncture, at the same time the organ weights were recorded, and tissue samples for histology were taken of the kidneys, liver and spleen. The ADF (11.08 vs. 7.51 g/d) and NDF (25.10 vs. 21.14 g/d) intake of rats fed the algae meal diet was greater ($P < 0.01$) than those fed the control diet. Subsequently, apparent DM and CP digestibility was slightly lower ($P < 0.03$) in the algae fed rats then the controls There were no apparent differences ($P > 0.10$) in final body weight, or CP balance. There were no differences in blood glucose ($P = 0.15$), base excess ($P = 0.79$) or BUN ($P = 0.69$). Additionally, there were no apparent differences ($P > 0.10$) in histology of the kidneys, livers or spleens of rats fed either the control or diet with algae meal. These data indicate that the algae meal of *N. oculata* may be a safe alternative protein source for non-ruminant animals, yet the digestibility may be limited by the increased fiber content of the algae meal.

Key Words: algae, biodiesel, digestibility

M266 The effect of supplementation with ginger on dietary oxidation stability. X. Zhao and Z. B. Yang*, *Shandong Agricultural University*, *Tai-an, Shandong, PRC*.

The experiment was conducted to evaluate the effect of supplementation with ginger on dietary oxidation stability. Treatments included control diet without ginger supplementation and test diets supplemented with 5, 10, 15, 20 g/kg of ginger. All of the diets were placed in plastic air-tight envelope that were distributed randomly in a 20°C oven for 60-d experimental period. Lipid was extracted from samples at 10-d intervals using the method of Soxhlet extraction (<45°C). The peroxide value (PV) was determined on the extracted oil using the AOCS method Cd 8–53 (Walker, 1989). The anisidine value (AV) was measured using the official IUPAC method (Paquot, 1979). Supplementation with ginger in poultry diets caused a greater ($P < 0.05$) increase in PV than the control diet during the first 30 d. But after that time, the PV showed no difference ($P > 0.05$) until last except the 0, 5g/kg of ginger supplementation diets were lower ($P < 0.05$) at Day 60. In contrast to the PV, the control diet caused the fastest ($P < 0.05$) rate of oxidation, whereas the 20 g/kg of ginger supplementation diet showed the lowest ($P < 0.05$) rate of oxidation during the first 30 d and then no significant differences ($P > 0.05$) in AV between the control and the test diets. Further analysis showed that AV of all the diets were linearly ($P < 0.05$) and tended ($P < 0.05$) to quadratically increased. In conclusion, AV and PV of the diets were strongly affected by time. Supplementation with ginger in poultry diets can decrease AV but increase PV. As all know, both PV and AV are important characteristic of the edible oils quality and appears as an indicator of the lipid oxidation and oil properties deterioration. PV measures the first products, hydroperoxides and peroxides, which are transient and decompose to aldehydes and ketones, whereas AV measures these secondary oxidation products. Through above analysis, ginger supplementation in poultry diets may effective to restrain the conversion of first oxidation products to secondary ones.

Key Words: ginger, poultry diets, oxidation stability

M267 Effects of dietary wild ginseng adventitious root meal on egg quality, egg production, and fatty acid content of yolk in egg produced by laying hens. H. J. Kim*, J. S. Yoo, J. P. Wang, Q. W. Meng, B. W. Yang, and I. H. Kim, *Department of Animal Resource and Science, Dankook University*, *Cheonan, Choongnam, Korea*.

This study was conducted to evaluate the effects of dietary wild ginseng adventitious root meal on the egg quality, egg production and fatty acid content of yolks in egg produced by laying hens. A total of 240 ISA Brown laying hens 55 wk of age were used in this 5–wk feeding trial. Dietary treatments included 1) CON (basal diet), 2) WGR1 (basal diet + 1% wild–ginseng adventitious root meal), and 3) WGR2 (basal diet + 2% wild–ginseng adventitious root meal). The laying hens were allotted into 3 dietary treatments with 40 replicate pens and 2 laying hens per pen in a completely randomized design. Evaluation of the egg quality revealed that the egg shell thickness, egg yolk color, egg yolk height and Haugh unit had no significant different among treatment groups ($P > 0.05$). Egg production was also significantly increased in the WGR1 and WGR2 groups when compared with the CON group ($P < 0.05$). The fatty acid content of yolk, palmitic acid, stearic acid, saturated fatty acid content and the saturated fatty acid/unsaturated fatty acid ratio were significantly lower in the WGR1 and WGR2 groups when compared with the CON group ($P < 0.05$). The linoleic acid, eicosenoic acid and unsaturated fatty acid content in the WGR group was higher than in the CON group ($P < 0.05$). In conclusion, the addition of wild-ginseng adventitious root meal improved egg quality, egg production and fatty acid content of yolk.

Key Words: wild ginseng, egg quality, laying hens

M268 Effect of a mixture of turmeric and capsicum oleoresins and of a garlic botanical on broiler chickens performance and intestinal histology. D. Bravo*[1], T. G. Petrolli[2], L. F. T. Albino[2], and H. S. Rostagno[2], [1]*Pancosma*, *Geneva, Switzerland*, [2]*Federal University of Viçosa, Department of Animal Science*, *Viçosa, Brazil*.

Our objective was to evaluate the effect of a mixture of turmeric and capsicum oleoresins (PF, Proflora) and of a garlic botanical (GB) on the performances and small intestine villus height and crypt depth of broiler chickens fed a corn soybean meal diet. One day-old male broiler chicks were distributed in a completely randomized block design with 6 treatments, 8 rep. and 20 birds per rep. (floor pen) in the starter (1–21d) and grower/finisher (21–40d) phases. T1 was the nonsupplemented control (positive control, PC, 3000 kcal/kg ME, 1.263% Lys, 0.574% Met). T2 (negative control, NC) was T1 with reduction of 75 kcal ME/kg and 2% AAs. T3 was T2 + 100 ppm of XT. T4 was T2 + 75 ppm of GB. T5 was T2 + 150 ppm of GB. Birds and feed were weighted at d1, 21 and 40. At d21, 1 bird of each rep. was sacrificed and a portion of jejunum was collected to determine villus height (VH), crypt depth (CD) and villus/crypt ratio (VC). The data were subjected to one-way ANOVA. Treatments effect was tested by the Newman Keul's Test ($P < 0.05$). From d 1 to 21, BWG and G:F were decreased by NC (−7.9%, −5.3%), improved by either XT (+5.3%, +3.6%), or 75 and 150 ppm of GB (BWG = +6.5%, +8.8%; G:*F* = +3.5%, +4.1%) and similar between T3, T4, T5 and PC. From d1 to 40, BWG and G:F were depressed by NC (−4.2%, −2.3%), improved by XT (+1.9%, +1.1%, $P > 0.05$) and by 150 ppm of GB (+5.3%, +3.4%). The NC diet decreased VH (−2.9%) and increased CD (+3.0%, $P > 0.05$). When compared with NC, birds fed XT improved VH (+19.5%) and reduced CD (−5.8%, $P > 0.05$), which was a 20.8% improvement of VC ratio. GB improved VH (−12.2% for 150 ppm, $P > 0.05$) and decreased CD (+8.9% for 75 ppm, $P > 0.05$). The results indicated that broilers on the NC diet had poorer performance and intestinal histology than those fed the PC diets (T1) and the NC plus

additives (T3, T4, T5). XT, and GB improved chicks BWG, G:F and intestinal histology to values similar to those fed the PC diets.

Key Words: essential oils, gut health, broilers

M269 Effects of dietary medicinal plants (Artemisia, Acanthopanax, and garlic) on productive parameters in pigs. J. H. Jung*[1], H. D. Jang[1], T. X. Zhou[1], S. H. Oh[2], R. C. Noble[2], and I. H. Kim[1], [1]*Department of Animal Resource and Science, Dankook University*, *Cheonan, Choongnam, Korea*, [2]*Department of Animal SCience, North Carolina A&T State University*, *Greensboro, North Carolin, United States*.

This study was conducted to determine the effect of supplemental medicinal plants (Artemisia, Acanthopanx and garlic) on productive parameters in pigs. In experiment 1, Three days before parturition, a total 90 multiparous (4.5 ± 0.3) sows were used in a 21–d performance assay. Sows fed treatments included 1) CON (basal diet; Control), 2) BM1 (CON + 0.1% medicinal plants) and 3) BM2 (CON + 0.2% medicinal plants). We detected the initial, final body weight, backfat and estrus interval of sows. Litter's average of birth and weanling weight and average dairy gain were checked. Backfat thickness difference from farrowing to weaning was significantly increase ($P < 0.05$) in CON treatment compared with medicinal plants treatments. The piglets weigh gain was higher ($P < 0.05$) in the medicinal plants treatments than in control. In experiment 2, a total of 60 finishing pigs [(Landrace × Yorkshire) × Duroc, 65.21 ± 1.04 kg average initial body weight] were used in a 56–d performance assay to determine the effects of supplemental medicinal plants (Artemisia, Acanthopanx, and garlic) on growth performance and carcass characteristics in finishing pigs. Finishing pigs fed treatments included 1) CON (basal diet), 2) BM1 (CON + 0.1% medicinal plants) and 3) BM2 (CON + 0.2% medicinal plants). During 4~8weeks and overall period, ADG was higher ($P < 0.05$) in the medicinal plants treatments than in control. CON treatment was higher pH of loin after 24 h of storage and cooking loss than BM1 treatment ($P < 0.05$). Water holding capacity and Drip loss after 1 d of storage were affected by the dietary BM treatments ($P < 0.05$). In conclusion, the results obtained from this feeding trial suggest that the medicinal plants mixture supplementation in diets for finishing pigs improved ADG, water holding capacity, cooking loss and sow decreased backfat loss and litter weight gain improved.

Key Words: medicinal plants, sow, finishing pigs

M270 Effects of cassava on production performance and relative organ weight in Korean native broilers. J. H. Lee*, H. D. Jang, J. P. Wang, T. X. Zhou, and I. H. Kim, *Department of Animal Resource and Science, Dankook University*, *Cheonan, Choongnam, Korea*.

This study was conducted to evaluate the effects of cassava for energy source on the performance and relative organ weight in Korean native broilers. A total of 528 broilers were allocated into the following 4 treatments: 1) CON (basal diet), 2) C5 (5% of cassava diet), 3) C10 (10% of cassava diet), and 4) C20 (20% of cassava diet). The broilers were allotted into 4 dietary treatments with 6 replicate pens and 22 chicks per pen in a completely randomized design and studied in a 9-wk experiment. During 9 wk, weight gain and feed intake was not affected by treatments ($P > 0.05$), however, feed/gain ratio was higher in C10 and C20 treatments compared with C5 treatment ($P < 0.05$). In liver, abdominal fat, leg and carcass percentage were not difference was observed. However, in breast meat percentage was higher in CON compared with C10 treatment ($P > 0.05$). In conclusion, this study demonstrated that the cassava for energy source in Korean native broilers can be used at up to 20% without negative effect on performance.

Key Words: cassava, relative organ weight, Korean native broilers

M271 Effects of cassava on production performance and egg quality in laying hens. J. H. Lee*, H. J. Kim, J. P. Wang, T. X. Zhou, and I. H. Kim, *Department of Animal Resource and Science, Dankook University*, *Cheonan, Choongnam, Korea*.

This study was conducted to evaluate the effects of cassava for energy source on the production performance and egg quality in laying hens. A total of 240 (ISA brown) 47 week old layers were allocated into the following 4 treatments: 1) CON (basal diet), 2) C5 (5% of cassava diet), 3) C10 (10% of cassava diet), 4) C20 (20% of cassava diet), and 5) C30 (30% of cassava diet). The laying hens were allotted into 5 dietary treatments with 24 replicate pens and 2 laying hens per pen in a completely randomized design and studied in a 35-d experiment. Egg production was significantly decreased in the C30 treatment when compared with other treatments ($P < 0.05$). Evaluation of the egg quality revealed that the egg weight, eggshell thickness, eggshell breaking strength, egg yolk height and Haugh unit was not affect by treatments ($P > 0.05$). However, in egg yolk color, C20 and C30 treatments were dramatically decreased from 2nd and 1st week ($P < 0.05$). In conclusion, this study demonstrated that the cassava for energy source in laying hens can be used at up to 20% without negative effects on performance, however consider pigment for yolk color.

Key Words: cassava, egg quality, laying hens

M272 Inclusion of shrimp heads meal (*Litopenaeus* spp.) and red crab meal (*Pleuroncodes planipes*) in rations for laying hens, and its effect on the egg physical and sensorial quality, at different time and temperature of storage. E. M. Carranco*[1], L. Sangines[1], E. Morales[2], E. Avila[3], B. Fuente[3], R. Ramirez[3], S. Carrillo[1], C. Calvo[1], and F. Perez-Gil[1], [1]*Instituto Nacional de Ciencias Medicas y Nutricion Salvador Zubiran*, *Mexico, D.F., Mexico*, [2]*Universidad Autonoma Metropolitana*, *Mexico, D.F., Mexico*, [3]*Universidad Nacional Autonoma de Mexico*, *Mexico, D.F., Mexico*.

The aim of this study was to determine if the inclusion of shrimp heads meal (SM) and red crab meal (RCM) in laying hen diets has an effect on the egg physical and sensory characteristics when is stored at 4°C and 20°C during 15 and 30 d. One hundred thirty-five laying hens were distributed in 3 treatments: Control diet, SM (20%), and RCM (4%). At the end of the trial, 250 eggs were taken: 50 fresh eggs were analyzed, 100 eggs were stored at 4°C and 20°C/15 d and another 100 at 4°C and 20°C/30 d. Egg physical quality and pH were measured, while the egg flavor and yolk color where evaluated, too. The results were analyzed using a 3 × 3 × 2 factorial design; the comparison among means was done with the multiple range test of Duncan ($P < 0.05$). There were no statistical differences ($P > 0.05$) in productive parameters, weight of shell and sensory evaluation. It was found that egg weight decreased at longest time and lowest temperature ($P < 0.05$). The albumen height and Haugh Units increased in old treatments in egg at 0 d at SM and RCM at 20°C, but decreased when eggs were stored at 4° and 20°C during 15 and 30 d. The yolk color decreased with SM and RCM at 15 and 30 d (20°C). Eggshell thickness presented the great loss at 30 d/4°C ($P < 0.05$). The pH was increased as the time was longer by itself. It was concluded the inclusion of SM and RCM in laying hen diets did not affect both productive variables and the sensory characteristics in eggs at 0 and 15 d (4° and 20°C) but the physical quality and pH were affected.

Key Words: egg quality, shrimp heads meal, red crab meal

M273 The effect of medicinal plants and plant extracted oils on broiler duodenum morphology and immunological profile. L. Stef*[1], G. Dumitrescu[1], D. Drinceanu[1], D. Stef[1], D. Mot[1], C. Julean[1], R. Tetileanu[1], and N. Corcionivoschi[2], [1]*Banat's University of Agricultural Sciences and Veterinary Medicine, Department of Animal Science*, *Timisoara, Romania*, [2]*University College Dublin*, *Ireland*.

It was previously reported that essential oils from aromatic plants have antimicrobial activity against many bacterial pathogens. We have conducted an in vivo experiment to study the effect of some aromatic plants and in particular to investigate the effect of oils extracted from these plants at the immune level and duodenal morphology. During the experiment 90 broiler chicken were divided in 3 experimental groups: control group (C), group 1 (G1) and group 2 (G2). Broilers from group G1 had received feed with 0.05% incorporated oils extracted from savory (*Satureja hortenis*), mint (*Mentha piperita*) and sea-buckthorn (*Hippophae rhamnoides*). Group G2 received a premix of plants (savory, mint, and sea-buckthorn) during daily feeding. The control group (C) received normal feed with no supplements. The amount of lysozyme detected at group G1 was doubled (28.55 μg/cm^3; $P < 0.05$) comparing G2 (13.2 μg/cm^3; $P < 0.01$) and the control (11.42 μg/cm^3; $P < 0.005$). The incorporation of extracted oils in food determine a powerful stimulation of intestinal mucous membrane, manifested by development of intestinal villi, the hypertrophy of villi, hyperplasic hypertrophy of capillary network and the stimulation of leukocytes infiltrate. The muscular hypertrophic processes and of leukocytes infiltrates are visible in the endomysium and perimysium of the muscular tunic. The microscopical images taken from the duodenum sections were sampled from the G2 group suggest the stimulation of angiogenesis ($P < 0.05$). The processes are however of smaller intensity comparative with experimental lot G1 ($P < 0.001$). This work shows that essential oils extracted from plants improve the immune response and also are able to determine changes of the duodenal mucosa with beneficial effects for the animal.

Key Words: medicinal plants, plant oils, broiler nutrition

M274 Effects of dietary polyphenol-rich grape products on gut morphology and intestinal microflora in broiler chicks. A. Viveros*[1], S. Chamorro[2], M. Pizarro[1], W. Siqueira[3], C. Centeno[2], I. Arija[1], and A. Brenes[2], [1]*Facultad de Veterinaria, UCM*, *Madrid, Spain*, [2]*Instituto del FRIO-ICTAN, CSIC*, *Madrid, Spain*, [3]*Faculdade de Veterinaria, Universidade Estadual do CEARA*, *Fortaleza, Brasil*.

Grapes have high amounts of phenolic compounds which can modulate the gut activity as well as to modify the structure and function of the gastro-intestinal tract. An experiment was conducted to study the effect of the inclusion of grape pomace concentrate (GPC) and grape seed extract (GSE) in broiler chick diets on performance, intestinal morphology (jejunum), and ileal and cecal microflora at 21 d of age. Dietary treatments included an antibiotic-free diet (CTL-), a positive control (CTL+, 50 mg/kg of avoparcin), and an antibiotic-free diet containing GPC (60 g/kg) or GSE (7.2 g/kg). Each treatment was randomly assigned to 5 pen replicates (5 birds each). Jejunum histology was examined to determine the villi height, crypt depth, villi-height-to-crypt depth ratio, and muscularis layer thickness. Ileal and cecal contents were assayed for *Escherichia coli*, lactobacilli, enterococci, and *Clostridium perfringens*. Performance was not affected by dietary treatments except in the case of birds fed GSE diet which showed a decrease of weight gain. CTL- fed birds had longer villi and deeper crypt depth than birds in any other treatment group. The best villi height: crypt depth ratio corresponding to birds fed GPC diet and the worst to those fed CTL- diet. Muscularis layer thickness was not affected by dietary treatment except in the case of CTL- group which was reduced. In the ileal content, birds fed CTL- and GSE diets had the highest population of lactobacilli. Compared with the CTL- diet, the CTL+, GPC and GPS diets increased the populations of enterococci and decreased the counts of *C. perfringens* in the ileal content. There were no differences in the ileal population of *E. coli* among all dietary treatments. In the cecal digesta, birds fed GPC and GSE diets had a higher population of *E. coli*, lactobacilli, enterococci, and *C. perfringens* than in any other treatment group. Based on the results of the present study, it can be stated that dietary polyphenol-rich grape products modify the intestinal microflora and gut morphology in broiler chicks.

Key Words: chicks, grape pholyphenols, gut morphology and intestinal microflora

M275 Effects of hemp oil on the expression of FADS1, FADS2, and ELOVL5 in laying hens. M. Jing*, N. Gakhar, E. Goldberg, and J. D. House, *University of Manitoba*, *Winnipeg, Canada*.

Hemp seed and oil products are rich and balanced sources of omega-3 and omega-6 polyunsaturated fatty acids (PUFAs). Hemp contains about 17% α-linolenic acid (ALA) and 56% linoleic acid (LA), which are precursors for omega-3 and omega-6 PUFAs, respectively. In conjunction with studies designed to evaluate the transfer efficiency of dietary ALA to table eggs, the present study investigated the effects of dietary hemp oil (HO) inclusion on 3 principal biosynthetic genes involved in PUFA metabolism: FADS1 (Δ5 desaturase), FADS2 (Δ6 desaturase), and ELOVL5 (elongation of very long chain fatty acids protein 5). Bovan White laying hens (n = 8 per diet) received wheat-barley-soy-based diets containing 12% supplemental oil as either corn oil (CO; 0% HO), blend of 33:67 (4% HO) or 67:33 HO:CO (8% HO), or HO (12% HO), with a gradual decrease in the LA:ALA ratio as HO inclusion increased. The hens were fed over a period of 12 weeks. All the diets were formulated with equal protein and energy. Liver tissue was freshly harvested at the end of the experiment and used for RNA isolation. The mRNA expression profile of the 3 genes was assessed by semiquantitative real-time PCR. Results revealed that the mRNA levels of FADS1 were significantly reduced by 39.48% ($P < 0.05$) in hens fed the diet containing 12% of HO, and FADS2 mRNA was decreased by 45.18% and 51.32% ($P < 0.05$) in hens fed the diet containing 8% and 12% of HO in comparison with the basal diet, respectively. However, the expression of ELOVL5 was unaffected ($P > 0.05$) by the treatment of HO. Overall, this study demonstrates that 2 desaturase genes including FADS1 and FADS2 are downregulated by the supplementation of hemp oil in laying hen diets, and these changes may be related to the ratio of the prevailing dietary fatty acids.

Key Words: hemp oil, gene expression, laying hens

M276 Dietary supplementation effects of oregano essential oils on intestinal digest microbial community in broilers under high altitude conditions. L. Betancourt*[1,2], V. Phandanouvong[3], F. Rodriguez[3], C. Ariza-Nieto[3], M. Hume[4], D. Nisbet[4], and G. Afanador-Téllez[2], [1]*Universidad de La Salle*, *Bogotá, Colombia*, [2]*Universidad Nacional de Colombia*, *Bogotá, Colombia*, [3]*CORPOICA*, *Bogotá, Colombia*, [4]*USDA, ARS, FFSRU, College Station*, *TX*.

Microbiota impact broiler health and production. Essential oils have been shown to play a significant role in the modulation of gut microflora and the colonization of pathogenic bacteria. The aim of this study was to test the effect of oregano essential oils (OEO) on the microbial community on broiler chickens reared at high altitude. Seven hundred and fifty 1-d-old Hybro male broiler chicks, maintained at high altitude, were placed in 30 brooder cages under a completely randomized design. Six treatments

were evaluated: 200 ppm of OEO from 3 varieties produced and ground in Sabana of Bogota-Colombia 1) *O. vulgare* H. (OH); 2) *O. vulgare* L. (OL) and 3) *O. majorana* (OM); 4) 50 ppm of EO from O. vulgare H. ground in Greece (OG); 5) 500 ppm Chlortetracycline (AB) and 6) control (C). Template DNA was isolated from pooled duodenal, ileal, and cecal contents of 5 chickens in each group, respectively, and analyzed by denaturing gradient gel electrophoresis (DGGE). Dendrogram analysis of amplicon profiles from duodenum, ileum and cecal bacterial DNA revealed 2 main groups, OEO-treated chicks and non-treated control chicks at 14 and 35d. The highest similarity coefficient (CS), CS > 90%, was observed for OM and AB in jejunum (21d), ileum (3 and 21d), cecal (3, 7 and 21d) and colon (7 and 21d). OM and AB presented the highest body weight at 21d. Comparison of bacterial DNA profiles from different gut compartments revealed diverse bacterial populations between duodenum, jejunum and ileum compared with cecal and colon. The results suggest that digestive microbial populations of these broilers from the Sabana of Bogotá (2650 AMSL) can be altered by addition of OEO in the diet. *O. majorana* essential oil was associated with increased body weight gain. A possible association was observed between the bacterial DNA profile of the intestine and body weight of broilers.

Key Words: DGGE, DNA bacterial, gut

Physiology and Endocrinology: Nutritional Effects on Reproduction and Development

M277 Effects of body weight loss on serum progesterone concentrations of non-lactating dairy cows. R. Rodrigues*[1], C. Trevisanuto[1], T. Leiva[1], M. Barbosa[1], R. Cooke[2], and J. Luiz Vasconcelos[1], [1]*FMVZ - UNESP*, *Botucatu, SP, Brazil*, [2]*Oregon State University*, *Burns*.

The objective of this study was to evaluate serum concentrations of nonesterified fatty acids (NEFA), cortisol, insulin, and progesterone (P4) of dairy cows maintaining or mobilizing body weight (BW). Eleven non-lactating, non-pregnant, and ovariectomized Gir × Holstein cows were stratified by BW and body condition score (BCS), and randomly assigned to one of 2 treatments on d −7 of the study: 1) BW loss (6 cows; LOSS) and 2) BW maintenance (5 cows; MAINT). Treatments were achieved through a grazing schedule utilizing 3 different pastures (A, B, and C). From d −7 to d 1 of the study, all cows were maintained in pasture A (adequate forage availability; 12 kg of dry matter/cow daily). From d 2 to d 30, LOSS cows were maintained in pasture B (minimal forage availability; less than 1.0 kg of dry matter/cow daily), whereas MAINT cows were maintained in pasture C (adequate forage availability; 12 kg of dry matter/cow daily). From d 3 to d 30 of the study, cows from both treatments were re-grouped daily into pasture A from 0600 to 1200 h to allow LOSS cows to consume, on average, 4.5 kg/d of forage dry matter. From d −66 to d 3 of the study, all cows were inserted with CIDR to promote P4 uptake by adipose tissues, which was replaced every 14 d and removed on d 3. Cow BW and BCS were assessed on d 0 and 30. Blood samples were collected daily, from d 0 to d 30, at 0600 and 1200 h. Changes in BW and BCS were greater in LOSS cows compared with MAINT cows (−0.95 vs. −0.07 kg of BW/d, SEM = 0.216; −0.30 vs. 0.00 of BCS change, SEM = 0.092). Within samples collected at 0600 h, serum NEFA concentrations were greater in LOSS cows compared with MAINT. Similarly, serum P4 concentrations were typically greater in LOSS cows compared with MAINT. Serum cortisol concentrations were also greater for LOSS compared with MAINT cows, but only on d 6, 28, and 29 of the study. In conclusion, data from this study indicates that BW loss increases circulating concentrations of P4 in non-lactating ovariectomized dairy cows, and this outcome can be mainly attributed to fat mobilization and consequent release of P4 stored in adipose tissues.

Key Words: adipose tissues, progesterone, weight loss

M278 Effects of maternal metabolizable protein supplementation in late gestation on uterine and umbilical blood flows in sheep. L. E. Camacho*[1], L. A. Lekatz[1], M. L. VanEnom[2], C. S. Schauer[2], K. R. Maddock Carlin[1], and K. A. Vonnahme[1], [1]*Center for Nutrition and Pregnancy, Department of Animal Sciences, North Dakota State University*, *Fargo,* [2]*Hettinger Research Extension Center, North Dakota State University*, *Hettinger*.

To examine effects of maternal MP supplementation in late gestation on uterine and umbilical blood flows, multiparous ewes (n = 11) were assigned to receive either 75% (LOW, n = 4), 100% (CON, n = 4), or 125% (HIGH, n = 3) of MP requirements from d 100 until d 130. At surgery on d 130, uterine blood flow was measured by Transonic Doppler flow probes and umbilical blood flow was measured using color-Doppler US. Throughout surgery, maternal blood pressure was monitored. After determination of blood flow, fetal and placental tissue were collected and weighed. Data were analyzed with PROC GLM and means separated with LSMeans. Data were considered significant if ($P < 0.05$. Fetuses from HIGH ewes were heavier ($P \leq 0.04$) than fetuses from LOW ewes with fetuses from CON ewes being intermediate. Total placental wt was not different ($P = 0.41$) among treatments. Uterine blood flow had a tendency ($P = 0.07$) to be greater in the LOW group compare with HIGH (818.0 vs. 447.3 ± 105.3 mL/min) with CON being intermediate. Uterine blood flow per fetus wt was increased ($P < 0.02$) in LOW ewes compare with CON and HIGH (0.42 vs. 0.22 and 0.12 ± 0.07 mL/min/g). Umbilical blood flow per fetus wt was not affected ($P = 0.14$; 0.20, 0.14, and 0.08 ± 0.04 mL/min/g for LOW, CON, and HIGH, respectively) by MP supplementation. Maternal blood pressure did not differ ($P = 0.19$) among groups. However, unprotected LSD means (used only in blood pressure analysis) showed that LOW ewes had increased ($P \leq 0.01$; 150.5 ± 13.5 mmHg) blood pressure compared with HIGH (113.6 ± 11.0 mmHg) and CON (124.8 ± 11.0 mmHg). Factors influencing uteroplacental blood flow appear to be associated with maternal MP intake and have yet to be determined.

Key Words: metabolizable protein, umbilical blood flow, uterine blood flow

M279 Effects of maternal protein supply on offspring somatotropic axis: Serum IGF-binding proteins-2 and -3 in pigs at weaning and market weight. A. Ooster*[1], U. Müller[1], H. Sauerwein[1], I. Lang[2], M. Peters[2], C. Rehfeldt[2], and C. C. Metges[2], [1]*University of Bonn*, *Bonn, Germany*, [2]*Leibniz Institute for Farm Animal Biology*, *Dummerstorf, Germany*.

Fetal growth is reflected in size at birth possibly associated with postnatal metabolic function and health. The GH/IGF axis is affected by intrauterine growth retardation and might be permanently readjusted. We aimed to characterize the plasma concentrations of IGF binding proteins (IGFBP) 2 and 3 in offspring of gilts fed with diets differing in protein content. Isoenergetic diets with low, adequate or high CP contents (6, 12 or 30%) were fed to a total of 40 gilts throughout pregnancy. At birth the piglets were cross fostered to nursing sows fed a 12% CP gestation diet and then a standard lactation diet. From weaning (d 28) to slaughter (d 185) offspring received standard fattening diets. Serum collected at d 28 and 185 from 144 piglets was assessed for IGFBP using a non-radioactive Western ligand blotting protocol optimized to yield quantitative data. The chemiluminescence signals were densitometrically evaluated and the bands corresponding to IGFBP-2 and -3 were compared. Maternal feeding group, sex, litter size and weight at birth classes and the respective interactions were considered fixed. Values were compared by t-test at d 28 and 185. At d 28 and 185, IGFBP-3 was not affected by either factor tested. For IGFBP-2, there were trends for feeding group and birth weight differences ($P = 0.093$ and 0.057, respectively) on d 28, without any interactions. Piglets from sows fed 6% CP had less IGFBP-2 than those from the 12% diet ($P = 0.037$). At d 185, IGFBP-2 was not affected by either factor tested. IGFBP-3 increased ($P < 0.05$) from d 28 to 185 in all groups, whereas IGFBP-2 was decreased ($P < 0.05$) solely in pigs from sows fed at 12% but remained unchanged in offspring from sows fed at 6 or 30% protein. Carry-over effects of maternal feeding during gestation on offspring IGFBP-2 resulting in divergent concentrations at weaning and in altered patterns of age-related changes are thus indicated.

Key Words: somatotropic axis, IGFBP, pig

M280 The impact of maternal obesity on offspring hypothalamic-pituitary-adrenal axis response to stress. N. M Long*[1], A. B. Uthlaut[1], P. W. Nathanielsz[2], and S. P. Ford[1], [1]*Center for the Study of Fetal Programming, Animal Science Department*, *University of Wyoming, Laramie,* [2]*Center for Pregnancy and Newborn Research, Department of Obstetrics and Gynecology*, *University of Texas Health Sciences Center, San Antonio*.

Multiparous Ramboullet × Columbia crossbred ewes were fed either 100% of NRC recommendations (Control, C) or 150% of NRC (Obese, OB) from d 60 d before mating until lambing. Lambs born to these dams (10 OB, 5 wethers, 5 ewes: and 8 C, 3 wethers and 5 ewes) were maintained as a group before and after weaning and fed a similar diet until 19 mo of age when they received jugular catheters and were subjected to a corticotrophin releasing hormone (CRH)/arginine vasopressin (AVP) challenge, an ACTH challenge, and an isolation stress test, on separate occasions. ACTH and cortisol responses to the isolation stress test and CRH/AVP challenge and cortisol responses to ACTH challenge were determined. Cortisol was quantified via RIA and ACTH was quantified using an Immulite 1000. Hormone data were analyzed using repeated measures analysis utilizing the MIXED procedure of SAS. Offspring from OB mothers tended ($P = 0.06$) to have a greater ACTH response after an intravenous CRH/AVP injection than offspring from C mothers (1234 ± 143 vs. 817 ± 157 pg/mL, respectively). The cortisol response of offspring to a CRH/AVP or ACTH challenge was not influenced by maternal nutrition ($P < 0.46$), and averaged 4.77 ± 0.2 and 1.94 ± 0.01 µg/dL. The ACTH response following the isolation stress test was also similar ($P = 0.82$) for OB and C offspring (147 ± 20 pg/ml). Cortisol response during the isolation stress test was also similar between C and OB offspring ($P = 0.64$, 5.25 ± 0.3 µg/dl).These findings suggest that maternal obesity before and during gestation does not affect stress responses by the offspring, but has an impact on hypothalamo-pituitary-adrenal sensitivity. The lack of differences in cortisol release under the influence of difference concentrations of ACTH during the CRH/AVP challenge could indicate adrenal dysfunction in OB offspring.

Key Words: maternal obesity, offspring, stress response

M281 Effects of two-stage and total vs. fenceline weaning on the physiology and performance of beef calves. C. Campistol*[1], H. G. Kattesh[1], J. C. Waller[1], E. L. Rawls[1], J. D. Arthington[2], T. E. Engle[3], and J. A. Carroll[4], [1]*University of Tennessee*, *Knoxville,* [2]*University of Florida - IFAS, Range Cattle Research and Education Center*, *Ona,* [3]*Colorado State University*, *Fort Collins,* [4]*Livestock Issues Research Unit, USDA-ARS*, *Lubbock, TX.*

Calves weaned using a 2-stage method, where nursing is prevented between cow-calf pairs before separation (Stage 1), experience less weaning stress after separation (Stage 2) based on behavior and growth measures. The aim of this study was to document changes in various physiological measures of stress in calves weaned using the 2-stage with total separation or temporary fenceline contact. Steer calves (n = 48; 314.1 ± 20.5 kg), housed on pasture with their dams, were blocked by initial BW and assigned randomly during Stage 1 to be fitted with a nose-flap weaning device (YD) or no device (ND) for 7 d preweaning. During Stage 2, calves (12 YD and 12 ND/group) were weaned by fenceline (Group 1) or total separation to a distant pasture (Group 2). After 7 d, Group 1 calves were moved to a pasture lot adjoining Group 2. Calves were weighed and bled on d −7, 0, 3, 7 (d of weaning), 10, 14, 21, and 42, and injected with ovalbumin on d 0. Blood was analyzed for total cortisol, IgG to ovalbumin, interferon-gamma (IFN-γ), haptoglobin (HAP), ceruloplasmin (CER), hematocrit (Hct), and neutrophil:lymphocyte ratio (N:L). Weight gain was similar ($P = 0.74$) among steers regardless of Stage 1 treatment. The YD calves had higher ($P < 0.05$) Hct than ND calves during Stage 1. Weight gain was greater ($P < 0.01$) in Group 1 versus Group 2 on d 14–42. Ovalbumin-specific IgG increased ($P < 0.01$) in all calves by d 10 unrelated to Stage. Both HAP and CER increased ($P < 0.01$) by d 3 in response to ovalbumin. Between d 7 and 10, CER, IFN-γ, and N:L increased ($P < 0.05$) in ND but not YD calves. In conclusion, 2-stage weaning may improve calf well-being when fenceline separation is employed.

Key Words: beef cattle, two-stage weaning, stress

M282 Effects of dietary n-3 fatty acids on timing of estrus onset and LH surge in synchronized estrous cycles of dairy cows. M. Zachut*[1,2], H. Lehrer[1], A. Arieli[2], L. Livshitz[1], and U. Moallem[1], [1]*Agriculture Research Organization*, *Bet Dagan, Israel*, [2]*Faculty of Agriculture, Hebrew University*, *Rehovot, Israel*.

In a previous study conducted in our lab we observed a delay in behavioral-estrus manifestation in cows fed flaxseed, which contained a high proportion of 18:3n-3. The objectives were to examine the effect of dietary extruded flaxseed (EF) on the interval between $PGF_{2\alpha}$ injection and LH surge in synchronized estrous cycles. Multiparous Israeli-Holstein dry cows (256 d pregnant) were assigned to 2 treatments (i) control (n = 22) were fed a dry cow diet and postpartum (PP) lactating cow diet, which consisted of 5.8% ether extracts and (ii) EF (n = 22) supplemented prepartum with 1 kg/d per cow of EF providing 141 g/d of 18:3n-3, and PP to 100 d in milk (DIM) a diet consisted of 9.2% EF providing on average 382 g/d of 18:3n-3. At 40 DIM ovaries were monitored by ultrasound to ensure normal cyclicity. Cows received a GnRH analog injection at d 0, and 7 d later were monitored by ultrasound for corpus luteum (CL) presence. Cows that had CL were injected with $PGF_{2\alpha}$ (d 7) followed 2 d later (d 9) by GnRH injection. Seven d later (d 16) cows were injected with $PGF_{2\alpha}$ to stimulate luteolysis and 5-d period of intensive follow-up was conducted. Cows were observed continuously (24 h a day) for onset of behavioral-estrus signs and thereafter blood samples were taken every 3 h during 24 h for LH detection. A total of 38 successful estrous cycles (16 controls and 22 EF) were obtained in 2 sessions. Interval from $PGF_{2\alpha}$ injection to behavioral-estrus onset was not significantly different (57.3 and 59.4 h for control and EF, respectively). LH peak in the controls occurred on average 5.8 h after estrus-onset, as compared with 7.6 h in the EF ($P < 0.03$). Interval from $PGF_{2\alpha}$ injection to LH peak tended to be longer in the EF than in controls (67.0 and 62.1 h, respectively; $P < 0.07$). These results imply that dietary n-3 fatty acids may delay timing of LH peak, perhaps due to changes in the secretion of prostaglandins E_2 that are involved in ovulation control.

Key Words: omega-3, LH surge

M283 The effects of ancient Mediterranean aphrodisiac capari (*Capparis ovata* Desf.) on some reproductive parameters of Lohmann roosters. A. Ata, M. S. Gulay*, and O. Yildiz-Gulay, *Mehmet Akif Ersoy University, Faculty of Veterinary Medicine*, *Burdur, Turkey*.

The focus of this research was to determine the effects of dietary supplementation of capari on some spermatological parameters in Lohmann roosters. Twenty-four week old roosters were randomly assigned to control and capari treatment groups (8 per group) and fed a standard diet. Roosters in control group received 10 mL of tap water, whereas roosters in treatment group received 1 g/kg of caper in 10cc tap water daily by oral gavages for 39 d (3 spermatogenesis duration). Semen was collected from each rooster by abdominal massages weekly and sperm analyses were performed on individual semen samples collected

39 d after introduction to capari. There were no difference between control and caper treated roosters on semen volume (44.3 ± 13.4 vs. 62.8 ± 11.3 μL), semen pH (8.24 ± 0.11 vs. 8.25 ± 0.14), percent morphologically normal sperm (89.2 ± 3.0 vs. 92.3 ± 2.7%), percent live spermatozoa by eosin-nigrosine staining mixture (87.4 ± 1.3 vs. 88.3 ± 1.3%), respectively. On the other hand, daily caper treatment increased the progressive motility (85.0 ± 0.84 vs. 87.6 ± 0.70%, $P < 0.04$) and sperm concentration (3.78 ± 0.59 vs. 5.45 ± 0.41 × 10^9 mL, $P < 0.04$). The results indicated that there is a merit to use dietary supplementation of capari to improve spermatological performance of roosters.

Key Words: caper, rooster, spermatological parameters

M284 Blood urea nitrogen and nonesterified fatty acid concentrations in the umbilical blood of fetal pigs at day 90 and 110 of gestation. T. A. Wilmoth*, C. O. Lemley, and M. E. Wilson, *West Virginia University*, *Morgantown*.

Speculation as to why fetal size variation occurs has led to the investigation of placental efficiency and function. Unequal nutrient delivery and usage by the fetus can be a result of fetal or placental inefficiency. Measuring the metabolites of nutrient degradation such as blood urea nitrogen (BUN) and nonesterified fatty acids (NEFA) may give insight to placental and fetal usage of these nutrients. The objective of this study was to determine the concentrations of BUN and NEFA in arterial and venous umbilical blood of fetuses at d 90 and 110 of gestation. Gilts (n = 13) were randomly assigned to be ovariohysterectomized on d 90 or 110 of gestation at the time of breeding. Arterial and venous umbilical blood samples were collected for the determination of BUN and NEFA. Tissue sections were fixed in paraffin for the determination of placental and endometrial vascular densities. Placental efficiency (fetal weight divided by placental weight) was determined for each fetus. Means and correlation coefficients were determined using the correlation procedure of SAS. On d 90 of gestation, arterial BUN concentrations were 198.7 mg/mL, while venous BUN concentrations were 212.2 mg/mL. Arterial and venous NEFA concentrations were 0.24 mg/mL. A trend for a negative correlation between placental efficiency and the arterial venous difference (A-V) in BUN existed ($r = -0.34$, $P < 0.1$). On d 110, arterial and venous BUN were 242.6 mg/mL and 128.6 mg/mL, respectively. Arterial NEFA was 0.23 mg/mL and venous NEFA was 0.18 mg/mL. A positive correlation between endometrial vascular density and placental efficiency existed ($r = 0.28$, $P < 0.05$). A negative correlation existed between placental vascular density and the A-V difference in BUN ($r = -0.35$, $P < 0.05$). The change in metabolites being delivered to and returning from the placenta changes between d 90 and 110 of gestation suggesting that there is an increased amino acid catabolism by the fetus at d 110 of gestation and a greater removal of urea from fetal circulation at d 110.

Key Words: placental efficiency, blood urea nitrogen, nonesterified fatty acids

M285 Effect of dry period lengths on follicular dynamics in early lactation Holstein cows. A. Soleimani*[1,2], A. Heravi Moussavi[2], M. Danesh[2], G. Golian[2], and S. Safa[2], [1]*Islamic Azad University-Kashmar Branch*, *Kashmar, Khorasan Razavi, Iran*, [2]*Ferdowsi University of Mashhad*, *Mashhad, Khorasan Razavi, Iran*.

The study was designed to test the effects of dry period lengths on follicular dynamics parameters during the subsequent lactation in Holstein cows. Cows (n = 42) were randomly assigned in 1 of 3 treatments: 1) traditional 60 d dry period (DP) (n = 14), 2) 35 d DP (n = 15) and 3) 20 d DP. Holstein cows were blocked in pairs based on their previous 305 d milk, parity, and expected calving dates. All cows were fed by routine ration of farm (total mixed diet) twice a day and had at all time free access to water. To monitor follicular parameters, ultrasound measurements of follicular activity were made on alternate days from d 10 to 35 postpartum to determine the characteristics and fate of the 1st follicular wave. The data were analyzed using the General Linear Model (GLM) for a completely randomized design. Number of follicles (≥5 mm in diameter) on d 10 and 14 postpartum were similar among the groups. Length of dry period had no effect on days postpartum to first ovulation ($P = 0.91$; 24.69 ± 2.2, 24.07 ± 2.2, and 23.27 ± 2.4 d, respectively), number of days until detection of a follicle ≥10 mm in diameter ($P = 0.42$; 11.53 ± 1.0, 11.64 ± 0.9, and 13.23 ± 1.0 d, respectively), diameter of the largest follicle at first ultrasound ($P = 0.92$; 10.8 ± 0.91, 10.46 ± 0.8, and 13.11 ± 0.9 mm, respectively), and also days open ($P = 0.88$; 170.25 ± 25.8, 159.10 ± 28.3, and 178.72 ± 27.0 d, respectively). Diameter of the first dominant follicle ($P < 0.05$; 18.76 ± 1.1, 19.80 ± 1.1, and 14.46 ± 1.1 mm, respectively) and diameter of the dominant follicle on d 14 ($P < 0.05$; 13.65 ± 0.8, 12.96 ± 0.7, and 9.95 ± 0.8 mm, respectively) were different among the groups. Results from this experiment demonstrated that dry period length had no apparent effect on most follicular dynamics parameters and days open during the subsequent lactation. Meanwhile, a short dry period reduced the diameter of dominant follicle.

Key Words: dairy cows, dry period, follicular dynamic

M286 The application of TARGET bovine CL progesterone test kit for early pregnancy diagnosis in ewes. W. Chen*, T. Wuliji, H. Wang, N. Li, and A. Qi, *Animal Biotechnology, University of Nevada-Reno*, *Reno*.

The objective of the experiment was to identify the applicability of TARGET Bovine CL progesterone test kit (TARGET) for early pregnancy diagnosis in ewes. TARGET is a commercial test kit to identify pregnant cows from non-pregnant cows in field. When the blood or milk sample progesterone level is high, the test kit shows a white color and the cow is diagnosed as pregnant, and the dark blue color indicates non-pregnant, whereas the light blue or faint blue indicates that there is no definite diagnosis, so a second test is required. Three other methods were applied to verify the accuracy of TARGET. They are ELISA analysis of the blood progesterone level, ultrasound scanning for the pregnancy diagnosis, and the lambing record. 82 ewes were assigned in a spring breeding flock, of which 52 ewes with the TARGET test, while 30 ewes were assigned with non-TARGET test group. Blood samples were collected from ewes on 20d of post-breeding and the serum samples were used for the TARGET test and the ELISA analysis. Sample color grade readings were assigned to the standard color grade chart provided by TARGET. Ultrasound scanning diagnosis was conducted on 50d of post-breeding. TARGET color grade readings, ELISA analysis, ultrasound scanning results, and lambing records were analyzed by the CORR procedure of SAS program. The correlation coefficients between ELISA analysis and Ultrasound scanning diagnosis was the highest as 0.89 ($P < 0.001$) when the serum progesterone level was 2ng/ml or higher. Therefore, this level is defined as the threshold for the status of pregnancy. Six possible color grades recombination within 4 color grades were evaluated. The correlation analysis was conducted with the results obtained from all 4 procedures. The combination of the color indicator with the TARGET kit standard chart showed the highest correlation ($P < 0.01$) with ELISA progesterone level, ultrasound scanning diagnosis, and lambing record which are 0.85, 0.89, and 0.62, respectively (Table 1). Therefore, the bovine TARGET test kit is applicable to the early pregnancy diagnosis in ewes with a high degree of accuracy.

Table 1. Correlation coefficients of TARGET kit color grade assignments for pregnancy diagnosis with three other pregnancy diagnostic methods

Groups	Pregnant	Unassigned	Non-Pregnant	ELISA	Ultrasound	Lambing Record
A	1	2,3	4	0.85**	0.89**	0.62**
B	1,2	3	4	0.75**	0.81**	0.56**
C	1,2,3	–	4	0.56**	0.64**	0.44**
D	1	2	3,4	0.74**	0.77**	0.55*
E	1	–	2,3,4	0.45**	0.42**	0.28**
F	1,2	–	3,4	0.65**	0.69**	0.49**

1 = white, 2 = light blue, 3 = faint blue, 4 = dark blue; $^{**}P < 0.01$, $^{*}P < 0.05$.

Key Words: progesterone, pregnancy, ewes

M287 Endocrine events during the periestrus period and the effect of various PMSG on estrus synchronization in shall ewes. T. Saberifar, H. Kohram*, and E. Dirandeh, *University of Tehran*, *Karaj, Tehran, Iran*.

The aim of the present study was to investigate the endocrinology of periestrus period and the days after until estrus in ewes (n = 40) synchronized out of breeding season and diagnosing the related pregnancies after laparoscopic insemination comparing to different doses of PMSG that was used. Animals treated for 12 d with CIDR followed by administration with different doses (0, 450, 550, 650, 750, 850 IU) of PMSG after CIDR withdrawal. Number of ewes in each group was 7 except for control group that was 5. 48 h after CIDR removal, ewes were inseminated by frozen semen using laparoscopy method. Blood samples were collected once daily from the jugular vein into heparinized tubes beginning at day CIDR removal until the day of estrus. Plasma was harvested and stored at −20°C until progesterone or estradiol assay. Concentrations of progesterone (Progesterone RIA, Biosource, Belgium) and estradiol (estradiol RIA, Biosource, Belgium) were determined. Pregnancies were diagnosed using ultrasonography at d 30 following insemination in ewes. Progesterone levels did not differ between groups during periestrus period. Estradiol levels also did not differ between groups during the days CIDR removal and one day later. However, estradiol levels in the control group comparing to groups 550 and 850 was significantly lower and higher (control: 12.14 pg/mL, 550:19.91 pg/mL, 850:8.98 pg/mL) at estrus, respectively. Pregnancy diagnosing showed that, the number of nonpregnant ewes was lower in group 550 and higher in group 850 comparing to control group (control:3, 550:0, 850:4). The result of this study demonstrated that 550 IU PMSG would be the best dose to increase the plasma estradiol at the onset of estrus and also for synchronizing Shall ewes out of breeding season and have the best lambing rate in this breed.

Key Words: periestrus period, PMSG, shall ewes

M288 Reproductive endocrine profile in ewes with different thickness of dorsal fat added with bypass fat. R. Nieto[1], T. Sánchez[1], O. Mejía[2], L. Olivares[3], J. Peralta[4], J. Cordero[1], P. Molina[1], M. Cárdenas[5], E. García*[6], and N. Cedillo[4], [1]*Colegio de Postgraduados*, *Montecillo, Edo. de México*, [2]*CEIEPO, FMVZ. UNAM*, *Tres Marías México*, [3]*Universidad Autónoma del Edo. de México*, *Edo. de México*, [4]*Universidad Autónoma del Edo. de Hidalgo*, *Tulancingo, México*, [5]*INNSZ*, *Mexico City, México*, [6]*CUCSur, Universidad de Guadalajara*, *Autlán, Jalisco, México*.

To determine the effect of bypass fat in serum concentrations of luteinizing hormone (LH), estradiol (E2), progesterone (P4) and insulin (INS) during 7d before removal of intravaginal sponges in Dorset ewes, ewes (n = 59) were classified by thickness of dorsal fat by ultrasonography with a 7.5-MHz transducer. Ewes with low (LDF, 2mm) and high (HDF, 4mm) thickness dorsal fat were subdivided in groups: Low thickness without (LDF0, n = 14) and with (LDF1, n = 14) the addition of 150 g of bypass fat; High thickness without (HDF0, n = 15) and with (HDF1, n = 16) the addition of 150 g of bypass fat, respectively. Estrous cycles were synchronized with sponges of flugesterone acetate (FGA, 20 mg), for 12 d, 10 d after insertion 15 mg of prostaglandins (PGF2α) were injected. LH was analyzed by PROC GLM and means by Tukey; P4, E2 and INS by PROC MIXED and mean values by least squares means (SAS). There were no differences ($P \geq 0.05$) by addition of fat, in onset, duration, and LH preovulatory peak, however, amplitude of LH preovulatory peak was different among treatments ($P \leq 0.05$). P4 concentration was higher in ewes without addition of fat compared with the added group ($P \leq 0.05$, 2.74 ± 0.2 vs. 2.58 ± 0.2 ng mL^{-1}). E2 and INS concentrations increased in ewes with HDF compared with LDF group ($P \leq 0.05$, 15.4 ± 11.8 pg mL^{-1}; 0.37 ± 0.02 ng mL^{-1} vs. 5.1 ± 11.8 pg mL^{-1}, 0.25 ± 0.02 ng mL^{-1}, respectively). It is concluded that the addition of bypass fat did not alter onset and duration of LH preovulatory peak, but decreased P4 concentration probably due to an early secretion of PGF2α, nevertheless, E2 and INS concentrations increased in ewes with HDF, which is attributed to an improved metabolic, nutritional and body animal status.

Key Words: ultrasonography, hormones, synchronized estrus.

M289 Effects of human chorionic gonadotropin on serum progesterone concentrations, embryonic survival and lambing rates in ewes. L. M. Lankford*[1], D. T. Yates[2], R. A. Halalsheh[1], P. L. Black[1], D. M. Hallford[1], and T. T. Ross[1], [1]*New Mexico State University*, *Las Cruces,* [2]*University of Arizona*, *Tucson*.

This study was conducted to determine if multiple injections of human chorionic gonadotropin (hCG) will increase circulating concentrations of progesterone (P4) in sheep following mating and prolong elevated levels through the period of fetal attachment. Fifty-nine nulliparous, primiparous, and multiparous Suffolk ewes (avg BW = 79.7 ± 2.5 kg) received an intravaginal P4-containing insert (CIDR, 0.3 g P4) for 12 d and were mated with fertile rams on the second estrus after CIDR removal. Ewes were randomly assigned to one of 2 treatments. The treated group received 200 IU (0.4mL) of hCG im and controls received 0.4 mL saline im on d 4, 7, and 10, after onset of estrus (d 0; mating). Blood samples were taken via jugular venipuncture beginning on d 0 and on alternate days until d 35. Serum P4 concentrations were similar ($P > 0.10$) between treatment groups through d 5. However, beginning on d 7, ewes treated with hCG had greater ($P < 0.01$) serum P4 concentration than controls, and P4 remained higher ($P < 0.05$) throughout the sampling period (d 35). Of ewes receiving hCG, 68% had 4 or more total CL present compared with 33% for controls ($P < 0.05$; determined by laparoscopy on d 25). Fetal numbers were determined via flank ultrasound on d 60 and 85% of hCG-treated ewes had multiple fetuses compared with 62% of controls ($P < 0.10$). In addition, 82% of hCG-treated ewes gave birth to 2 or more lambs compared with 63% of control ewes ($P = 0.17$). In conclusion, hCG administration on d 4, 7, and 10 after mating resulted in elevated serum P4 concentrations from d 7 through d 35, with more ewes carrying multiple fetuses.

Key Words: hCG, progesterone, lamb crop

M290 Administration of genistein does not alter anterior pituitary concentrations of LH and IGF-I in ovariectomized gilts. C. Paulson*, A. Taylor, and J. Clapper, *South Dakota State University*, *Brookings*.

Previously we have shown that administration of genistein to barrows increases anterior pituitary (AP) concentrations of IGF-I and LH and increased expression of AP IGF receptor. However, whether similar changes occur in ovariectomized gilts remains to be determined. Therefore, the objective of this experiment was to determine if short-term administration of genistein alters serum and anterior pituitary (AP) concentrations of LH and IGF-I and expression of AP GnRH receptors and LHβ subunit. Sixteen cross bred gilts of similar weight (95.5 kg)

were ovariectomized and assigned to either control (C; n = 8) or genistein (G; n = 8) groups. G pigs received 8oo mg of genistein in DMSO while C pigs received an equal volume of DMSO i.m. on d 0, 1, 2, and 3. Blood samples were obtained by jugular venipuncture on d 0, 1, 2, and 3. Pigs were slaughtered on d 4 when blood and AP were collected. Serum and AP concentrations of LH and IGF-I were determined in duplicate by RIA. Relative expression of GnRH receptor and LHβ subunit were determined by real time RT-PCR, and fold changes analyzed using the REST software. Differences in serum and AP concentrations of LH and IGF-I were determined using the Proc Mixed procedure of SAS. Serum concentrations of LH were not different ($P > 0.05$) in G pigs compared with C pigs on d 0, 1, 2, 3 and 4. Serum concentrations of IGF-I were not different ($P > 0.05$) between C and G pigs on d 0 through d 4. AP concentrations of LH and IGF-I did not differ ($P > 0.05$) between C and G pigs. Relative expression of LHβ subunit and GnRH receptor did not differ ($P > 0.05$) between C and G pigs. These preliminary data suggest that short-term administration of genistein does not increase serum and AP concentrations of LH or IGF-I, or expression of GnRH receptors and LHβ subunit in the ovariectomized gilt.

Key Words: genistein, IGF, pigs

M291 Changes in plasma concentrations of growth hormone and luteinizing hormone in ewes following central and peripheral treatment with kisspeptin. B. K. Whitlock*[1], J. A. Daniel[2], B. P. Steele[3], and J. L. Sartin[3,4], [1]*Department of Large Animal Clinical Sciences, College of Veterinary Medicine, The University of Tennessee*, *Knoxville,* [2]*Department of Animal Science, Berry College*, *Mt. Berry, GA,* [3]*Department of Anatomy, Physiology and Pharmacology, College of Veterianry Medicine, Auburn University*, *Auburn, AL*, [4]*Agricultural Experiment Station, Auburn University*, *Auburn, AL*.

Kisspeptin (KP), a neuroendocrine regulator of gonadotropin releasing hormone, has been hypothesized as an integrator of nutrition and hormones critical to metabolism and regulation of reproduction. Recent evidence suggests growth hormone (GH) secretion may be influenced by KP. The objective of this study was to determine if the GH stimulatory effect of KP is due to actions on the hypothalamus or anterior pituitary gland in ewes. Adult ovariectomized ewes (n = 8) were fitted with intracerebroventricular (ICV) cannula to facilitate central administration of experimental treatments. Ewes received one of 8 treatments [4 intravenously (IV) and 4 ICV]. Peripheral treatments [0 (Veh), 100, 200, or 1000 pmol/kg body weight (BW) KP-10 (human KP 45–54; 4389-v, Peptide Institute, Inc., Osaka, Japan) in saline] were administered as a bolus via jugular cannula and ICV treatments [Veh, 50, 100, or 200 pmol/kg BW KP-10] were administered via the ICV cannula. Blood samples were collected from a jugular cannula at −15, 0, 10, 20, 30, 45, 60, and 75 min relative to treatments. Experiments were repeated until all ewes received each treatment. Plasma GH and luteinizing hormone (LH) concentrations were determined by radioimmunoassay. Effects of treatment on plasma concentrations of LH and GH were tested using procedures for repeated measures (SAS Institute Inc., Cary, NC). The 200 and 1000 pmol/kg IV KP-10 increased ($P < 0.05$) plasma concentrations of LH. However, there was no effect of IV KP-10 on plasma GH. Conversely, 100 and 200 pmol/kg KP-10 administered ICV increased ($P < 0.05$) plasma GH concentrations. Maximum GH responses occurred 30 min following ICV KP-10 injection and were greater ($P < 0.05$) than both Veh and the 50 pg/ml KP-10 ICV. In addition to activating the gonadotropic axis, KP can activate the somatotropic axis in ruminants and present data support a central site of action.

Key Words: sheep, kisspeptin, growth hormone

M292 Temporal changes during the periparturient period on metabolic and endocrine parameters of spring-calving beef cows in grazing conditions. A. L. Astessiano*[1], R. Pérez-Clariget[1], G. Quintans[2], P. Soca[1], and M. Carriquiry[1], [1]*School of Agronomy, UdelaR*, *Uruguay*, [2]*Instituto Nacional de Investigación Agroprcuaria*, *Treinta y Tres, Uruguay*.

Primiparous crossbred cows (Hereford/Angus, n = 20), classifiedby BCS at calving (scale 1-8), were used in a randomizedblock design, to study temporal changes on metabolic andendocrine parameters during the peripartum in grazingconditions. Cows grazed together a native pasture paddock (60 ha) with an average forage mass available of 453 kg DM/ha (13.2% CP, 24.4% ADF). Means from repeated measure analyses were considered to differ when $P<0.05$. Cow BCS throughout the period evaluated was greater for BCS >3.75 than BCS ≤3.5 calved cows. Concentrations of NEFA were affected ($P < 0.01$) by day postpartum (DPP) as NEFA were elevated at −45 DPP, peaked at −7 DPP and were reduced thereafter for all cows. However, NEFA levels were less from −45 to −15 DPP but greater at −7 DPP for BCS >3.75 than BCS ≤3.5 calved cows, while no differences between groups were observed during the postpartum. Glucose, urea, and total protein concentrations were affected ($P < 0.01$) by DPP and there was an interaction ($P < 0.03$) between BCS at calving and DPP for urea and total protein levels. Glucose concentrations tended ($P = 0.07$) to decrease from −7to 30 DPP while urea concentrations were elevated at −45DPP, peaked at −7 DPP and decreased thereafter. However, changes in urea were steep around parturition for BCS >3.75 but not for BCS ≤3.5 calved cows. Total protein concentrations were elevated during the last month of gestation, decreased at parturition and remained reduced until 45 DPP. Cows with BCS >3.75 at calving had greater total protein at −15 DPP but less around parturition than cows with BCS ≤3.5. There were no differences in circulatinginsulin levels along the period evaluated, however, insulinwas less for BCS >3.75 than BCS ≤3.5 calved cows dueto a drastic increase of insulin levels after 15 DPP in the lastones. Metabolic and endocrine parameters reflected the negative energy balance during the prepartum of cows grazing native pastures in winter.

Key Words: peripartum, metabolites, cattle

M293 Metabolic measurements in the sow and relationship to post-weaning reproductive performance. L. A. Rempel*, J. L. Vallet, and D. J. Nonneman, *USDA, ARS, USMARC*, *Clay Center, NE*.

Extreme weight (wt) loss during lactation is an indicator ofcatabolism in exchange for maintaining metabolic output andcan have adverse effects on reproductive parameters. Creatine is a nonprotein nitrogen that acts as a phosphagen and aids in tissue repair. Creatine may be indicative of a sow's ability to support offspring as well as the postpartum uterus. Our objective was to establish creatine and body condition measurements at periods of physiological changes due to parturition and lactation in the sow and how these components related to post-weaning (pw) reproductive performance. First and 2nd parity sows were bled and weighed at d110 gestation (d110), d1 post-farrowing (d1PF), and at weaning(wn) Plasma was assayed for creatine. Loin eye area (LEA)and 10th rib backfat (bft) were measured by ultrasound atd110, wn, and following pw estrus (pwE). Weaning to estrus interval (WEI), pwE within 14d, and subsequent ovulation rate (OR) were recorded. Day 110 bft and change in bft from wn to pwE was negatively associated (-ASSOC; $P<0.05$) with pwE in 1st parity sows. Creatine at d110 tended ($P<0.10$) to be -ASSOC with pwE in 1st parity sows as well. Body wt change in 2nd parity sows from d110 to d1PF and d1PF to wn tended ($P < 0.10$) to be positively associated (+ASSOC) with pwE, and change in body wt from d110 to wn was +ASSOC ($P < 0.05$) with pwE. Creatine at wn

and change in creatine from d1PF to wn were -ASSOC ($P < 0.05$) with pwE in 2nd parity sows only. 1st parity WEI was -ASSOC ($P < 0.05$) with d1PF creatine and +ASSOC ($P < 0.05$) with change in creatine from d1PF to wn. OR was +ASSOC ($P < 0.05$) with LEA at wn of 1st parity sows whereas OR in 2nd parity sows was +ASSOC ($P < 0.05$) with wn wt. Creatine at wn in 1st parity sows was -ASSOC (P<0.05) to both wn wt and LEA at wn. Backfat in 1st parity sows was associated with pwE whereas creatine at wn in 2nd parity sows was coupled with pwE. First parity WEI was related to creatine at d1PF, which may reflect stress events associated with parturition. These data suggest that body wt, bft, LEA, and creatine contribute to the complex trait of pw reproduction but may respond differently dependent upon female maturity.

Key Words: swine, reproduction, metabolism

M294 Lipoic acid decreases progesterone clearance rates in ovariectomized ewes. R. S. Mottet*[1], C. O. Lemley[2], E. L. Berg[1], E. P. Berg[1], and K. A. Vonnahme[1], [1]*North Dakota State University*, *Fargo,* [2]*West Virginia University*, *Morgantown*.

Lipoic acid is a naturally occurring compound that has been shown to modulate insulin sensitivity when supplemented to the diet. Elevated blood insulin concentrations have been shown to decrease progesterone catabolism in several species by modulating expression and/or activity of cytochrome P450 2C (CYP2C) or 3A (CYP3A). We hypothesized that lipoic acid would decrease progesterone catabolism by the liver. The objective was to determine how supplementation of lipoic acid impacted progesterone clearance rate in ovariectomized ewes. Eight ovariectomized ewes were fed an alfalfa-grass ration at 95% of ad libitum for the duration of the experiment. Ewes were randomly assigned to lipoic acid treatment [an empty bolus administered by gavage (n = 4; CON), or lipoic acid supplemented at 32 mg/kg BW administered by gavage (n = 4; LA)]. Progesterone was administered via CIDR devices on d 5 to all ewes. Daily blood samples were collected from d 5 to 10. On d 10, liver biopsies were obtained from each ewe to determine CYP2C and CYP3A activity. On d 11, serial blood samples were collected after CIDR removal to determine progesterone clearance from the blood stream. Ewes treated with LA had decreased ($P < 0.03$) serum progesterone clearance compared with CON ewes; however, no difference ($P > 0.20$) in hepatic enzyme activity was found. We conclude that while lipoic acid decreases progesterone clearance in the blood, it does so without affecting hepatic CYP2C or CYP3A enzyme activity; therefore, the mechanism of action is yet to be elucidated.

Key Words: lipoic acid, progesterone, liver

M295 Zearalenone increases reproductive tract development, but not skeletal muscle signaling in prepubertal gilts. W. T. Oliver*[1], J. R. Miles[1], D. E. Diaz[2], J. J. Dibner[2], G. E. Rottinghaus[3], and R. J. Harrell[2], [1]*USDA, ARS, U.S. Meat Animal Research Center*, *Clay Center, NE,* [2]*Novus International, Inc.*, *St. Charles, MO,* [3]*Veterinary Medical Diagnostic Laboratory, University of Missouri, Columbia*.

Zearalenone (zea) is a potent mycotoxin that has estrogenic properties. In vitro results indicate that zea metabolites are capable of downregulating proteins associated with protein synthesis (mammalian target of rapamycin, mTOR) and cellular proliferation (extracellular signal-regulated kinase, ERK) in muscle. The objectives were to determine the effect of zea consumption by prepubertal gilts on: 1) growth performance, 2) reproductive tract development, and 3) skeletal muscle mTOR and ERK activation. Gilts were weaned at 21 d of age and allowed to adjust for 1 wk on a commercial diet. After 1 wk (d 0), gilts were randomly assigned to consume a commercial basal diet (C, n = 9) or C + 1.5 mg/kg zea (n = 10) for 4 wk, at which time gilts were killed, urine collected, and tissue collected and frozen. Zearalenone, α-zearalenol, and β-zearalenol were detected at levels of less than 4 μg/kg in urine of C gilts, but were increased (292 ± 76, 113 ± 20, and 15 ± 3 μg/kg, respectively) in pigs consuming zearalenone ($P < 0.01$). No differences were observed in ADG, ADFI, or G:F between treatments ($P > 0.28$). Reproductive tract size was increased 1.5-fold (20.9 ± 4.3 vs. 50.6 ± 3.8 g) in zea gilts ($P < 0.01$). Uterine endometrial gland development was increased 50% in gilts consuming zea ($P < 0.01$). In uterus, estrogen receptor (ER)-α mRNA and protein were unchanged ($P > 0.28$), but gilts consuming zea had 2- and 3-fold higher abundance of ER-β mRNA and protein, respectively, compared with the C group ($P < 0.01$). No differences were observed in mTOR and ERK protein phosphorylation or total abundance in skeletal muscle ($P > 0.36$). The consumption of zea had no effect on growth performance or skeletal muscle signaling in prepubertal gilts, but zea increased reproductive tract size and glandular development, possibly due to altering the expression of ER-β.

Key Words: swine, uterus, zearalenone

M296 Quantitative bioluminescence imaging of porcine antral follicles in vitro. S. Jung* and S. T. Willard, *Mississippi State University*, *Mississippi State*.

Determining the relationships between optimal imaging time, plasmid DNA dose and luciferase expression for quantitative bioluminescence imaging is critical to the development of new biophotonic paradigms. In this study, we analyzed the time course of luminescence emitted from transfected porcine whole follicle units. We used cationic lipid transfection with increasing doses of plasmid DNA (pGL4) encoding a luciferase reporter gene. Follicles between 5.5 to 6 mm in diameter were dissected from the ovaries. DNA–lipid complexes were formed at a DNA (μg):lipid (μL) ratio of 2:5 in PBS, by adding FuGene 6 diluted in PBS to 0 μg, 1 μg, 2 μg or 3 μg of pGL4 and introduced into each follicle unit by injection using a microinjector. A total of n = 48 follicles were randomly allocated in 4 groups (negative control, 1 μg, 2 μg and 3 μg groups) and cultured at 39°C under 45% O_2; 50% N_2; 5% CO_2 for 20 h. The luminescence from each follicle unit was detected using an IVIS 100 imaging system after 300 μg of luciferin was injected. An imaging series of 30-s exposures were collected up to 10 min. The signal intensity was reported as mean ± SEM of photon counts (PC; n = 12 per group), and the experiment was repeated 6 times. Data were analyzed by repeated measures ANOVA. The means of the negative control group at individual peak time points served as a background signal and subtracted from means of 1 μg, 2 μg, and 3 μg groups. The signal intensity reached a peak at 1.5 min ($1.08 \times 10^6 \pm 0.47 \times 10^6$ PC) in the 3 μg group, and at 1 min in both 1 μg ($2.45 \times 10^5 \pm 0.88 \times 10^5$ PC) and 2 μg ($4.60 \times 10^5 \pm 1.62 \times 10^5$ PC) groups after the injection and declined gradually afterward. The luciferase expression level of follicles in the 3 μg group tended to be greater than the 1 μg group ($P = 0.09$), but did not differ from the 2 μg group ($P = 0.18$). Overall, a higher level of luciferase expression was observed in follicles transfected with 3 μg of pGL4, with an optimal time for quantification at 1.5 min after luciferin injection. These data are the first to demonstrate luciferase detection and quantification, indicative of transcription, within whole antral follicle cultures in vitro.

Key Words: bioluminescence imaging, antral follicle, in vitro culture

M297 Feed restriction and pre-synchronization on progesterone concentration and LH peak in ewes on a synchronization program. P. Molina[1], T. Sánchez[1], M. E. Ortega[1], L. Olivares[2], O.

Mejía[3], M. Cárdenas[4], E. García*[5], J. Cordero[1], J. Peralta[6], and R. Nieto[1], [1]*Programa de Ganadería, Colegio de Postgraduados*, *Texcoco, México*, [2]*UAEM*, *Edo. México*, [3]*CEIEPO, UNAM*, *Tres Marías, México*, [4]*INNSZ*, *Mexico City*, [5]*CUCSUR*, *Autlán, Jalisco, México*, [6]*ICAP, UAEH*, *Hidalgo, México*.

To evaluate the effect of pre-synchronization and feed restriction in progesterone concentration and characterization of onset, duration and amplitude of LH peak, 69 Dorset ewes were randomly assigned to 4 treatments: Treatment 1 n = 18 (T1): Ewes received 1 kg of commercial supplement (16% protein) for 30 d and were synchronized with FGA sponges (40 mg) for 12 d; Treatment 2 n = 17 (T2) ewes received the same diet as T1, but they were synchronized with 2 doses of $PGF_{2\alpha}$, 16 and 8 d before sponges; Treatment 3 n = 17 (T3) ewes were feed restricted and received 1 kg of oat hay during 30 d, and synchronization regimen as T1; and Treatment 4 n = 17 (T4) received the same diet as T3 and the synchronization regimen as T2. Estrus was determined when ewes allowed the ram for mount after sponge removal. All groups showed 100% of estrus. Progesterone concentrations were greater in pre-synchronized groups ($P \leq 0.05$) compared with non pre-synchronized. Feed regimen affected onset of LH peak ($P \leq 0.05$), with a faster increase on groups with commercial supplement (T1 y T2), compared with groups feed with oat hay (T3 y T4). For synchronization program no differences were observed ($P \geq 0.05$). Duration and amplitude of LH were not affected ($P \geq 0.05$) for type of feed, synchronization program neither interaction between effects. Under the present experimental conditions, it is concluded that nutrition influenced onset of pre-ovulatory LH peak, while greater P4 concentration was observed in ewes pre-synchronized during the luteal phase, as a result of corpus luteum secretion.

Key Words: $PGF_{2\alpha}$, ewes, flugesterone acetate

M298 Progesterone and insulin concentration on ewes with different body condition fed bypass fat in a superovulatory program. P. Molina[1], T. Sánchez[1], M. E. Ortega[1], L. Olivares[2], O. Mejía[3], M. Cárdenas[4], E. García*[5], J. Cordero[1], J. Peralta[6], and R. Nieto[1], [1]*Programa de Ganadería, Colegio de Postgraduados*, *Texcoco, México*, [2]*UAEM*, *Edo. México*, [3]*CEIEPO, UNAM*, *Tres Marías, México*, [4]*INNSZ*, *México City*, [5]*CUCSUR UADG*, *Autlán Jal., México*, [6]*ICAP UAEH*, *Hidalgo, México*.

Dorset ewes in body condition score of 3 (1–5 scale) wererandomly assigned to two treatments: In T1 (n=26) eweswere fed with commercial supplement and in T2 (n=21)ewes were fed with oat hay to reduce the body condition ofthese ewes and both groups received this diet for a month. Then six ewes of each group were superovulated (donors) and the rest remained as recipient ewes. At the beginning of the superovulation treatment dorsal fat was 2.5 and 1.97 mm and body weight was 69 and 65 kg, for T1 and T2, respectively. During the first 8 days of synchronization and superovulation treatment both groups received 100 g of protected fat and same diet as T1, synchronization for donors and receptors was performed by sponges of flugesterone acetate (FGA, 40 mg) during 12 days. Recipient ewes received 200 IU of eCG 12 h before sponge removal. Donor ewes were superovulated with decreasing doses of FSHp for 4 d and embryos were obtained and transferred 7 d later. At synchronized estrus ewes of T1 and T2 weighed 72 and 69 kg ($P > 0.05$) and dorsal fat measures were 3.5 and 3.29 mm ($P > 0.05$) respectively. All ewes from T1 (100%) responded to superovulation, while in T2 only 67% responded. Progesterone and insulin secretion were greater ($P < 0.05$) in ewes of the T1 group, compared to those of the T2 group. There were differences in number of corpora lutea present (9.5 vs. 14.7) for T1 and T2 groups, respectively, and also in rate of recovered embryos (93 vs. 71%). There were no differences in gestation rate ($P > 0.05$), with 35 and 31.5% for T1 and T2 groups, respectively. Based on the present experimental conditions, it is concluded that previous undernutrition affects ovulatory rate, and serum concentrations of progesterone and insulin but not pregnancy rate.

Key Words: FSH, embryos, Dorset ewes

Physiology and Endocrinology: Reproductive Management

M299 Effect of prepartum somatotropin on milk production, metabolism and reproduction in primiparous Holstein dairy cows. A. Schneider*, E. Schwegler, P. Montagner, L. T. Hax, M. M. Antunes, E. Schmitt, F. A. B. Del Pino, I. Bianchi, and M. N. Corrêa, *Federal University of Pelotas*, *Pelotas, RS, Brazil*.

The aim of this work was to evaluate the effect of prepartum somatotropin (bST) injection on metabolic adaptation and resumption of ovulatory cycles in primiparous dairy cows. For this study 31 primiparous Holstein cows in a commercial dairy herd were used. The cows had a mean body weight (BW) of 568.8 ± 47.8 kg and 3.4 ± 0.4 of body condition score (BCS) at the beginning of the experiment. Cows in the bST group (n = 15) received subcutaneous injections of bST (500 mg, Boostin) at −32.2 ± 6.9 d and −18.9 ± 6.9 d, and, if pertinent, at −4.7 ± 7.1 d from calving date. Control cows (n = 16) did not receive any treatment and were managed in the same conditions of treated cows. Blood samples were collected weekly from −35 d to 45 d after calving for glucose, non-esterified fatty acids (NEFA), insulin-like growth factor I (IGF-I) and progesterone assays. Postpartum cows were milked twice daily and production was recorded. A cow was considered ovulated when blood progesterone exceeded 1 ng/mL after calving. Data was compared between groups by ANOVA for repeated measures. Ovulatory status was compared among groups by the Chi-squared test. A value of $P < 0.05$ was considered significant. The positive effect of prepartum bST on milk production and resumption of ovulation could be related to the better adaptation, as seen by the reduced postpartum BCS loss, and, also to the exposure of mammary and reproductive tissues to higher IGF-I concentrations. In conclusion, prepartum somatotropin injection reduced BCS loss, percentage of anovulatory cows, and improved milk production during the first 45 DIM.

Table 1. Variables analyzed for control and prepartum somatotropin treated (bST) groups

	Treatment			P
Variables	Control	bST	SEM	Treat
Prepartum				
BW, kg	568.7	559.7	6.4	0.32
BCS	3.1	3.2	0.0	0.36
Glucose, mmol/L	3.1	3.0	0.1	0.85
NEFA, mmol/L	0.9	1.0	0.0	0.004
IGF-I, ng/mL	84.1	127.8	7.3	<0.0001
Postpartum				
BW, kg	532.9	524.7	4.7	0.22
BCS	2.6	2.8	0.0	<.0001
Glucose, mmol/L	3.2	3.2	0.1	0.49
NEFA, mmol/L	0.9	0.9	0.0	0.28
Milk production, kg/day	22.6	25.3	0.5	<0.0001
Anovulatory at 45 DIM, %	62.5	20.0	-	0.016

Key Words: dairy cows, prepartum bST, postpartum ovulation

M300 Effect of dietary energy on ovarian development and fertility in postpuberal beef heifers. S. E. Echternkamp*, R. A. Cushman, and C. L. Ferrell, *USDA, ARS, U.S. Meat Animal Research Center*, *Clay Center, NE*.

Beef producers are advised to develop replacement heifers to 65% of mature BW, but reports indicate this BW could be reduced to lower input costs. To determine whether lower dietary intake impedes ovarian development and fertility in purebred or crossbred heifers, Angus (n = 60) and MARC II (1/4 Angus, 1/4 Hereford, 1/4 Gelbvieh, and 1/4 Simmental; n = 60) heifers were fed either a high (HE) or low (LE) energy diet for 180 d postweaning to achieve 65 vs. 53% of mature BW at first breeding. At 14 mo of age, heifers were housed with fertile bulls for 47 d. Estrus was monitored for 21 d, and 12 h after estrus, ovaries were ultrasounded in one-half of the heifers to measure ovarian length and height, preovulatory follicle diam., and total number of antral follicles (AFC); corpus luteum (CL) diam. and blood progesterone were measured 7 to 14 d after estrus. Data were analyzed by SAS PROC GLM or GLIMMIX with diet and genetic line as independent variables; 2-way interactions were not significant. Initial BW (282.8 kg) did not differ but, at breeding, HE heifers were heavier (429.4 vs. 344.8 ± 7.1 kg) and fatter (6.9 vs. 5.0 ± 0.1 BCS) than LE heifers ($P < 0.01$); experimental ADG was 0.81 vs. 0.35 ± 0.02 kg/d ($P < 0.01$). Puberty occurred in 93.3% of heifers prebreeding. Size of preovulatory follicle (13.7 ± 0.2 mm), ovary (length = 24.2 ± 0.3 mm; height = 13.3 ± 0.2 mm), CL (19.4 ± 0.5 mm), and AFC (23.4 ± 1.3) did not differ between HE and LE, but follicle diam. (14.3 vs. 13.1 ± 0.3 mm; $P < 0.01$) and ovarian length (25.1 vs. 23.1 ± 0.7 mm; $P = 0.05$) were greater for MARC II vs. Angus heifers. Ovarian size was correlated with AFC (r = 0.64; $P < 0.01$). Plasma progesterone was greater for HE vs. LE heifers (5.3 vs. 4.3 ± 0.3 ng/mL; $P < 0.05$), but CL diam. (19.4 ± 0.5 mm) was not affected by diet or line. Pregnancy rate did not differ between diets but tended ($P = 0.07$) to be greater for MARC II vs. Angus (80 vs. 65%). Developing yearling beef heifers to 53% of mature BW did not impede ovarian development or heifer pregnancy rate.

Key Words: beef heifers, diet, fertility

M301 The pH decreases in the vaginal portion of the cervix in mares near ovulation. J. J. Parrish*, *University of Wisconsin*, *Madison*.

The objective was to determine if vaginal pH in mares varies during the estrous cycle and could be a predictor of time to breed. In this study, wireless transmitting boluses were obtained from Kahne Limited, New Zealand, that were capable of measuring pH, temperature and pressure. Boluses of 15 × 3 cm, were originally designed for remote rumen measurements but modified in our lab for limited time use in mares. The boluses were sterilized in Nolvasan followed by rinsing in distilled water and calibration with pH standards. The mare's vulva was disinfected with 3 washes of detergent as done for artificial insemination. The bolus was inserted with a lubricated gloved hand into the vagina. The tip of the bolus was inserted deep into the anterior vagina and into the folds of the vaginal portion of the cervix. This location was chosen as air entering the vagina produced unstable pH readings when the bolus was left in just the anterior vagina. Pressure measurements demonstrated the vagina was 10 mbar below ambient pressure and influx of air occurred at unpredictable times. The pH was recorded at 5 s intervals and the average pH determined over a mean ± SEM of 4.1 ± 0.3 min (225 measurements) per mare. Data was obtained on 3 mares on days −7, −2, −1 and 0 relative to ovulation as detected via ultrasonography. Mares exhibited estrus on days −2, −1 and 0. The mean ± sem pH across mares was 7.02

± 0.01, 6.95 ± 0.02, 6.88 ± 0.02, and 6.75 ± 0.07 for days −7, −2, −1 and 0 respectively. Using Dunnett's procedure, days −7 and −2 had greater pH values than d 0 ($P < 0.05$) but d 0 was not different from day −1 ($P > 0.05$). Temperature measured along with pH did not vary over stage of cycle ($P > 0.05$). If left in the vagina overnight, the boluses were ejected at 12 – 24 h and often damaged. Vaginal pressure changes were detected when an estrus mare was brought into contact with a stallion. The experiment demonstrated that the pH of the vaginal portion of the cervix in mare's is neutral in diestrus and decreases near the time of ovulation and thus could be a suitable marker of the time to breed. The boluses were the generous donation of Kahne Limited.

Key Words: vaginal pH, estrous cycle, ovulation

M302 Main endocrine-metabolic differences between 1st and 2nd lactation of the dairy cows around calving. G. Bertoni*, R. Lombardelli, F. Piccioli-Cappelli, and E. Trevisi, *Istituto di Zootecnica, Universitá Cattolica S. Cuore*, *Piacenza, Italy*.

Dairy cows yield less milk in the 1st lactation in comparison to the following one and this seems to be mainly due to mammary gland development, although other factors can be involved (e.g., level of DMI, digestive tract development, different experience of stress). With the aim to better clarify the influence of metabolic-endocrine changes on differences in milk yield between 1st (L1) and 2nd (L2) lactation, 8 healthy Italian Frisian cows reared under very similar conditions (housing, diet, climate), were checked in their first 2 lactations. Cows were individually fed with corn silage, chopped alfalfa and grass hays distributed every 12 h, and concentrate, fed in 2 (dry period) or 8 (lactating period) meals at regular intervals. Cows have been daily checked for milk yield, DMI, and fortnightly for BW and BCS. Blood samples were weekly withdrawn, before the morning meal, from −28 to 120 DIM to determine metabolites and hormones. During 1st month of lactation, L2 showed higher milk yield (40.0 vs. 30.8 kg/d), DMI (20.5 vs. 17.9 kg/d) and lower BCS (2.36 vs. 2.49 score). The negative energy balance was more accentuated in L2 as suggested by the lower glucose for 3 weeks (3.43 vs. 3.78 mmol/L; $P < 0.01$) and higher BHBA (0.64 vs. 0.89 mmol/L; $P < 0.05$), despite NEFA were similar. Hormones with an apparent relationship with lactation start were bST and glucagon (increased) and IGF-I, insulin and perhaps triiodothyronine (T3) (reduced); nevertheless, in the periparturient period very small differences has been observed, according to parity, for bST, glucagon and T3. Otherwise, the average values (end pregnancy - first two months of lactation) were lower in L2 for insulin (5.9 vs. 7.6 mcU/mL; $P < 0.01$) and IGF-I (47 vs. 63 ng/mL; $P < 0.01$). These last differences suggest that the more negative energy balance of L2, due to higher milk yield, is the main cause of lower glucose and, consequently, of lower insulin and IGF-1. This explanation seems confirmed by the good correlation between glucose recovery and that of insulin and IGF-1 in the 1st month of lactation. To conclude, higher milk yield in the 2nd lactation does not seem to be affected by hormonal changes, but it indirectly causes a reduction of insulin and IGF-1.

Key Words: milk yield, parity, hormone

M303 Effect of thermal preconditioning during the prebreeder period on breeder turkey hens' reproductive performance. S. W. Kang*, S. Kosonsiriluk, S. J. Welch, and M. E. El Halawani, *University of Minnesota*, *St. Paul*.

Breeder turkey hens photostimulated in the month of May are highly susceptible to a sudden increase in environmental temperature which has a detrimental effect on egg production. The objective of this study was to investigate the effects of thermal preconditioning before photostimulation on enhancing egg production during the summer months. Hens were reared under the photoperiod 14L/8D daily with day length reduced to 6L/18D from 17 to 30wk. At 30wk, hens were photostimulated (15L/9D). In experiment 1: Hens were subjected to temperature treatments at 20 wks of age (6hrs/day). Treatments included: 1) Control, no temperature treatment. 2) 10 wks: subjected to 75°F, increasing by 5°F every 2 wks. 3) 5 wks: same as treatment (2) excepting each temperature cycle was only for one wk. 4) 3 wks: treatment started at 27 wk, starting at 85°F, increasing by 5°F for the next 2 wks. In experiment 2: Treatments included: 1) Control, same as experiment 1. 2) 3wks: subjected to 85°F at 27 wk, increasing by 5°F every wk. 3) 2 wks: subjected to 90°F at 28 wk, increasing by 5°F at 29 wk. 4) 1 wk: subjected to 95°F at 29 wk. Peak egg production was comparable among all treatment groups between wk 1–4 of photostimulation. In experiment 1, average egg production was highest in the 3 wks preconditioning group (4.16 eggs/hen/wk) during the 27 wks production period. Lowest average egg production was that of hens receiving 10 wks of preconditioning (3.43 eggs/hen/wk). Control group was 3.86 eggs/hen/wk. In experiment 2, average egg production of the 1 wk preconditioning group (3.96 eggs/hen/wk) was 37.5% higher than that of control (2.88 eggs/hen/wk). There was no significant difference among treatment groups (1, 2, and 3 wks). The results clearly indicate that thermal preconditioning can be beneficial or detrimental to egg production of hens photostimulated in the month of May depending on the preconditioning temperature schedule and age of hens at the time of treatment initiation.
Supported by Minnesota Turkey Growers Association, Willmar Poultry Co., and Minnesota Agricultural Experiment Station.

Key Words: turkey reproductive performance, heat stress, thermal preconditioning

M304 In vitro investigation of anti-*Escherichia coli* O157:H7 effects of free fatty acids under acidic conditions. J. Yang*[1,2], X. Hou[1], P. S. Mir[2], and T. A. McAllister[2], [1]*Inner Mongolia Agricultural University*, *Hohhot, P. R. China*, [2]*Agriculture and Agri-Food Canada Research Centre*, *Lethbridge, AB, Canada*.

Preventing acid-tolerant *Escherichia coli* O157:H7 from colonizing the lower gut of cattle could reduce fecal shedding of this zoonotic pathogen. This study aimed to test the antimicrobial effects of fatty acids (FA) against *E. coli* O157:H7 at acidic pH. From 4 strains of *E. coli* O157:H7 (E32511, E318N, H4420N and R508N) screened for acid tolerance, strain H4420N was selected for further study of the influence of pH on bactericidal activities of 6 FA (capric, lauric, palmitic, oleic, linoleic, and linolenic). Strain H4420N was cultured at pH 2.5, 4.3 and 7 for 6 h at 37°C in the presence (20 m*M*) of selected FA in Luria-Bertani broth containing 4% (v/v) Tween 80. Triplicate cultures were prepared for each FA × pH combination, and the entire experiment was repeated. Bacterial numbers were $\log_{10}$ transformed for statistical analysis. Differences were identified using the Least Squares Means of GLM (SAS Institute, Cary, NC). None of the FA exhibited bactericidal activity at pH 7.0. At pH 4.3, capric acid (C10:0) caused a 5 $\log_{10}$ reduction in cfu/mL and both lauric and linoleic acids reduced ($P < 0.001$) viability of H4420N. None of the other FA showed bactericidal activity at pH 4.3. At pH 2.5, oleic (C18:1) and linolenic acids (C18:3) had modest effects on the H4420N viability, whereas capric (C10:0), lauric (C12:0) and linoleic acids (18:2) resulted in ≥ 5 $\log_{10}$ reductions in cfu/mL. Capric and lauric acids were examined further at pH 2.5 at concentrations ranging from 0.15 to 20 m*M*. After 10 min of exposure, 5 $\log_{10}$ cfu/mL reductions were achieved by lauric acid at 2.5 m*M* and by capric acid at 0.31 m*M*. Acid stress increased the sensitivity of *E. coli* O157:H7 to FA, particularly capric, lauric and linoleic acids. Thus, the ability of this pathogen to survive passage to the lower gut may be reduced if these fatty acids are included in diets for cattle.

Key Words: fatty acids, pH, *E. coli* O157:H7

M305 A more specific and sensitive detection method for avian influenza H5N1 using antibodies against N1 subtype and red blood cell amplification in an impedance biosensor. J. Lum*[1], R. Wang[1], D. Abi-Ghanem[2], B. Hargis[1], L. Berghman[2], S. Tung[1], and Y. Li[1], [1]*University of Arkansas*, *Fayetteville,* [2]*Texas A&M University*, *College Station*.

Avian influenza (AI) H5N1 was first discovered in the 1990s and since then has become a likely source of a global pandemic and economic loss. Current specific detection methods are time consuming, expensive, and require special training or facilities. A rapid, sensitive, and specific screening method is needed for in-field or bedside testing of AI virus to implement quarantines and medications. An impedance biosensor has been developed to meet this need, but it is not ready to detect AI H5N1 subtype at very low concentrations. Therefore, the objective of this study was to improve the specificity and sensitivity of this impedance biosensor for rapid screening of AI H5N1 using secondary antibody against N1 subtype and red blood cell (RBC) amplification. Three major components of the developed biosensor are immunomagnetic nanoparticles for separation of AI virus, a microfluidic chip for sample control, and an interdigitated microelectrode for impedance measurement. In this study, polyclonal antibody against N1 subtype was immobilized on the surface of the microelectrode to generate more specific impedance signal, and red blood cells were mixed with the sample to amplify impedance value. The impedance of the nanoparticle-virus-RBC complex was measured and compared with the negative control. The change in impedance could be correlated with the concentration of AI H5N1 virus. Using polyclonal anti-N1 along with red blood cell amplification, the impedance biosensor was capable of detecting AI H5N1 at levels down to 100 EID50/ml in less than 3 h. Red blood cell amplification caused a significant increase ($P < 0.001$) in impedance change as compared with antibody immobilization alone.

Key Words: avian influenza, biosensor, rapid detection

M306 Survival of *Escherichia coli* O157:H7 incubated with corn- or wheat-based dried distillers' grains with solubles in ruminal or fecal inoculum. H. E. Yang[1,2], W. Z. Yang[1], J. J. McKinnon[2], T. W. Alexander[1], Y. L. Li[1], and T. A. McAllister*[1], [1]*Agriculture and Agri-Food Canada Research Centre*, *Lethbridge, AB, Canada*, [2]*University of Saskatchewan*, *Saskatoon, SK, Canada*.

Including corn-based dried distillers grains with solubles (DDGS) in feedlot diets may increase fecal shedding of *E. coli* O157:H7 by cattle. In western Canada, wheat-based DDGS is also available to finishing cattle. This study investigated whether corn- or wheat-based DDGS (CDDGS, WDDGS) replacing 0, 20 or 40% of barley grain in substrate for in vitro batch culture affected survival of *E. coli* O157:H7 in ruminal content- or feces-based inoculum. Donors for ruminal and fecal inoculum were 2 ruminally cannulated non-lactating Holstein cows fed diets containing both corn- and wheat-based DDGS, in equal proportions, to ensure that microbial populations associated with digesta from both forms of DDGS were present in the digestive tract. Triplicate incubation vials (200 mg substrate + 20 mL ruminal or fecal inoculum) were prepared for time points 0, 4, 12 and 24 h and each of 5 substrates (ground barley grain replaced with 0, 20 or 40% CDDGS or WDDGS). After inoculation with a 4-strain (E318N, E32511, R508N, and H4420N) mixture of *E. coli* O157:H7 (total 10^8 cfu/mL), vials were sealed and incubated at 39°C. Neither type nor level of DDGS affected fermentation or survival of *E. coli* O157:H7 in ruminal contents. In fecal inoculum, however, a time × DDGS interaction ($P = 0.05$) was observed. At 4 and 12 h of incubation, numbers of *E. coli* O157:H7 in feces were similar across treatments, but at 24 h, they were greater in 40% WDDGS and 40% CDDGS than in other treatments. Additionally, *E. coli* O157:H7 concentrations at 24 h were greater in fecal incubations with CDDGS than with WDDGS. Differences in numbers of *E. coli* O157:H7 were not attributable to changes in pH or VFA concentrations. These results suggest that inclusion of high levels of either corn- or wheat-based DDGS in feedlot diets for cattle may encourage the persistence of *E. coli* O157:H7 in feces.

Key Words: *E. coli* O157:H7, distillers grains, ruminal contents

M307 The effect of fungus myceliated grain supplementation in different feeding phases on coccidiosis and production performance of broilers. W. L. Willis, O. S. Iskhuemhen, S. L. Hurley, D. Wall*, R. C. Minor, and E. I. Ohimain, *North Carolina Agricultural and Technical State University*, *Greensboro*.

A 49 d experiment was conducted to evaluate fungus myceliated grain (FMG) supplemental inclusion levels in different feed phases on coccidiosis and production performance in broiler chickens. This study utilized 294 straight-run broiler chicks that were randomly weighed and distributed into 7 treatment (trt) groups with 3 replications of 14 chicks each on recycled litter as follows: 1) Control- no myceliated grain, 2) Starter

feed-FMG 5%, 3) Grower feed-FMG 5%, 4) Starter/grower/finisher feeds-FMG 5%, 5) Starter feed-FMG 10%, 6) Grower feed-FMG 10% and 7) Starter/grower/finisher feeds-FMG 10%. Assessment data were taken on male/female BW, fecal *Eimeria sp.* egg count, bursa and spleen wts, and mortality. BW of males and females broilers was significantly depressed in trt 5 when compared with the control 2.00 vs. 2.52 kg males and 1.83 vs. 2.10 kg females. Treatments 1 and 2 had the highest growth of *Eimeria sp.* with the other trts had varying levels of reduced counts. Trts 6 and 7 had the lowest counts though not significantly different from trts 3, 4 and 5 ($P > 0.05$), but significantly ($P < 0.05$) different from trts 1 and 2. Male relative bursa wts were highest in trt 4 (0.021) vs the control (0.017), while trt 6 had the lowest (0.013) vs the control (0.017). Average feed consumed did not differ greatly among trts. The results from this study reflect a positive response of fungus myceliated grain fed at the 10% inclusion level throughout the entire feeding phases for anticoccidial control and production performance.

Key Words: broilers, fungus myceliated grain, coccidiosis

M308 Tibial dyschondroplasia in four crosses of male commercial broilers and its relationship to gait score. P. Y. Hester*[1], P. N. Talaty[1], and M. N. Katanbaf[2], [1]*Purdue University*, *W. Lafayette, IN*, [2]*Cobb-Vantress, Inc.*, *Monticello, KY*.

The objective of the following study was to determine the incidence of tibial dyschondroplasia (TD) among 4 crosses (crosses A, B, C, and D) of male meat-type commercial broilers and its relationship to gait score at 6 wk of age. At 38 and 39 d of age, 360 birds were evaluated individually for gait score. Three male chickens/pen with good walking ability (gait score of 0 or 1) and 3 male chickens/pen with poorer walking ability (gait score of 3) were killed and individual BW determined at 6 wk of age. Both drumsticks were retrieved and the distal and proximal tibia were scored for TD lesion (0 = no lesion; 1 = mild lesion; 2 = moderate lesion; and 3 = severe lesion). Data were analyzed via ANOVA using the mixed model procedure of SAS. Very few birds showed TD lesions. The TD scores were similar among crosses even though gait scores differed among genotypes with cross C having better gait scores than crosses A and B but did not differ from cross D. The TD lesion scores did not differ between male broilers with a gait score of 0 or 1 (mean TD lesion score of 0.03 ± 0.03) as compared with those with a poorer walking ability and a gait score of 3 (mean TD lesion score of 0.08 ± 0.03). The proximal end of the right and left tibia had similar TD lesion scores. The TD lesions scores were higher for the right proximal tibia when compared with the distal ends of the right and left tibia. These results suggest the poorer walking ability of male broilers in this study was not due to TD lesions.

Key Words: tibial dyschondroplasia, male broiler, gait score

M309 Impact of egg storage on blastodermal cell viability and embryonic metabolism in broiler breeders. J. A. Hamidu*[1], Z. Uddin[1], G. M. Fasenko[2], and D. R. Barreda[1], [1]*University of Alberta*, *Edmonton, Alberta, Canada*, [2]*University of New Mexico*, *Albuquerque*.

The objective of the current study was to investigate the impact of short-term (4 d) and long-term (14 d) egg storage on blastodermal cell viability and embryonic metabolism. Two separated experiments were conducted using Ross 308 broiler strains after egg storage (4 d vs. 14 d) at 18°C and 80% RH. Study–1 involved separation of individual blastoderms into individual cells. The cells were pooled together in each treatment and stained with Annexin V-FITC and propidium iodide. A flow cytometer (BD FACScan) was used to analyze the cell suspensions and separated into percentages of live cells (Annexin V–/PI–), early apoptotic cells (Annexin V+/PI–), necrotic cells (Annexin V–/PI+) and late apoptotic/necrotic cells (Annexin V+/PI+). In study–2, eggs from each treatment were placed in metabolic chambers inside an incubator. Measurements of O_2 consumption and CO_2 production were used to calculate embryonic heat production. Daily dry embryo weights (4 to 21 d of incubation) were measured and used to determine heat production/g embryo weight. All data were analyzed by the proc mixed model procedure of SAS ($P \leq 0.05$). The PDIFF procedure in SAS was applied to separate LSmeans between storage treatments. The percentage of live cells decreased significantly as egg storage duration increased (4 d = 81.17 ± 2.13% vs. 14 d = 68.18 ± 2.15%). The percentage of early apoptotic cells increased in 14 d (17.88 ± 1.87%) vs. 4 d (4.32 ± 1.89%). While daily embryo weight and heat production decreased with egg storage, the heat production/g embryo weight increased. Though embryos from 14 d stored eggs were metabolizing at a higher rate than 4 d storage group, they had reduced embryonic metabolism. The study indicates that reduction in blastodermal cell numbers following egg storage for 14 d is primarily due to events of apoptosis. Examining genes that induce apoptosis in broiler breeders could be used to slow down the events of apoptosis and increase cell viability, improve embryonic metabolism and embryo survival during incubation.

Key Words: egg storage, viable and apoptotic cells, embryonic metabolism

M310 Influence of hen's age and phenotypic correlation between external and internal traits of eggs. O. T. F. Abanikannda* and A. O. Leigh, *Lagos State University*, *Ojo - Lagos, Nigeria*.

Table egg remains the cheapest source of animal protein, however competing demands for nutrients by the hen for its maintenance and production at different stages of lay impact on the quantity and quality of eggs produced. This study investigates the influence of hen's age on quality of egg's external and internal traits. A total of 300 eggs derived from Harco Black layers from 5 ordinal groups based on age [A (22–32), B (33–43), C (44–54), D (55–65) and E (66–76) weeks] consisting of 60 eggs from each group were sampled and measured. Data were analyzed using JMP (7.0.1) statistical software for basic descriptives, correlation, regression and ANOVA. The overall mean ± SE for egg weight (EGGWT), egg length (EGGLT), egg width (EGGWD), shape index (SHPINDX), vertical circumference (VTCIRC) and horizontal circumference (HTCIRC) are 55.65 ± 0.28 g, 56.09 ± 0.15 mm, 42.40 ± 0.08 mm, 75.69 ± 0.19%, 15.67 ± 0.03 cm and 13.41 ± 0.03 cm, respectively. The effect of hen's age was highly significant ($P < 0.01$) on all external traits, and accounted for 0.26, 0.22, 0.16, 0.07, 0.27, and 0.33, respectively, of the total variation. Age Group A consistently had the least mean values for all external traits except shape index, while group D recorded the highest. The internal traits exhibited similar trend as the external traits across different age groups, with overall mean values of 15.66 ± 0.12g, 33.53 ± 0.21g, 6.46 ± 0.04g, 28.15 ± 0.17%, 60.93 ± 0.22%, 11.64 ± 0.06%, 46.56 ± 0.41% and 0.36 ± 0.01mm respectively for yolk weight (YLKWT), albumen weight (ALBWT), shell weight (SHLLWT), yolk ratio (YLKRAT), albumen ratio (ALBRAT), shell ratio (SHLRAT), yolk:albumen ratio (YKALBRT) and shell thickness (SHLLTKN). Largest correlation was recorded between Albumen weight and all external traits ($P < 0.05$) except for shape index which was low and not significant. Yolk ratio, albumen ratio and yolk:albumen ratio had very low correlation against all external traits and were not significant ($P > 0.05$). The study revealed that hen's age significantly ($P < 0.05$) affect both external and internal traits of eggs and that some of the internal traits had moderate to high correlation with most of the external traits studied.

Table 1. Phenotypic correlations between external and internal traits of egg

	YLKWT	ALBWT	SHLLWT	YLKRAT	ALBRAT	SHLRAT	YKALBRT	SHLLTKN
EGGWT	0.591*	0.877*	0.603*	–0.071	0.017	–0.260*	0.052	0.138*
EGGLT	0.444*	0.621*	0.488*	–0.030	0.071	–0.128*	0.040	0.013
EGGWD	0.476*	0.701*	0.505*	–0.060	0.052	–0.190*	0.062	0.119*
VTCIRC	0.518*	0.763*	0.546*	–0.058	0.109	–0.202*	–0.076	0.020
HTCIRC	0.499*	0.682*	0.436*	–0.017	0.015	–0.252*	–0.009	0.130*
SHPINDX	–0.100	–0.109	–0.133*	–0.016	–0.027	–0.024	–0.010	0.064

*= Statistical Significance ($P < 0.05$).

Key Words: egg, hen age, phenotypic correlation

M311 Effects of heat stress on egg production and quality in two strains of layers. L. A. Mack*[1], J. N. Felver-Gant[1], R. L. Dennis[2], and H. W. Cheng[2], [1]*Purdue University*, *West Lafayette, IN*, [2]*LBRU, USDA-ARS*, *West Lafayette, IN*.

Heat stress is a problem for both egg production and bird well-being. Given a stressor, genetic differences can alter the type and degree of birds' responses and their adaptation. This study examined heat stress responses of 2 strains of White Leghorns: DeKalb XL (DXL), an individually-selected, commercial strain and a strain of kind, gentle birds (KGB) genetically-selected on high group productivity and survivability. Ninety 28wk-old birds (48 DXL, 42 KGB) were randomly paired, housed by strain, and assigned to hot (H) or control (C) treatments for 14 d (mean: H = 32.6°C, C = 24.3°C). Birds' egg production (egg number, EN; egg weight, EW; shell thickness, ST; and percentage of broken eggs, PB), behavior, and physical variables (BW; ovary weight, OW; number of mature follicles, FN; and crop feed weight, CF) were measured. Data were analyzed in SAS using the mixed models procedures. Compared with C birds, EN, EW, and ST were lower in H birds across both strains ($P < 0.05$). In H birds but not in C birds, both EN and EW increased over time while ST decreased. The PB tended to be greatest in the H-DXL, intermediate in the C birds, and lowest in the H-KGB birds, but a significant difference was found between H-DXL and H-KGB only ($P < 0.5$). Behaviorally, comparing treatments, H birds spent more time drinking and resting, and less time sitting ($P < 0.05$) than C birds. Comparing strains, DXL birds rested more on d 1 ($P < 0.05$) and tended to drink more on d 13 than KGB birds ($P < 0.1$). C-KGB birds ate more frequently than C-DXL birds on d 6 and 11 ($P < 0.05$) but no strain difference was evident in responding to heat stress ($P > 0.05$). H-KGB birds tended to have lower CF than C-KGB birds at both wk 1 and 2, while H-DXL birds tended to have higher CF than C-DXL birds at wk 1 only ($P < 0.1$). Body weight, d 14 OW and FN were all reduced in the H birds compared with relative controls ($P < 0.05$). Although heat stress reduced production variables in both strains of birds, genetic background shaped both the nature and intensity of the response.

Key Words: heat stress, egg quality, behavior

M312 Effect of litter type and wetness on foot pad dermatitis in broiler chickens. O. Cengiz*[1], J. B. Hess[2], and S. F. Bilgili[2], [1]*Adnan Menderes University*, *Aydin, Turkey*, [2]*Auburn University*, *Auburn, AL*.

An experiment was conducted to determine if wetting fresh or used litter for a short period of time during the latter part of the grow-out could influence the incidence and severity of foot pad dermatitis (FPD) in broiler chickens with and without existing lesions. A total of 2 hundred male broiler chickens with and without existing FPD lesions were selected from a 52-d old (Ross 708) flock and reared to 67 d of age in a design consisting of 2 × 2 arrangement of litter type (fresh or used) and added moisture (with or without added water). Broilers (8 treatments; 5 birds per pen; 40 pens total) were reared in floor pens (3 × 4 ft) prepared with used or fresh pine shavings bedding (8 cm deep). One half of the pens were wetted with a gallon of water daily for 5 d starting on Day 52. Litter samples were collected, pooled and analyzed for moisture at 56 and 67 d of age. FPD incidence and severity were assessed at the end of the study by using a 3-point scale. A common withdrawal feed and water were freely available; lighting was continuous throughout the study. Data were analyzed as a factorial design by the GLM procedure of SAS, Inc. Moisture level was higher with used than fresh litter on Day 56 ($P < 0.05$) but not on Day 67 of the trial. Wetting increased the moisture level from an average of 24 to 54% on Day 56. Litter moisture remained high in fresh wetted pens, but was equalized between the two litter types by Day 67. Placing the birds with FPD lesions on fresh bedding significantly reduced the incidence at 67 days of age (78 and 50% for used and fresh litter, respectively). Similarly, FPD severity was also reduced from 42 to 14% with fresh, as compared to used litter. Wetting treatment did not affect FPD incidence, but reduced mild ($P < 0.06$) and severe ($P < 0.07$) lesions at 67 days of age. Neither litter type nor litter wetting influenced FPD incidence or severity in adult birds without existing FPD lesions. These findings indicate that FPD may be occurring early in the grow-out and that improvements in litter quality can reverse the severity of lesions in market age broilers. In addition, in older broiler chickens, exposure to wet litter conditions for short periods prior to marketing is not sufficient to induce FPD.

Key Words: broiler, foot pad dermatitis, litter moisture

M313 Eggshell quality of Japanese quail (*Coturnix japonica*) after long-term selection for egg production. M. M. Fathi*[1], A. E. El-Dlebshany[2], and M. Bahie El-Deen[2], [1]*Al-Qassim University*, *Buridah, Al-Qassim, Saudi Arabia*, [2]*Alexandria University*, *El-Shatby, Alex., Egypt*.

An experiment was conducted to evaluate egg quality and ultrastuctural measurements of eggshell using scanning electron microscopy (SEM) in 2 lines (selected and control) of Japanese quails. Selection program was applied over 22 consecutive generations for higher egg production and lower broken egg percentage. The results revealed that the females of selected line significantly ($P < 0.01$) produced higher egg mass compared with that of control line. Also, selection procedure resulted in significantly improvement in feed conversion ratio. The eggshell of selected line had a higher breaking strength compared with that of control line, although there was no difference between them in shell thickness. Significantly higher wet ($P < 0.01$) and dry ($P < 0.05$) eggshell percentages were found in selected line. In general, the eggshells of selected line had a lower total score (good) of ultrastructural evaluation compared with control line. According to scanning electron microscopy data, the incidence of certain structural variants is more common in eggshell of control line suggesting poor shell strength. Alignment appearance was more prevalent in control eggshells compared with selected ones, suggesting lower resistance to breakage. Late fusion and large interstitial spaces of palisade layer indicating decrease resistance to fracture were observed in control eggshells. It could be concluded that long-term selection for egg production over 22 generations improved mammillary layer measurements and in turn breaking strength.

Key Words: Japanese quail, ultrastructural measurements, eggshell quality

M314 Effects of ambient temperature on body weight, cloacal temperature and blood traits in Pekin ducks. J. F. Huang*[1], C. H. Su[1], C. C. Lin[2], J. H. Lin[1], and S. R. Lee[1], [1]*Ilan Branch, Livestock Research Institute*, *Ilan, Taiwan*, [2]*National Ilan University*, *Ilan, Taiwan*.

This study aimed to investigate the effects of ambient temperature on body weight, cloacal temperature, and blood traits in Pekin ducks. A total of 36 Pekin ducks at 10–11 weeks of age were randomly assigned into 3 temperature groups: (1) 25 ± 1°C (LT), (2) 30 ± 1°C (MT), and (3) 35 ± 1°C (HT) and raised in an individual cage in a climate chamber. The relative humidity was 80–85% for all groups. This study lasted for 3 weeks. Body weight, feed intake, cloacal temperature and blood traits were determined once a week. The data was analyzed by the General Linear Model procedure of the Statistical Analysis System. The most dramatic decrease in body weight was observed in the HT group, followed by MT and then LT groups. Although there was a trend

of lower feed intake in the MT and HT groups, no significant differences among treatments were observed. After one week of treatment, significant differences in cloacal temperature were observed between the LT and HT groups. However, this significance disappeared after 2 weeks of treatment, probably due to adaptation of ducks to high ambient temperature. The cloacal temperatures in the MT and HT groups after 2 week of treatment were lower compared with those measured after one week of treatment. The blood traits showed that levels of calcium, sodium, magnesium, chloride ions, glucose, and total cholesterol were decreased in the MT and HT groups after one week of treatment, but were increased thereafter. However, the levels of the blood traits were relatively stable in the LT group throughout this study. The high ambient temperature caused the most remarkable decrease in body weight and blood traits and the most remarkable increase in cloacal temperature in the first week.

Key Words: ambient temperature, blood trait, Pekin duck

M315 The study on correlation between the liver enzyme activity and dioxin contents in the eggs of laying Brown Tsaiya ducks. C. C. Lin*[1], T. H. Ueng[2], Y. H. Lin[1], J. F. Huang[3], and S. R. Lee[3], [1]*National Ilan University*, *Ilan, Taiwan*, [2]*National Taiwan University*, *Taipei, Taiwan*, [3]*Ilan Branch, Livestock Research Institute*, *Ilan, Taiwan*.

The objective of this study was to study the correlation between the liver enzyme activity and dioxin contents in the eggs of laying Brown Tsaiya ducks. One hundred Brown Tsaiya ducks (119 d old) were raised in the Hsiangsi township (dioxin- contaminated area) and Wuchieh township (not dioxin-contaminated area), respectively. In each township, 50 ducks were raised on the ground and 50 ducks were raised in the cage. This study lasted for 7 mo. In each month, we collected duck liver microsomes to detect 7-ethoxy resorufin O-deethylase (EROD), 7-pentoxyresorufin O-dealkylase (PROD), and 7-ethoxycoumarin O-deethylase (ECOD) activity and also collected the egg samples for analysis and calculation of dioxin toxic equivalency (TEQ_{DF}) by high-resolution gas chromatography/mass spectrometry (HRGC/HRMS). Then, the correlation coefficient was calculated between liver enzyme activity and HRGC/HRMS results. An average correlation coefficient of 0.95 was observed between duck liver EROD and duck egg dioxin TEQ_{DF}. In contrast, a very low correlation coefficient was observed between liver PROD or ECOD activity and dioxin TEQ_{DF} in duck eggs. Furthermore, we used real-time PCR to determine CYP1A4 mRNA expression in duck liver. It showed the highest value of CYP1A4 expression was observed in the liver of ducks raised on the ground of dioxin-contaminated area compared with those in other treatments. The high correlation coefficient between liver EROD activity and dioxin TEQ_{DF} in duck eggs suggests that EROD is a valuable bio-marker of dioxin contamination in Brown Tsaiya ducks.

Key Words: Brown Tsaiya duck, dioxin, EROD

M316 Safety of industrial hemp as feed ingredient in the diets of laying hens and its impact on their performance. N. Gakhar*, E. Goldberg, and J. D. House, *University of Manitoba*, *Winnipeg, MB, Canada*.

Despite the utility of industrial hemp (*Cannabis sativa* L.) as a source of fiber and seed, its cultivation in N. America in the past was deemed illegal, due to concerns over the presence of the psychoactive compound tetrahydrocannabinol (THC) in the plant components. Regulatory changes undertaken by the Canadian government in 1998 permitted the use of cannabis cultivars containing lower concentrations (<0.3%) of THC. These changes present an opportunity to exploit the immense untapped potential of industrial hemp. Keeping this in perspective, a total of sixteen 19-wk-old individually housed Bovan White laying hens were fed one of the 2 diets containing 10 and 20% of hemp seed (HS). Concurrently, a total of twenty-four 19-wk-old individually housed Bovan White laying hens were fed one of the 3 diets containing 4, 8 and 12% of hemp oil (HO). Eight birds fed wheat, soy and corn oil based diets served as control. The diets were fed over a period of 12 weeks. All the diets were formulated to be isonitrogenous and isoenergetic. Daily egg weights, egg production, average daily feed intake (ADFI), feed efficiency (FE) and weekly body weights were recorded for the entire 12 weeks. Shell thickness and Haugh units (HU) were recorded from the eggs collected in wk 4, 8 and 12. Data were subjected to statistical analysis using Proc Mixed procedure of SAS. Daily egg weights (55.13 vs. 51.49 ± 1.2 g), FE (1.74 vs. 1.88 ± 0.04) and body weights (1.47 vs. 1.43 ± 0.02 kg) were higher ($P < 0.05$) for the birds fed 20% HS in comparison to the control. ADFI was lower ($P < 0.05$) in all HO treatments as compared with the control. Hen day egg production (91.12 vs. 96.84 ± 0.07%) and HU (83.8 vs. 86.8 ± 1.53 HU) were lower ($P < 0.05$) in 4% HO group whereas HU increased ($P < 0.05$) in 8% HO group as compared with the control. FE was higher ($P < 0.05$) in 12% HO group (1.70 vs. 1.85 ± 0.04) as compared with the control. In conclusion, this study allays concerns over the safety of feeding industrial hemp to the laying hens and demonstrates the positive impact of feeding HS on their performance.

Key Words: laying hens, hemp seed, hemp oil

M317 Duckweed as a feed ingredient in laying hen diet and its effect on egg production and composition. K. E. Anderson*, Z. Lowman, A. Stomp, and J. Chang, *North Carolina State University*, *Raleigh*.

Duckweed is a native North Carolina aquatic plant that can be used for bio-fuels (ethanol) and animal feeds. Researchers at North Carolina State University have worked for a decade and have developed a system to produce high-protein duckweed biomass utilizing the nutrient-rich effluent from anaerobic digestion of swine wastewater. This aspect of the project was to evaluate data generated in a feeding trial utilizing the duckweed biomass as a protein source in laying hen feed. First, the nutrient and energy composition of the Duckweed grown in these conditions was determined, and found to contain 29.05% CP, 25.08% C Fiber, and 695 kcal/kg AMEn based on a feeding trial with marker. Then a completely randomized design study to evaluate the impact of duckweed on the performance of a commercial layer egg production and feed conversion was conducted. Two layer diets were formulated to be iso-nitrogenous (18.1% crude protein) and Iso-caloric (2930 kcal/kg). The Control (C) no Duckweed and Duckweed (D), using the analysis to formulate the diet containing 12.6% duckweed. The study, utilized 60, 76 wk old Hy-Line, W-36 hens that were individually caged such that 30 hens received the C diet and the remaining 30 hens received the D diet. During the 12 wk study performance criteria were monitored daily and each week USDA grades, Haugh unit, shell strength, vitelline membrane strength, and yolk color data was collected on 1 d production. The data was analyzed using the Proc T-Test procedure, with significant differences of ($P < 0.05$) determined by *t*-test. On wk 3, 7, and 11 whole 6 egg pooled samples were collected and sent in for nutrient composition laboratory analysis. Diet had no impact on the hen-day production. There was a significant increase ($P < 0.05$) in the percent grade B eggs in the hens fed the D by 2% over the C hens. Surprisingly, there was no difference in the nutrient composition of the eggs except for omega-3 fatty acids concentration which were 0.06% higher ($P < 0.0001$) than in the C hens. The results indicate that duckweed can be fed at a 12.6%

inclusion rate and not impact the performance of laying hens and may be a means of enhancing omega-3 fatty acid concentration in eggs.

Key Words: laying hen, duckweed, egg nutrient composition

M318 Blood lipid concentration and performance parameters of broiler was fed by tomato pomace and turmeric powder under heat stress condition. S. J. Hosseini-Vashan[1,2], A. Golian*[1], A. Yaghobfar[2], H. Lotfolahian[2], and P. Esmaeilinasab[3], [1]*Ferdowsi University of Mashhad*, *Mashhad, Khorasan Razavi, IR Iran*, [2]*Animal Science Research Institute*, *Karaj, Tehran, IR Iran*, [3]*Birjand University*, *Birjand, Khorasan Jonobi, IR Iran*.

The effects of including tomato pomace and turmeric powder in dietary broiler chickens, on performance and lipid concentration were evaluated. 440 one-day old Arian broiler were randomly allotted into 20 pens which were assigned to 5 dietary treatments containing 0 (control), 3 or 5% tomato pomace, or 0.4 or 0.8% turmeric powder. Each dietary treatment was replicated 4 times with 22 broilers per pen. Feed and water were offered ad libitum. The ambient temperature was increased from 22 to 32°C for 5 h (10–15 h) on study d 28 to 42 (simulating diurnal temperature during heat stress). Relative humidity ranged from 50% to 65%. On study d 42, one bird from each replicate was randomly selected, slaughtered and blood samples taken from the jugular vein. Data were pooled and analyzed using the general linear model of SAS, and means were separated by Tukey test when $P < 0.05$. Dietary treatments did not influence ($P > 0.05$) body weight gain and feed intake. Feed conversion (intake/gain) was not affected by dietary treatments until d 28, after which it decreased ($P < 0.05$) in birds fed diets with a high content of tomato pomace and turmeric powder. Total cholesterol and triglyceride content of serum did not differ ($P > 0.05$) among dietary treatments. Birds fed diets with high contents of tomato pomace had higher ($P < 0.05$) concentration of HDL cholesterol in serum and no differences were found among birds fed the control diet and diets containing turmeric powder. The lowest serum LDL cholesterol was observed when birds were fed the diet containing 5% tomato pomace. It is concluded that supplementation of 5% tomato pomace and 0.8% of turmeric powder could alleviate the effects of heat stress on feed conversion and they could modulate the serum concentration of LDL and HDL cholesterol.

Key Words: tomato pomace, turmeric powder, heat stress

M319 Reduction of *Clostridium perfringens* colonization in turkey poults by feeding Primalac. S. Rahimi[1], J. L. Grimes*[2], S. Kathariou[2], and R. Siletzky[2], [1]*Tarbiat Modares University*, *Tehran, Islamic Republic of Iran*, [2]*North Carolina State University*, *Raleigh*.

Clostridium perfringens (CP) is recognized as an enteric pathogen in humans, domestic animals, and livestock. This organism is associated with necrotic enteritis, gangrenous dermatitis, clostridial dermatitis (turkeys) and gizzard erosion in poultry. This study was conducted to evaluate the effectiveness of a direct-fed microbial (DFM), Primalac (PM), as a preventative or mitigator of intestinal colonization by *C. perfringens* in turkey poults. One hundred and 20 8 d-old Large White Turkey poults were randomly divided into 4 treatments with 4 replicates (8 birds/pen) consisting of 1) basal diet (C); 2) basal diet supplemented with PM (1.5 kg/ton); 3) basal diet with poults gavaged with *C. perfringens* (C+CP); 4) basal diet supplemented with PM and poults gavaged with *C. perfringens* (PM+CP). Feed and distilled water were provided ad libitum throughout the trial. On d 3 and 7, each bird in CP groups were gavaged with 1 mL of *C. perfringens* (10^8cfu/mL). On d 21, 2 birds per pen were killed. Spleen and bursa of Fabricius (BF) were collected and weighed. On d 21, cecal contents were used for C. perfringens enumeration. Feed consumption (FC), BW and feed conversion ratio (FCR) were calculated weekly and cumulatively. Data were analyzed using GLM of SAS ($P < 0.05$). The *C. perfringens* in ceca were C – 5.88^{bc}, C+CP – 7.26^{a}, PM – 5.35^{c}, PM+CP – $6.19^{b} \pm 0.36$ $\log_{10}$ cfu/g. No differences were observed for BW, FC, FCR, organ weights, or relative organ weights. Further studies are needed to fully ascertain the potential of using DFM (Primalac) to reduce the colonization of *C. perfringens* in the gastrointestinal tract of turkey poults.

Key Words: *Clostridium perfringens*, direct fed microbial, turkey

M320 Influence of *Bacillus subtilis* PB6 (CloSTAT) on the performance of Hyline W-98 layers from 68 to 102 weeks of age. M. Elliot[1], R. Myers[2], A. Lamptey[2], and A. G. Yersin*[2], [1]*A&E Nutrition Services, LLC*, *Lititz, PA,* [2]*Kemin AgriFoods*, *Des Moines, IA*.

The microbial population of the gastrointestinal tract is influenced by several factors, including pH, substrate availability, toxins, antibodies, and other bacteria. Birds possess an unstable microbial ecosystem and poorly digested nutrients and anti-nutritional factors can lead to undesirable microbial growth, often resulting in a negative impact on performance. Periods of stress can cause a shift in the microbial profile from positive to negative. Products, such as CloSTAT Dry Direct-Fed Microbial, a DFM based on a patented *Bacillus subtilis* PB6 organism, assist in maintaining intestinal microbial balance. A study was conducted at a commercial laying operation to evaluate the effect of CloSTAT on the performance of Hyline W-98 layers from 68 to 102 weeks of age. One house, utilizing a split feeding system, was utilized in the study. This arrangement allowed one group of 136,000 hens to be fed the control diet and another group of 136,000 hens to receive the DFM treatment under similar housing conditions. CloSTAT was added at 1 lb/ton (0.5 kg/tonne) to normal second cycle diets 2–3 weeks before induction of the molt and fed for an additional 34 weeks. Egg production, egg weight, body weight, feed intake and mortality were measured weekly. Egg production and mortality tended to be improved in the CloSTAT group throughout the trial, resulting in an increase of 1.9 eggs per hen-housed and 0.57 lb (0.25 kg) of egg per hen-housed and a 1.5% reduction in mortality in the CloSTAT group. Feed intake and body weight were slightly elevated in the CloSTAT group through approximately 83 weeks of age, after which there was no discernible difference between treatment groups. The results of this trial suggest that the use of CloSTAT will result in improved production, improved hen-housed eggs and decreased mortality in second cycle Hyline W-98 layers.

Key Words: *Bacillus subtilis*, layers, egg yield

M321 Do dietary protein:energy ratios modify growth and frame size of young broiler breeder females? E. Mba*, R. A. Renema, A. Pishnamazi, and M. J. Zuidhof, *University of Alberta*, *Edmonton, AB, Canada*.

Feeding practices to minimize muscling of broiler breeder pullets could improve maternal support for early egg production and long-term maintenance of lay. A total of 1,140 Ross 708 broiler breeder females were divided into 30 pens (38/pen) and fed a common starter ration until 3 wk of age, when experimental diets began. Pens were randomly assigned to a high energy (HE), standard energy (STD) or low energy (LE) treatment and a low protein (LP) or high protein (HP) treatment in a 3 × 2 factorial with 3 energy (2,600 kcal, 2,800 kcal and 2,950 kcal) and 2 crude protein levels (14% and 16%). Pen BW was determined 2×/wk to allow feed allocation changes to maintain a common BW target. Individual BW was recorded every 2 wk from 3 wk of age and frame size parameters

(shank length, keel length, and thoracic width) measured every 4 wk. Results were assessed with the proc MIXED procedure of SAS, with significance assessed at the $P < 0.05$ level. Feed intake varied widely to achieve BW targets, ranging from 47.9 (HP-HE) to 54.2 g/bird/day (LP-LE) by 9 wk of age. Differences in feeding level did not impact growth as measured by shank or keel length. On average, LE birds ate 9% more feed than HE or STD birds (P=0.002). Hence, the HE ration provided no growth benefit to the birds compared to the STD diet. Birds fed the LP diet consumed approximately 10% more feed than HP birds to maintain a similar rate of BW gain ($P = 0.001$). Increased diet density had the potential to improve BW uniformity. The higher density HP/HE feed resulted in a BW CV of 13.7 compared to 15.1 for birds fed the lower density LP-LE diet. Impact of diets that elevated ME intake at the expense of CP were of interest. The HE-LP diet resulted in the highest overall ME intake/g feed (0.43/g) while providing average feed volume and measures of BW CV. However, when total intake of CP or ME per g of BW gain was measured, there were no differences among treatments. In this phase of growth, the degree of feed restriction limits lipid deposition, which may be masking the impact of unbalanced CP or ME intake.

Key Words: broiler breeders, CP, ME

M322 Population densities impact on feed intake and growth performance in Japanese quail. D. Cardoso-Jiménez[1], A. Z. M. Salem*[1,2], R. Rojo[1], S. R. Rebollar[1], and A. Perez-Cháves[1], [1]*Universidad Autónoma del Estadode México*, *Centro Universitario UAEM-Temascaltepec, Estado de México, México*, [2]*University of Alexandria*, *Department of Animal Production, Faculty of Agriculture (El-Shatby), Egypt*.

Two-hundred seventy-six Japanese quail (*Coturnix cournix japónica*) of 17 d of age were used to investigate the impact of population densities on quail feed intake and growth performance. A complete random design of 3 population densities (80 (PD80), 100 (PD100), and 120 (PD120) birds/m^2) of 4 repetitions were used during 17 d of the experiment in floor housing system of 4 pens for each population densities type. Dry matter intake (DMI), average daily gain (ADG), Feed conversion (FC) and mortality were evaluated. DMI was improved ($P < 0.05$) at PD120 than PD100 or PD80 (380, 313 and 310g DM/bird, respectively). No significant differences were observed among treatments in ADG, whereas the FC was significantly ($P < 0.05$) improved at PD80 compared with PD100 and PD120 (3.7, 4, 5.6, respectively). A similar mortality of 1% was observed at the 3 experimental treatments. Population densities may be a very important factor that could affect on quails growth performance. Data suggested that, population sizes at 80 birds/m2 was better than the other densities used

Key Words: Japanese quail, population density, growth performance

M323 Effects of dietary energy and broiler breeder hen energetic efficiency on egg production and fertility. T. G. V. Moraes*, M. J. Zuidhof, A. Pishnamazi, and R. A. Renema, *University of Alberta*, *Edmonton, Alberta, Canada*.

The effects of dietary energy and broiler breeder hen efficiency on production traits and duration of fertility were examined. At 21 wk, 192 Ross 708 pullets were individually caged in 1 of 6 environment chambers, and photostimulated at 23 wk. Birds were fed either a high energy (HE; 2900 kcal/kg) or low energy (LE; 2700 kcal/kg) diet. At 41 wk of age, individual energetic efficiency was determined through calculation of residual MEm (RMEm), which was the difference between observed and predicted maintenance requirements relative to ME intake. The highest and lowest efficiency hens (n = 32/group) were inseminated on 2 consecutive days. Eggs were collected for 21 d to measure duration of fertility. Results were analyzed with the MIXED procedure of SAS. Efficient hens were 266 g heavier than inefficient hens (P<0.0001), which did not affect egg size. Though egg numbers were similar, efficient hens produced 1.52 g/d more egg mass than inefficient hens ($P = 0.025$). At dissection (46 wk of age), inefficient hens had less breast muscle (19.8%) than efficient hens (20.8%), but neither % fatpad nor fertility were affected by hen efficiency. Egg weight in the LE treatment was 0.9 g more than HE eggs ($P = 0.056$), likely a result of 0.91 g/d higher CP intake with LE feed ($P = 0.13$). Duration of fertility of hens on the LE diet was 12.8 d compared to 11.8 d in HE treatment ($P = 0.034$). Hatch of fertile was similar among all treatment groups (mean=92.7 ± 1.5%). Breast muscle was larger in LE hens (20.7%) vs. HE hens (19.9%) and fatpad was 0.41% lower ($P = 0.0004$). These results suggest that the higher ME:CP ratio may reduce fertility due to lower CP intake.

Key Words: broiler breeder efficiency, metabolizable energy, fertility

M324 Growth performance of Pearl Grey guinea fowl subjected to varying floor densities from hatch to fourteen weeks of age. S. Nahashon*, J. Tyus, and D. Wright, *Tennessee State University*, *Nashville*.

Little is known of the required floor density for optimum performance of the Pearl Grey guinea fowl. The objective of this study was to assess the effect of varying floor densities on growth performance of the Pearl Grey guinea fowl. In 3 replicates, 786 1-d-old French guinea keets were weighed individually and randomly assigned to floor pens covered with pine wood shavings at 80, 69, 60 and 53 birds/pen, equivalent to densities of 18, 15.6, 13.6, and 12 birds/m^2, respectively. Birds in these floor densities were allowed feeder space of 2.3, 2.7, 3.1, and 3.5 cm/bird, respectively, and water space of 1.2, 1.4, 1.6, and 1.8 cm/bird, respectively. All birds received 23 h and 12 h lighting regimen at 0–8 and 9–14 weeks of age (WOA) and were fed diets comprising 3,000 and 3,100 kcal of ME/kg of diet at 0–5 and 6–8 WOA, respectively, and 24% CP. The birds were fed diets comprising 3,100 kcal ME/kg of diet and 18% CP at 9–14 WOA. Feed and water were provided for ad libitum consumption. Body weight and feed consumption (FC) were measured weekly. Overall body weight gains (BWG) were higher ($P < 0.05$) and feed conversion ratios (FCR) were significantly lower in birds reared on floor density of 18 birds/m2 when compared with birds on floor densities of 12, 13.6 and 15.6 birds/m^2 at 0–8 WOA. However at 9–14 WOA, birds in floor densities of 12 birds/m2 exhibited higher BWG and feed consumption and significantly lower FCR ($P < 0.05$) than those reared on 13.6, 15.6 and 18 birds/m2. Therefore, pearl gray guinea fowl seem to exhibit superior performance when reared at floor densities of 18 birds/m^2 at 0–8 WOA and 12 birds/m2 at 9–14 WOA.

Key Words: Pearl Grey guinea fowl, floor density, growth performance

M325 Feedlot performance and carcass traits of hairsheep lambs treated with a β-adrenergic agonist during summer. J. V. Velázquez-Morales, F. D. Álvarez-Valenzuela, N. G. Torrentera-Olivera, J. Rodríguez-García, U. Macías-Cruz, A. Correa-Calderón, and L. Avendaño-Reyes*, *Instituto de Ciencias Agricolas, Universidad Autonoma de Baja California*, *Ejido Nuevo Leon, Valle de Mexicali, Baja California, Mexico*.

The objective of this study was to determine the effect of feeding the β-agonist zilpaterol hydrochloride to female lambs on growth traits and carcass characteristics during hot ambient temperatures. Twenty female lambs from hairsheep crossbreeds with an average initial BW of 32.2 ± 0.58 kg were used in a 33 d feeding study. The lambs were blocked by initial BW and assigned individually to 20 pens in a closed calf rearing unit provided with fans during summer. Data were analyzed under a completely randomized block design. Treatments were: 1) Control (C: no β-agonist in the diet), comprising a formulation of wheat grain, molasses, alfalfa hay, soybean meal, wheat straw, and a mineral supplement; and 2) a treated group supplemented (as fed basis) with 10 mg of zilpaterol hydrochloride (ZH; Zilmax, Intervet, Mexico City, Mexico) per head per day. The ZH feed additive was mixed into 100 gr of wheat grain and was offered daily in the morning before offering the finishing diet. Climatic conditions during the study revealed a severe heat stress conditions, with an average ITH of 88.2 units during the study. Lambs fed ZH had similar ($P > 0.05$) feedlot performance (daily weight gain, final weight, fed intake, feed conversion, and gain:feed ratio) than control lambs. The β-agonist increased hot and chilled carcass weights, with carcasses from ZH lambs being 13% and 12% heavier ($P < 0.01$) than carcasses from C lambs respectively. Dressing percentage was higher in ZH lambs (53.8%; $P < 0.01$) than in C lambs (46%). The rib-eye area was larger ($P < 0.05$) in ZH lambs (18.9 cm2) than in C lambs (15.5 cm2), as well as carcass conformation (7.0 vs 6.0 units for ZH and C lambs, respectively). There was no difference ($P > 0.05$) in carcass length, fat thickness, kidney, pelvic and heart fat, and shear force between ZH and C lambs. Hide and head weights, as well as weight of several internal organs (heart, lungs, liver, kidneys, small intestine, and rumen, omasum and abomasum) did not differ between treatments ($P > 0.05$). Even though the severe hot ambient conditions observed during the study, some carcass traits were improved in hairsheep female lambs supplemented with zilpaterol hydrochloride.

Key Words: female lambs, zilpaterol hydrochloride, heat stress

M326 Genetic factors affecting survival rate and litter size of Pelibuey ewes under two times of weaning in northwestern Mexico. U. Macías-Cruz[1], F. D. Alvarez-Valenzuela[1], A. Correa-Calderón[1], L. Molina-Ramírez[2], and L. Avendaño-Reyes*[1], [1]*Instituto de Ciencias Agrícolas, Universidad Autónoma de Baja California*, *Ejido Nuevo León, Valle de Mexicali, Baja Cañifornia, México*, [2]*Centro de Bachillerato Tecnológico Agropecuario No. 41*, *Poblado Benito Juárez, Valle de Mexicali, Baja California, México*.

The aim of this study was to evaluate the effect of sire breed, type of birth and lambing year on some traits of Pelibuey ewe productivity in 2 times of weaning. As part of a hairsheep crossbreeding program between Pelibuey (Pb) ewes and Dorper (Dr), Katahdin (Ka) and Pb rams, data from 250 ewes lambed during 2003 and 2008 were used to characterize Pb ewe productivity with breeds specialized in mutton production. Response variables were litter size, and survival rate at 0 (lambing), 30, 60 and/or 90 d post-lambing per ewe lambed. Weaning time at 60 d occurred from 2003 to 2005, and weaning time at 90 d from 2005 to 2008. The information was divided based on weaning time, 60 or 90 d. Two models based on a factorial design, which included fixed effects of lambing year, type of birth (1, 2, or > 3) sire breed (3) and double interactions among them were performed. For 60 d weaning time, sire breed did not influence ($P > 0.05$) litter size or survival rate at lambing; but at 30 and 60 d post-lambing, survival rate was greater ($P < 0.01$) in litter of ewes mated by Ka sires (0.96 ± 0.05 and 0.95 ± 0.05) than those mated by Pb sires (0.78 ± 0.05 and 0.68 ± 0.06). Ewes with multiple lambing ($P < 0.05$) had higher litter size (3.20 ± 0.06, 2.44 ± 0.12 and 2.18 ± 0.14 lambs/ewe lambed at 0, 30 and 60 d, respectively) but lower survival rate (0.78 ± 0.05 and 0.70 ± 0.05 at 30 and 60 d, respectively) than those ewes with single or twin lambing during all pre-weaning period. For 90 d weaning time, there was higher ($P < 0.05$) litter size at 30, 60 and 90 d in ewes with multiple lambing and mated by Dr or Ka sires than all other ewes. At 30, 60 and 90 d, ewes with multiple lambing had the lowest ($P < 0.05$) survival rate than those of single or twin lambing. Survival rates at weaning time (60 and 90 d) were affected ($P < 0.05$) by lambing year in both models. Collectively, these results suggest that survival rate and litter size of Pb ewes could be improved through crossbreeding schemes including Dr or Ka. Type of lambing had a marked influence on survival rate and litter size.

Key Words: hair sheep, ewe lambed, weaning

M327 Artificial insemination in reindeer using frozen-thawed semen. M. P. Shipka*[1], J. E. Rowell[1], and S. Bychawski[2], [1]*University of Alaska Fairbanks*, *Fairbanks,* [2]*Optimum Genetics*, *Regina, Saskatchewan, Canada*.

Traditional practices of extensive reindeer ranching on the Seward Peninsula, Alaska, are being modified to accommodate a rapidly changing environment. Holding reindeer in large enclosures during vulnerable times of the year (breeding and calving season) is a practice being tried by some herders. Enclosing reindeer, even temporarily, requires the adoption of management strategies more typical of traditional agriculture. However, such strategies need to be modified to cope with the extreme logistics imposed by an arctic environment. Artificial insemination has been proposed as an alternative to maintaining rutting bulls in enclosures. Our objective was to evaluate the practicality of using AI in the Alaska reindeer industry. Semen was collected from a 15 mo-old reindeer bull in Saskatchewan, Canada, processed to a final dilution of 3.5×10^7 sperm per 0.5cc straw, frozen and shipped to Alaska. Sperm motility was 70% (fresh) and 45% (thawed) with 68% normal sperm. We applied a white-tailed deer AI protocol to 8 nulliparous, 2.5 yr-old captive reindeer at the UAF Agricultural and Forestry Experiment Station. The female reindeer were synchronized with CIDR-b, modified to fit the smaller reindeer vagina, using a 2 CIDR, 14 d schedule. At removal of the second CIDR, the females received 200 IU PMSG I.M. (either PG 600, n = 4; or PMSG, Sigma Chemicals, n = 4). At the time of breeding, one female's vagina was too small to accommodate the speculum and she was dropped from the study. The remaining 7 females exhibited signs of estrus (copious, clear mucus) at insemination. Intracervical insemination took place 55 h after CIDR removal. PSPB assay of serum collected 11 wks post-insemination indicated 1 pregnant female, 1 female possibly undergoing pregnancy loss and 5 open females. Options for increasing pregnancy rate within the context of the logistics imposed by an arctic reindeer industry require further research.

Key Words: reindeer, artificial insemination

M328 Constant long artificial days increase milk production in Alpine goats in northern Mexico. R. Rodríguez-Martínez*[1], C. A. Meza-Herrera[2], M. A. De Santiago-Miramontes[1], M. Mellado[3], and F. G. Véliz[1], [1]*Universidad Autónoma Agraria Antonio Narro*, *Torreón, Coahuila, Mexico*, [2]*Universidad Autónoma Chapingo, Unidad Regional Universitaria de Zonas Áridas*, *Bermejillo, Durango, México*, [3]*Universidad Autónoma Agraria Antonio Narro*, *Buenavista, Saltillo, Coahuila*.

The aim of this study was to determine if the use of an artificial long-day photoperiod scheme during winter and spring improves milk production in Alpine goat raised in Northern Mexico. Alpine multiparous goats (n = 40) were randomly assigned to one of 2 experimental groups: Control Group (CG; n = 21), exposed to naturals photoperiod variations of the region during the whole experimental period (10 h and 19 min in the winter solstice), and the Experimental Group (EG; n = 19), subject, from December 28th to may 12th, to a constant long day photic treatment (16 h light/8 h dark). Both groups were fed 300 g concentrate/animal/day, and alfalfa hay ad libitum. From the beginning of the trial (d 0 = 13 ± 0.6 postpartum days) up to d 14 (weaning of kids). Milk yield was daily recorded and data were analyzed by means of 2 factors ANOVA (time and treatment) followed by Student's *t*-test, to find differences between experimental groups. Milk yield did not differ ($P > 0.05$) between groups. However, from 28 d to 112 d, 20% increase of milk yield was observed in the EG-group (3.3 ± 0.1 vs. 2.6 ± 0.04 L/day/animal EG vs. CG; $P < 0.02$). These results show that, during winter and at the beginning of spring, exposure to a long day artificial photoperiod scheme induced an increase in milk production in Alpine goats raised in northern Mexico. Further studies are required to evaluate the effect of a long-day photoperiodic scheme upon milk production during the prepartum period as well as how this photoperiodic treatment could affect the hormonal reproductive status in goats.

Key Words: milk yield, milk composition, photoperiod

M329 Blood selenium levels in mule deer in eastern Washington. E. López-Pérez*[1], L. A Shipley[2], and W. Myers[3], [1]*Universidad Autónoma Chapingo*, *México*, [2]*Washington State University, Pullman,* [3]*Washington Department of Fish and Wildlife*.

Mule deer have been declining in the western United States over the last few decades, including eastern and north-central Washington. Because eastern Washington is naturally deficient in selenium (Se), Se deficiencies can affect the productivity of ungulates, and little is known about the natural concentration of Se in mule deer, we examined the range and spatial distribution of the concentration Se in mule deer across eastern Washington. We captured 115 female mule deer by net-gunning from a helicopter in 2002–2003 in 7 study areas ranging from shrub-steppe to montane coniferous forests. We collected 10 mL of whole blood from each animal by jugular venipuncture, and determined the concentration of Se in the blood using neutron activation. Individual blood Se concentration varied over 4 orders of magnitude, ranging from 0.000084 to 0.497 ppm. Study area means varied from a low of 0.04 ± 0.02 in 2 shrub steppe habitats to a high of 0.090 ± 0.02 and 0.125 ± 0.01 in 2 montane habitats ($F = 2.47$, $P < 0.01$, Table 1). Surprisingly, patterns of blood Se did not correspond with soil Se values, which are lower in the more northern and western montane habitats. These values are low when compared with livestock standards of >0.1 ppm which may indicate a potential for Se deficiency. On the other hand, mule deer, may have a lower Se requirement than do livestock and are adapted for soil and plant conditions in northeastern Washington.

Table 1. Blood selenium levels (ppm) in mule deer does from north central eastern Washington

Study areas	Habitat	Spring n	Spring blood Se content (ppm)	Winter n	Winter blood Se content (ppm)
Chelan	Montane forest	22	0.062±0.012	18	0.124±0.012
Flagstaff	Montane forest			5	0.076±0.028
Okanogan	Montane forest	5	0.094±0.023	4	0.088±0.025
Vulcan	Montane forest	9	0.060±0.006	7	0.060±0.012
Cofee pot	Shrub-steppe			12	0.048±0.015
Revere	Shrub-steppe			13	0.061±0.010
Colville	Shrub-steppe	6	0.047±0.021	17	0.060±0.012

Key Words: deer, selenium, blood

M330 Breeding performance of rams in two Wyoming producer flocks. B. M. Alexander*[1], N. Cockett[2], T. L. Hadfield[2], and G. E. Moss[1], [1]*University of Wyoming*, *Laramie,* [2]*Utah State University*, *Logan*.

Poor mating behavior results in increased ram costs, extended lambing seasons, and decreased genetic progress from sires with desired production traits. Producers recognize the importance of ram libido; however, time, labor, and facility constraints generally limit its routine evaluation. Although approximately 23% of all rams were predicted to exhibit poor-mating behaviors, breeding performance of individual rams in multi-sire flocks typical of Wyoming range operations has not been determined. Therefore, goals of the current experiment were to determine the incidence of low- and high sexually performing rams and numbers of lambs sired by each ram in 2 representative range flocks. All rams successfully passed breeding soundness evaluations conducted before the onset of the breeding season. Blood samples were collected from all rams, and approximately one-third of the lambs and their dams for paternal genotyping using microsatellite markers. Assuming each ram had equal opportunity to mate with ewes in estrus, number of lambs expected to be sired by each ram was established by calculating 99% confidence intervals for the mean in each flock. In flock one, sires (n = 24) for 290 lambs (80% of lamb samples) were successfully identified. Of those rams, 7 (29%) sired less than, 11(46%) equal to, and 6 (25%) sired more lambs than predicted (siring 6.9, 47.6, and 45.5% of the sampled lambs, respectively) based on the 99% confidence interval. In the second flock, sires (n = 13) for 170 lambs (85% of lamb samples) were successfully identified. Similar to flock one, 3 (23%) rams sired less than, 7 (54%) equal to, and 3 (23%) sired more lambs than predicted siring 8.2, 54.4, and 39.4% of the sampled lambs, respectively. These data emphasize the importance of identifying and eliminating poor-sexually performing rams to reduce sire costs. In addition, the identification and use of high-sexually performing rams with desired genetic traits is a requisite to the timely incorporation of those traits into a flock.
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Key Words: ram, parental genotyping, breeding performance

M331 Breaking resistance of lamb ears according to ear tag insertion position and sheep breed. G. Caja*[1], H. Xuriguera[2], M. A. Rojas-Olivares[1], S. González-Martín[2], A. A. K. Salama[1], S. Carné[1], and J. J. Ghirardi[1], [1]*Universitat Autònoma de Barcelona*, *Bellaterra, Barcelona, Spain*, [2]*Universitat de Barcelona*, *Barcelona, Spain*.

A total of 167 lamb ears tagged with official plastic ear tags were obtained after harvesting in a commercial slaughterhouse and used to study the resistance to breakage when submitted to tensile forces

under laboratory conditions. Ears were washed (cold and warm water) and classified according to breed (Lacaune, n = 26; Manchega, n = 45; Ripollesa, n = 60; other, n = 36), side (left, right), ear tag insertion position (distal, central, proximal) and preservation method (fresh, 1-7 d in a refrigerator, 2 to 4 wk in a freezer). Breaking force was measured by submitting the ears to a tensile test using a computer-controlled universal testing machine (PCM Mecmesin, Horsham, UK). Ears were locked to a fixed clamp at the insertion base and ear tags fixed to a mobile clamp to be tested by pulling the ear tag at a constant displacement rate (500 mm/min) until the ears broke. On average, ears measured 107 ± 1 mm long and 51 ± 0.4 mm wide, have ear tags adequately inserted (12% distal, 40% central and 24% proximal) and broke longitudinally at 191 ± 5 N (9.8 N = 1 kgf). No ear tags broke or opened during the test. Ear breaking force varied quadratically ($R^2 = 0.999$, $P < 0.001$) according to ear tag insertion position (distal, 93 ± 6; central, 188 ± 5; proximal, 251 ± 8 N) and by breed (Lacaune, 205 ± 11; Manchega, 193 ± 8; Ripollesa, 233 ± 8; other, 107 ± 6 N), but did not vary according to side or short-term preservation method ($P > 0.05$). Freezing reduced the force to break the ears ($P < 0.01$). In conclusion, ear tag position was a key factor for ear breakage. New ear tag design, taking into account ear resistance may improve sheep welfare and ear tag retention rate for long-term identification.

Key Words: identification, eartag, sheep

M332 Animal weight gain in a pastured hog production system. S. Pietrosemoli*[1,2], J. C. Guevara[2], J. Cardona[3], W. Maradiaga[3], A. Lobo[3], and J. T. Green[4,2], [1]*Animal Science Dept., North Carolina State University*, *Raleigh,* [2]*Alternative Swine Research and Extension Project*, *Raleigh, NC,* [3]*Universidad Nacional de Agricultura*, *Catacamas, Olancho, Honduras.*, [4]*Crop Science Dept., North Carolina State University*, *Raleigh.*

At the Center for Environmental Farming Systems (CEFS) located in Goldsboro NC, 60 crossbred (Yorkshire, Landrace, Hamsphire and Duroc) commercial hogs (35.7 ± 2.1 kg and 125.7 ± 2.3 kg initial and final live weight, respectively) were used in a 98-d trial (May–August 2009) to evaluate the effect of stocking rate (SR; 37, 74, 111, and 148 heads/ha) and sexual condition (SC; castrated male [CM] or female [F]) on average daily weight gain (ADG). Animals were managed under a continuous grazing system on bermudagrass (*Cynodon dactylon*) plots sized to match the SR, and had ad libitum access to a concentrate feed (16% CP). The average pig concentrate intake (ACI) was estimated for each plot. Five hogs were allotted to each one of 12 plots, but data from only 4 (2 CM and 2 F) animals were included in the statistical analysis. The experimental design was a randomized complete block, with 4 × 2 factorial arrangement of treatments and 3 field replicates. ANCOVA was performed using the PROC GLM procedure of SAS, v. 9.1 with initial live weight as a covariate. Differences were observed for ADG between replicates ($P = 0.0009$); SR ($P = 0.0566$) and SC ($P < 0.0001$). Animals in the lowest SR (37 heads/ha) had the lowest ADG (0.85 kg) whereas the other treatments were similar (0.94, 0.96 and 0.90 kg ADG, respectively, for 74, 111 and 148 heads/ha). ADG of CM was 17.9% higher than of F (0.99 vs 0.84 kg, respectively). ACI differed between replicates ($P = 0.0027$) and SR ($P = 0.0182$). The lowest intake was recorded for pigs in the lowest SR (37 heads/ha, 2.90 kg/head/d) compared with the other SR (2.96; 2.96; 2.94 kg/head/d, for 74, 111 and 148 heads/ha, respectively). Results indicated that performance of pasture-finishing pigs was influenced by SR and SC.

Key Words: outdoor swine, bermudagrass, weight gain

M333 Analysis of the effect of complexed trace minerals on the prevalence of lameness and severity of claw lesions in stall-housed sows. S. S. Anil*[1], L. Anil[2], J. Deen[1], S. K. Baidoo[2], M. E. Wilson[3], and C. Rapp[4], [1]*Veterinary Population Medicine, University of Minnesota*, *St Paul,* [2]*Southern Research and Outreach Center, University of Minnesota*, *Waseca,* [3]*Zinpro Corporation*, *Eden Prairie, MN*, [4]*Zinpro Performance Minerals*, *Boxmeer, the Netherlands*.

When considering the development of claw lesions, mineral nutrition is an important factor to examine. Trace minerals such as Cu, Zn and Mn are reported to be critical in the keratinization process. Both the quantity and form (organic or inorganic) determine the bioavailability of the trace minerals. The objective of the present study involving 229 sows was to evaluate the effect of supplementing complexed trace minerals on the prevalence of lameness and lesions in different claw areas (side wall, heel, including overgrown heel, sole, heel-sole junction, white line, and overgrown dew claw and toe) of stall-housed gestating sows. The sows were randomly allocated to 2 groups and fed either a control diet (ITM, inorganic sulfate minerals, n = 113; Zn–125 ppm, Mn–40 ppm and Cu–15 ppm) or a diet containing complexed trace minerals (CTM, n = 116) as a partial substitution of inorganic minerals Zn-50 ppm, Mn–20 ppm and Cu–10 ppm) fed at isolevels of total trace mineral supplementation. The lesions in different claw areas of these sows were scored by a trained person in one or 2 consecutive parities at mid-gestation. The total score for each claw area was obtained by adding the scores for that area in different claws. The sows were assessed for lameness while they were moved for lesion scoring. The scores for lesions in different claw areas among the sows fed ITM or CTM were compared using Kruskal-Wallis Test. The proportions of lame sows among the groups were compared using 2-sample proportion test. The results indicated that total claw lesion score and total lateral claw lesion score were lower ($P \leq 0.05$ for both) in the sows fed CTM. The total score for horizontal side wall cracks was higher ($P \leq 0.05$) for the sows fed CTM. The proportion of lame sows was lower ($P \leq 0.05$) in the sows fed CTM (34.5% vs. 51.0%). The results show a protective effect of complexed trace mineral supplementation on claw lesions and lameness in stall-housed sows.

Key Words: claw lesions, lameness, trace mineral supplementation

M334 Comparison of the production performance of group-housed sows receiving complexed trace minerals. S. S. Anil*[1], L. Anil[2], J. Deen[1], S. K. Baidoo[2], M. E. Wilson[3], and T. L. Ward[3], [1]*Veterinary Population Medicine, University of Minnesota*, *St Paul,* [2]*Southern Research and Outreach Center, University of Minnesota*, *Waseca,* [3]*Zinpro Corporation*, *Eden Prairie, MN*.

Trace minerals are important to maintain the high production performance of the modern sow. The bioavailability of trace minerals depends on both the quantity and form (organic or inorganic). The objective of the present study, involving 386 sows housed in group pens with electronic sow feeders was to compare the production performance of sows fed diets containing complexed trace minerals (CTM) with sows fed diets containing trace minerals in inorganic form (ITM). The CTM diet contained trace minerals as a partial substitution of inorganic minerals (Zn, 50 ppm, Mn, 20 ppm and Cu, 10 ppm) fed at isolevels of total trace mineral supplementation. The ITM diet contained inorganic sulfate minerals, Zn 125 ppm, Mn, 40 ppm and Cu, 15 ppm). The sows were allocated randomly to CTM (n = 197) and ITM (n = 189) diet groups. 1056 parity records (ITM, n = 527; CTM, n = 529) of these sows pertaining to 1, 2, 3 or 4 farrowings were obtained during the study period. Information on farrowing and weaning performances and lactation feed intake were collected from the PigCHAMP database of the research unit and sow cards, and compared using 2 sample *t*-test (SAS v. 9.1). Results indicated differences ($P < 0.05$ for all) between the sows fed ITM and CTM in terms of still born (1.3 in ITM vs. 1.1 in CTM), average piglet weight at weaning (14.0 in ITM vs. 14.3 lbs in CTM) and weight of the sow at weaning (543.4 in ITM vs. 531.6 lbs in CTM). The groups did not differ ($P > 0.05$) in terms of piglets born alive, mummies, average birth weight of pigs and average lactation feed intake.

Key Words: complexed trace minerals, production performance, sows

M335 Risk factors associated with frequency of abortion in swine farms. N. M. Rainho[1], M. Aparicio[1], M. A. de Andrés[1], J. Morales[1], R. Pallás[2], V. Rodríguez-Estévez[3], and C. Piñeiro*[1], [1]*PigCHAMP Pro Europa*, *Segovia, Spain*, [2]*Kubus, SA*, *Madrid, Spain*, [3]*Universidad de Córdoba*, *Spain*.

Current swine production is linked to a proper analysis and monitoring of results. Literature has described references for most of the reproductive factors, but interactions between them have not been studied in depth.

The objectives of the present study were to investigate the relationship between the relative frequency of abortion (percentage; AP) and number of parity (NP), weaning to first mating interval (WSI), number of services (NS), and day of week for service (DW). More than 870,000 mating records through 4 years (2005–2008) corresponding to about 80,000 sows in 161 farms from Spain, Portugal and Italy registered with PigCHAMP software were used. Each factor was categorized in different groups: NP in 1, 2, 3–6 and ≥ 7 parities; NS in first-serviced (FS), first re-serviced (FRS) and second-reserviced (SRS); WSI in ≤ 3, 4–7, 8–11 and ≥ 12 d; and DW in weekday and weekend. Data were analyzed using the MIXED procedure of SAS (v 9.00). Mean value of AP was 0.78 ± 0.03%. Among NP, mean AP in parities 1 and ≥ 7 was higher than those in parities 2 and 3–6 ($P < 0.001$), showing a quadratic effect that explains the higher risks in both gilts and old sows. A lineal effect was found for WSI, when AP in WSI ≤ 7 was lower than those of WSI ≥ 8 ($P < 0.001$). AP also depended on DW, and it was higher for matings during the weekend ($P < 0.001$). Finally mean AP for NS increased with the number of estrus repetition, showing 0.45, 2.87, 4.26% for FS, FRS, SRS respectively ($P < 0.001$). Some interactions between the main factors studied were found, being the most interesting one between WSI and DW: sows with ≤ 3 WSI showed no differences between DW; sows with normal WSI (4–7 d) showed a higher risk during weekends (0.63 vs 1.29%; $P < 0.001$); AP in later mated sows served 8–11 d post weaning was lower in matings during weekend (1.24 vs 0.75%; $P < 0.001$). These results add more information about the relative information of some classical factors as NP, NS or WSI, and show a new factor as it is DW.

Key Words: abortion risk factors, swine, abortion

M336 Analysis of the effect of high ambient temperature on growing pigs performance: A meta-analysis approach. D. Renaudeau* and J. L. Gourdine, *Institut National de la Recherche Agronomique, UR143*, *Petit-Bourg, French West Indies*.

The high ambient temperature has been recognized as the most important climatic factor influencing pig performance during summer heat waves in temperate climate and all the year in tropical climate. However, results from experiments dealing with the effects of high temperature on pig performance are remarkably variable. In the present work, a meta-analysis was carried out to analyze the results from different studies designed to evaluate the effect of elevated temperature on average daily feed intake (ADFI) and average daily gain (ADG) in growing finishing pigs. Data were extracted from 86 and 80 trials for ADFI and ADG, respectively, from studies published in scientific journals in PubMed, Science direct and proceedings of scientific meetings updated trough December 2009. Data on ADFI and ADG were analyzed with a linear mixed model that included the linear and the quadratic effects of temperature (T) and pig body weight (BW), the interaction between T and BW as covariates. The trial has been included as block random variable. The effects of housing conditions (n = 2; individual vs. group) and the year of publication of the trial (n = 3; 1970–1989, 1990–1999, and 2000–2009) were tested on the intercept and the linear slope of T. Results showed that high T had a curvilinear effect of ADFI and ADG and that this effect was highlighted in heavier pigs. Whatever the temperature level, the ADFI was lower when pigs were group-housed. The intercept and the slope for T were significantly affected by the year of the study publication. The effect of elevated T was greater in earlier works suggesting that modern genotypes could be more sensitive to heat stress than low growth potential pigs. In conclusion, results of this meta-analysis confirm that a large between-study variability exits for the effects of high T on pigs' performance. A part of this variability is explained by changes in pig BW and to a lesser extent by the year of the study publication.

Key Words: pig, heat stress, performance

M337 Weight gain of Duroc pigs managed in a Sudangrass (*Sorghum bicolor*) pasture. S. Pietrosemoli*[1,2], J. C. Guevara[2], A. Lobo[3], J. Cardona[3], W. Maradiaga[3], and J. T. Green[4,2], [1]*Animal Science Department, North Carolina State University*, *Raleigh,* [2]*Alternative Swine Research and Extension Project*, *Raleigh, NC,* [3]*Universidad Nacional de Agricultura*, *Catacamas, Olancho, Honduras.*, [4]*Crop Science Department, North Carolina State University*, *Raleigh.*

To reduce potential upload of soil nutrients in pastured swine systems and improve their spatial distribution, producers have the possibility to implement strategic movements of equipment. Therefore, the impact of either stationary (S) or mobile (M) shade and drinking structures on average daily weight gain (ADG) were investigated with female (F) or castrated male (CM) pigs. Mobile structures were moved on a weekly basis. Seventy-two Duroc pigs (31.9 ± 0.76 and 96.9 ± 1.69 kg initial and final live weight, respectively) were used in summer 2009 at the Center for Environmental Farming System (CEFS) in Goldsboro, NC. Twelve pigs were randomly assigned to each of 6 sudangrass paddocks (0.16 ha, 74 head/ha) and were managed under a continuous grazing system during 12 weeks. Pigs had ad libitum access to a concentrate feed (16% CP) and water. Individual pig concentrate intake (CI) was estimated from paddock average. Data from only 8 pigs (4 F and 4 CM) per paddock were included in the statistical analysis. The experimental design was a randomized complete block with a 2 × 2 factorial arrangement of treatments (S or M; F or CM) and 3 field replicates. ANOVA was performed using PROC GLM of SAS v 9.1. Initial weight (IW) was used as a covariate for ADG . Weekly movements of structures influenced CI ($P = 0.0572$) (2.37 vs 2.25 kg/head/d for S and M, respectively). Sexual condition ($P < 0.0001$) and IW affected ADG (0.71 vs 0.84 kg/day for F and CM, respectively). According to the results of this study, weekly movements of shade and drinking structures did not affect pig average daily weight gain.

Key Words: outdoor pigs, sudangrass, weight gain

M338 Heat challenge effect on peripheral blood mononuclear cells viability: comparison of a tropical and a temperate pig breed. J. C. Bambou, R. Grondin, J. L. Gourdine, and D. Renaudeau*, *Institut National de la Recherche Agronomique, UR143*, *Petit Bourg, French West Indies, France*.

Evidence was found that local Caribbean pigs (Creole) are better adapted to seasonal climatic changes of tropical climate than exotic breeds imported from Europe. We evaluated the effect of heat challenge on peripheral mononuclear blood cells (PBMC) isolated from Creole (CR) and Large White (LW) pigs, on cell viability, concanavalin A– induced proliferation and heat shock proteins (HSPs) mRNA expression. PBMC from Creole (CR) and LW growing pigs of 7 to 12 weeks of age were isolated, cultured for 9 h at 37°C, and thereafter subjected to one of the 3 trials. In trial 1, cells from 18 CR and 18 LW pigs were exposed to 42°C or 45°C for 2, 4, 6 and 9 h and cell viability was monitored using the trypan blue method. In trial 2, we evaluated mitogen–induced proliferation of PBMC from 5 CR and 5 LW pigs after for 2 and 9 h heat exposure at 45°C followed by 24 h-stimulation at 37°C with concanavalin A. The aim of trial 3 was to measure induction of HSP70.2 and HSP90 mRNA expression in PBMC from 5 CR and 5 LW pigs after a heat challenge at 45°C for 3, 6 and 9 h. Viability was affected by breed and temperature ($P < 0.01$) but no effect of breed × temperature or breed × exposure

time interactions was observed. The decrease in viability caused by heat challenge was greater for LW than for CR pigs. For mitogen-stimulated PBMC, incubation at 45°C reduced lymphoblastogenesis ($P < 0.001$). However, this reduction was not influenced by breed ($P > 0.05$). When compared with PBMC cultured at 37°C, the mRNA expression of HSP70.2 and HSP90 increased at 45°C. After 9 h exposure at 45°C, PBMC from CR pigs showed a decreased expression of HSP90 mRNA when compared with the LW pigs. In contrast, the temperature × breed interaction was not significant for HSP70 mRNA expression. In conclusion, breed differences in resistance to heat challenge at the whole organism scale is also reflected at the cellular level. Neither HSP70.2 nor HSP90 mRNA expression level could explain this effect.

Key Words: pig, breed, heat stress

M339 Manipulation of rumen fermentation and ecology of swamp buffalo by coconut oil and garlic powder supplementation. P Kongmun*[1,2], M Wanapat[1], and Z Yu[2], [1]*Khon Kaen University*, *Khon Kaen, Thailand, 40002*, [2]*The Ohio State University*.

This experiment was conducted to investigate the effect of coconut oil (CO) and garlic powder supplementation on digestibility of nutrients, ruminal fermentation, ecology, microorganisms and methanogen diversity. Four, 3-year old, rumen fistulated swamp buffalo bulls were randomly assigned in a 4 × 4 Latin square design to receive 4 dietary treatments; 7% CO, 7% CO with 50 g/d of garlic powder, 7% CO with 100 g/d of garlic powder and non-supplemented (control). During the experiment, concentrate was offered at 0.5% of BW while rice straw was given on ad libitum basis. It was found that supplementation of 7% CO had significantly influenced on total DM intake, OM, NDF and ADF digestibilities while supplementation of 7% CO with garlic powder (50 and 100 g/d) were not significantly different when compared with the control. Blood urea nitrogen was significantly higher in supplemented groups. Total VFA concentration, proportion of C2 and C2:C3 ratio was reduced by supplementation. Proportion of C3 was increased ($P < 0.05$) when supplemented with 7% CO and 7% CO with 100 g/d of garlic powder. Methane production was dramatically reduced ($P = 0.005$) in supplemented treatments and was 10% reduced in 7% CO supplementation. Amylolytic and proteolytic bacteria were increased ($P = 0.007$ and $P = 0.024$) while protozoal population by decreased 68 – 75% ($P < 0.01$) by supplementation. Total bacterial population was increased by supplementation while total fungi and total methanogens were not significantly different among treatments. Percentage of cellulolytic bacterial population was not different among treatments. However, dietary supplementations were reduced ($P < 0.001$) percentage of F. succinogenes population. However, methanogen diversity was not changed using PCR-DGGE as technique. Based on this study, supplementation with 7% CO plus 100 g/d of garlic powder could be efficiently utilized in the rumen and thus, could provide good fermentation end-products and improve rumen ecology for the host swamp buffaloes particularly in reducing 9% methane gas production without changing nutrient digestibilities.

Key Words: garlic powder, coconut oil, swamp buffalo

M340 Adding whole hops to high concentrate diets enhances *in vitro* ruminal fermentation. N. Narvaez*, Y. Wang, Z. Xu, and T. McAllister, *Agriculture and Agri-Food Canada*, *Lethbridge, AB, Canada*.

To assess the potential of hops (*Humulus lupulus*) as an alternative to antimicrobials for improving ruminant production, whole hops (pelleted and ground) were included in batch culture in vitro ruminal incubations (500 mg substrate + 40 mL inoculum) of barley grain (Exp 1) and barley grain:barley silage-finishing diet (Exp 2). Hops were included at 0, 50, 100, 200 and 400 μg/mL in Exp. 1; in Exp. 2, at 0, 200, 400, 800, and 1600 μg/mL, with and without polyethylene glycol (PEG; 250 μg/mL). PEG was included to selectively deactivate condensed tannins (CT). In Exp. 1, ^{15}N-labeled $(NH_4)_2SO_4$ was used to measure microbial protein (MP) synthesis. Gas production and methane concentration were measured at 3, 6, 12, and 24 h in both Exps. Concentrations of VFA and ammonia (NH_3-N), starch disappearance and MP synthesis were determined at 3, 6, 12, and 24 h in Exp 1. Total VFA, NH_3-N and apparent DM disappearance (DMD) were analyzed after 48 h in Exp. 2. Adding PEG did not alter the in vitro rumen fermentation suggesting that hop CT were not responsible for altering microbial activity. With hops inclusion, gas production from barley grain was linearly increased ($P = 0.029$) but from finishing diet, it was linearly ($P < 0.001$) decreased. Apparent dry matter disappearance (DMD) from finishing diet and starch disappearance from barley grain increased linearly ($P < 0.001$) with increasing hops content. Hops linearly increased ($P < 0.001$) VFA production from the finishing diet but with barley grain, VFA were decreased by hops only at 100 μg/mL. The acetate:propionate ratio was decreased quadratically ($P < 0.001$; minimum at 800–1600 μg/mL) by hops added to finishing diet, but A:P was unaffected by hops during incubation with barley. Methane production from both diets was quadratically reduced ($P < 0.01$) by hops. These results suggest that including hops in high-grain diets for ruminants may have potential to improve feed efficiency, possibly by reducing enteric methane emissions.

Key Words: barley grain, ruminal methane, β-acids

M341 Effects of hops on in vitro ruminal fermentation of high forage diets. N. Narvaez*, Y. Wang, Z. Xu, and T. McAllister, *Agriculture and Agri-Food Canada*, *Lethbridge, AB, Canada*.

Hops (*Humulus lupulus)* exert selective antimicrobial effects against gram-positive bacteria and may have potential as an alternative to antimicrobials for growth promotion in livestock. The effects of whole hops on ruminal fermentation of mixed forage (MF; Exp 1) or a barley silage:barley grain-based backgrounding diet (BD; Exp 2) were assessed during 48 h incubations (n = 4). Hop pellets (var. Tea Maker) were included in cultures (500 mg substrate + 40 mL inoculum) at 0, 50, 100, 200 and 400 μg/mL in Exp. 1 and at 0, 200, 400, 800 and 1600 μg/mL in Exp. 2. In Exp. 1, microbial protein (MP) synthesis was determined using $^{15}(NH_4)_2SO_4$, enabling true DM disappearance (TDMD) to be estimated. In Exp. 2, vials were prepared with and without polyethylene glycol (PEG) to bind condensed tannins (CT) and indirectly assess their effects on ruminal fermentation. Lack of any effect of PEG on fermentation suggested that CT in hops do not influence ruminal fermentation. Including hops linearly decreased ($P < 0.001$) gas production from MF and BD. Whereas true DMD from MF was linearly increased ($P < 0.001$) by hops, apparent DMD from BD was linearly decreased ($P < 0.001$). In Exp. 1, a quadratic ($P < 0.001$) response of MP synthesis to hops was observed. With BD, total VFA content was linearly reduced ($P < 0.001$) by hops, but with MF, the response was quadratic ($P = 0.002$). The acetate:propionate ratio was linearly increased ($P < 0.001$) with MF but quadratically decreased ($P < 0.001$) with BD. Hops quadratically reduced ($P < 0.05$) methane emissions from MF and BD. Hops have the potential to decrease methane production and may improve fermentation efficiency in ruminants consuming forage-based diets.

Key Words: hops, methane, β-acid

M342 Microencapsulation strategies to protect plant extracts against heat process of manufacture diets. P. W. Cardozo*[1], D. Ribera[1], A. Viso[1], H. Mengel[2], and M. Coenen[3], [1]*Research and Development Department, Carotech Technologies S.A*, *Tarragona, Spain*, [2]*KoVet, Coordination Staff for Veterinary Clinical Studies, Faculty of Veterinary Medicine, University of Leipzig*, *Leipzig, Germany*, [3]*Institute Animal Nutrition, Nutrition Diseases and Dietetics, Faculty of Veterinary Medicine, University of Leipzig*, *Leipzig, Germany*.

The purpose of this study was to evaluate the thermo-stability of standard combination of cinnamaldehyde and garlic oil in a protection capsule

(WEC) versus without encapsulation (WOEC) and the possible consequences after pellet process. Raw materials were provided by Carotenoid Technologie S.A. (Carotech, Tarragona Spain). Treatments were mixed at the rate of 5 g/ kg of a typical dairy concentrate diet, and were pelleted for 2 min at 80°C. Samples of both groups were taken before and after the pelleting process and the recovery of active ingredients was analyzed by HPLC technique. As expected, before pelleting, the recovery concentration of active ingredients in both treatments was similar ($P > 0.05$; average of 2.15 mg cinnamaldehyde/ g of feed, and average of 0.35 mg garlic oil/ g of feed). However, pelleting process (2 min at 80°C) affected the stability of active ingredients of WOEC recovering only 79.93% of cinnamaldehyde and 69.70% of garlic oil ($P < 0.05$), respectively. In the case of the encapsulated product, both cinnamaldehyde (98.65%) and garlic oil (95.78%) were not affected by pellet process ($P > 0.05$). The results of this trial showed that the stability was significantly higher in WEC than WOEC. The potential contribution of this study is focused on the technology used in this trial that allowed incorporating 100% of active ingredients with a percentage of active compounds recovered of approximately 98% after pelleting process. Further studies are necessary to determine the effectiveness of these active ingredients encapsulated on in vivo rumen microbial fermentation and animal performance.

Key Words: plant extracts, encapsulation system, pellet process

M343 Encapsulated combination of cinnamaldehyde and garlic oil as rumen modifiers in early-lactating dairy cows. X. Guozhong[1], X. Junxin[1], P. W. Cardozo*[2], and D. Yingying[2], [1]*Institute of Shanghai Dairy Science*, *Shanghai, China*, [2]*Research and Development Department*, *Tarragona, Spain*.

Two hundred lactating cows (DIM <60 d) were used in a completely block design (15 d of adaptation and 60 d for sampling period) to evaluate the effects of encapsulated combination of 129 mg/cow/d of cinnamaldehyde and 21mg/animal/d of garlic oil (Next Enhance 300; NE 300). Results obtained during the first 15 d were considered as covariant in the model. Milk yield was recorded every 15 d. Milk samples were taken at 15, 30 and 60 d to determine milk protein, fat percentage as well as milk urea nitrogen (MUN) and somatic cell count (SCC). Differences were declared at $P < 0.05$. Animals fed NE 300 increased ($P < 0.05$) milk production (over 1.7 kg/d) compared with control (37.38 kg/d vs. 35.73 kg/d). There was no overall effect ($P > 0.05$) of feeding NE 300 in milk fat (average 3.32%) and protein (average 2.95%) contents compared with control. However, cows fed with NE 300 showed an important reduction ($P < 0.05$) in milk urea nitrogen (14.7 mg/ dL) and SCC (168 × 1000)/mL) compared with control (15.5 mg/dL, and 337 × 1000)/mL, respectively). This study shows that the inclusion of an encapsulated combination of cinnamaldehyde and garlic oils (Next Enhance 300) in the early-lactating dairy diet has potential to influence milk production and milk composition, especially reducing MUN when fed to dairy cows in early lactation. Further studies are necessary to confirm that this encapsulated combination can be as useful as modifiers of rumen fermentation lactating dairy cows.

Key Words: dairy cows, cinnamaldehyde, garlic oil

M344 Effect of chestnut tannins on rumen activity of dairy sheep grazing on pasture. A. Nudda*[1], G. Battacone[1], R. Boe[1], R. Rubattu[1], A. H. D. Francesconi[1], M. Decandia[2], and G. Pulina[1], [1]*Dipartimento di Scienze Zootecniche, University of Sassari*, *Sassari, Italy*, [2]*Agricultural Research Agency of Sardinia - AGRIS Sardegna*, *Sassari, Italy*.

A 4-wk trial was conducted to investigate the effect of pasture supplementation with a concentrate (300 g/d; 87.1% DM; 29.4% NDF, 16.9% ADF, 17.6% CP, on a DM basis) containing 3 levels of commercial chestnut hydrolyzable tannin (0, 6 and 12%, on a DM basis; T0, T6, T12, respectively) on rumen activity of dairy ewes. Thirty-six 2- to 4-yr-old Sarda ewes (12 per experimental group), in mid lactation (90–120 DIM) and grazing on pasture of 70% *Medicago polymorpha* (27.5% DM; 44.3% NDF, 29.5% ADF, 18.3% CP, on a DM basis) and 30% of *Lolium rigidum* (39.6% DM; 58.3% NDF, 31.2% ADF, 9.4% CP, on a DM basis) were used. Rumen fluid samples were collected with a stomach tube 3 times (every 10 d) during the experimental period from 5 animals/group. Concentrate intake was measured daily. The pH, VFA (acetic, propionic and butyric acids), ammonia N (NH3-N) and the fatty acid profile of the rumen samples were determined. Data were analyzed by ANOVA including tannin level, sampling and their interaction. Concentrate intake of T6 and T12 were, respectively 10% and 25% lower than that of T0. Rumen pH was higher in T6 than in T0, being intermediate in T12. The T6 group contained the lowest content of acetic acid and the highest of butyric acid. Tannins also influenced the percentages of C18:2 n6 and C18:3 n3, which were lower in the control group, even if its C18:2 n6 content did not differ significantly from T6. The NH3-N tended to be reduced by the inclusion of tannin in the diet. These results suggest that the lack of effect of tannins on rumen activity in T12 was probably related to its lower intake of concentrate.

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Key Words: dairy sheep, rumen activity, tannin

M345 Effect of the inclusion of treated apple waste on in vitro ruminal fermentation of alfalfa hay. Y. Castillo-Castillo[1], O. Ruiz-Barrera*[2], C. Arzola-Alvarez[2], C. Rodriguez-Muela[2], A. Elias-Iglesias[3], C. Angulo-Montoya[2], O. La O-Leon[3], and J. A. Ortega[2], [1]*Universidad Autónoma de Ciudad Juárez.*, *Nuevo Casas Grandes, Chih, México*, [2]*Universidad Autónoma de Chihuahua.*, *Chihuahua, Chih, México*, [3]*Instituto de Ciencia Animal.*, *La Habana, Cuba.*

Feed produced by solid-state fermentation (SSF) has been satisfactorily added to ruminant fibrous diets due to an improvement on the ruminal fermentation patterns, including dry matter digestibility. The objective of this work was to evaluate the effect of the addition of fermented apple waste (FAW) on ruminal pH, ammonia nitrogen ($N\text{-}NH_3$), volatile fatty acids concentration (VFA), in vitro dry matter digestibility (IVDMD), lactic acid content (LA), and microorganisms counting (yeast, total bacteria and protozoa) of good quality alfalfa hay incubated in an in vitro ruminal ecosystem. Four levels of FAW inclusions were evaluated (0, 0.25, 0.50 and 0.75 g DM replacing 1.5 g DM of alfalfa hay and incubated at several times of fermentation (0, 4, 8, 12 and 24 h.) using a completely at random experimental design with repeated measures in time. Results showed that yeast concentration in the ruminal ecosystem was greater in the treatments with FAW addition up to the 12 h of incubation (2.4×10^6, 1.7×10^6 and 3.2×10^6 CFU/mL $\log^{10}$) in relation to the control (1.2×10^6 CFU/mL $\log^{10}$) and 0.75 g FAW addition exhibited the greatest concentration ($P < 0.0001$). LA content also increased at 12 h of incubation in response to the addition of FAW ($P < 0.001$) (13.86, 16.84 and 14.57 µg/ml, respectively) in relation to the control (10.61 µg/ mL). However, other measured variables as ruminal pH, $N\text{-}NH_3$, VFA, IVDMD total bacteria and protozoa counting remained unaffected by the treatments. According to these results, we concluded that substitution of alfalfa hay by FAW incubated in an in vitro ruminal ecosystem during 24 h only modified positively the population of viable yeast and

AL content, with no effect on other fermentative and microbiological parameters of the ruminal environment.

Key Words: fermentation, apple, ruminants

M346 Effects of hops on rumen fermentation, growth, carcass traits and shedding of *Escherichia coli* by feedlot cattle. Y. Wang*[1], A. V. Chaves[1,2], F. L. Rigby[3], M. L. He[1], and T. A. McAllister[1], [1]*Agriculture and Agri-Food Canada Research Centre*, *Lethbridge, AB, Canada*, [2]*The University of Sydney*, *Sydney, NSW, Australia*, [3]*Yakima*, *WA (deceased)*.

Hops (*Humulus lupulus*) have antimicrobial properties, which may have potential in livestock production. Experiments were conducted to evaluate the effects of hops on ruminal fermentation, fecal shedding of *Escherichia coli* and the growth of feedlot cattle. Sixty individually penned British × Charolais steers were randomly assigned to treatment for a 160-d feeding trial (55 d growing + 105 d transition/finishing) using barley grain:barley silage-based diets (n = 15). Hop cone pellets were added to the growing diet at levels of 0, 119, 238 and 476 mg/kg DM and to the finishing diet at 0, 238, 476 and 952 mg/kg DM. Fecal samples were collected every 28 d to assess the effects of hops on fecal shedding of *E. coli*. Feed deliveries were recorded daily and feed refusals were weighed weekly. The steers were weighed every 28 d and warm carcass weight, longissimus muscle area, marbling score and saleable meat yield were recorded at slaughter for each steer. Including hops in the diet did not affect ($P \geq 0.05$) growth (DMI, ADG or feed conversion efficiency) or carcass characteristics of steers, nor fecal shedding of *E. coli*. During both the growing and finishing periods, however, ADG was 6% improved ($P = 0.11$) with the highest levels of hops compared with the controls. In corresponding 24-h batch culture incubations of the 8 diets (n = 6), hops inclusion with the growing diet increased ($P \geq 0.001$) DM disappearance (IVDMD), gas production, and VFA accumulation, with linear increases ($P \geq 0.001$) of IVDMD and total VFA. The proportion of propionate in VFA was increased ($P < 0.001$) and acetate proportion and acetate:propionate ratio were decreased ($P < 0.001$). With the finishing diet, a linear increase ($P = 0.002$) in gas production was observed. However, these in vitro improvements were not reflected in improved growth or efficiency of feedlot cattle. Inclusion of higher levels of hops in the diet may be favorable for ruminant production.

Key Words: growth performance, rumen fermentation, *Humulus lupulus*

M347 Effect of phlorotannins from brown seaweed on ruminal bacteria. Y. Wang*, L. J. Yanke, Z. Xu, and T. A. McAllister, *Agriculture and Agri-Food Canada Research Centre*, *Lethbridge, AB, Canada*.

Brown seaweed has been used as feed additive to mitigate *E. coli* O157:H7 in feedlot cattle, but its impact on rumen bacteria is not clear. The effects of phlorotannins (PT) isolated from the brown seaweed, *Ascophyllum nodosum*, on ruminal bacteria were investigated in pure culture studies. *Prevotella bryantii*, *Ruminobacter amylophilus*, *Selenomonas ruminantium* and *Streptococcus bovis* were cultured through 10 serial 24-h transfers in ruminal fluid medium containing 0 or 50 μg PT/mL. The 4 strains, each non-exposed or pre-exposed to PT, were then inoculated into media containing 0, 75, 150 or 300 μg PT/mL and 24-h growth curves were determined (n = 6). The ruminal cellulolytic bacteria (CB) *Ruminococcus flavefaciens*, *Fibrobacter succinogenes* and *Ruminococcus albus* were also pre-cultured through 10 serial 72-h transfers in ruminal fluid medium containing 0 or 12.5 μg PT/mL and then, for 72 h, on Whatman no. 54 filter paper as a sole carbohydrate source in medium containing 0, 25, 50 or 75 μg PT/mL for the determination of filter paper digestion (n = 4). The effects of PT on growth of non-cellulolytic bacteria (NCB) were species-dependent, and were also affected by their having been pre-exposed to PT or not. At 24 h of incubation, growth of all 4 NCB was inhibited ($P < 0.01$) by as little as 75 μg PT/mL irrespective of their having been pre-exposed. Pre-exposed *P. bryantii* exhibited greater ($P < 0.01$) growth at 24 h in 75 μg PT/mL medium than did its non-exposed counterpart. At PT concentration of 75 μg PT/mL, *Sel. ruminantium* and *P. bryantii* exhibited more growth ($P < 0.01$) between 16 and 24 h of incubation than did *Str. bovis* or *Rb. amylophilus*. Phlorotannins inhibited digestion of filter paper by all 3 CB, but *F. succinogenes* was less ($P < 0.05$) sensitive to PT than were *Rc. flavefaciens* or *Rc. albus*. Pre-exposure to PT did not affect filter paper digestion by the 3 CB. Phlorotannins from *A. nodosum* inhibit both NCB and CB, but CB exhibit greater sensitivity than NCB. Thus, PT could negatively affect fiber digestion if brown seaweed is fed to ruminants.

Key Words: phlorotannins, ruminal bacteria, pure culture

M348 Additives (sodium monensin, salinomycin, and virginiamycin) for Nellore bulls feedlot fed high concentrate finishing rations. C. Sitta*, F. A. P. Santos, G. B. Mourão, A. M. Pedroso, R. Carareto, J. R. R. Dórea, T. G. Neri, and D. A. Rodrigues, *University of Sao Paulo*, *Piracicaba, SP, Brazil*.

The aim of the present study was to compare the effect of different additives on the performance of Nellore bulls fed high concentrate rations. One hundred and 30 4 Nellore bulls with initial weight of 330 kg were tested in a 102 d finishing trial, of which 21 d comprised adaptation to the high concentrate diet. Animals were grouped according to initial live weight and allotted to 24 pens. The final diet contained 12% tifton hay, 78.1% finely ground corn, 6% sugar cane molasses, 1.4% urea, 2.5% mineral and vitamin premix and respective additives. Treatments consisted in: 1) Control (without additives); 2) Sodium monensin 30ppm; 3) Sodium monensin 20ppm + Virginiamycin 15ppm; 4) Sodium monensin 30ppm + Virginiamycin 15ppm; 5) Virginiamycin 17ppm; 6) Virginiamycin 15ppm + Salinomycin 13ppm. Data were analyzed with Proc. Mixed from SAS (1999), version 9.2 for Windows, and the pens were used as experimental units. Dry matter intake and daily weight gain were not affected by treatments ($P > 0.05$). Feed conversion (DMI/ADG) was lower for the treatments containing monensin (M20 + V15; M30 + V15) and salinomycin (S13 + V15), both in combination with virginiamycin. Diet net energy for gain was higher for the treatments with monensin, monensin with virginiamycin, virginiamycin and salinomycin with virginiamycin ($P < 0,05$). The combination of monensin 30 ppm and virginiamycin 15 ppm resulted in an increase in the energy density of the rations in comparison with the other treatments (Table 1).

Table 1. Dry matter intake (DMI), average daily gain (ADG), feed conversion (DMI/ADG) and net energy (NE) of finishing Nellore bulls fed different additives

	Control	M 30	M20 + V15	M30 + V15	V 17	S13 + V15	P-value
DMI (kg DM/day)	9.89	9.20	9.29	8.98	9.76	9.85	0.0600
ADG (kg/day)	1.33	1.33	1.39	1.44	1.45	1.49	0.1784
FC (DMI/ADG)	7.40a	6.90ab	6.66bc	6.21c	6.72bc	6.62bc	0.0429
NEg obs (Mcal/Kg)	1.05a	1.14ac	1.17bc	1.26bd	1.15ac	1.16bc	0.0428
NEg obs/act (Mcal/Kg)	0.78a	0.85ac	0.86bc	0.93bc	0.85ad	0.86bc	0.0413

Key Words: additives, effect, Nellore

M349 In vitro effect of peppermint (*Mentha piperita*) essential oil and non-fiber carbohydrates on gas production parameters of alfalfa hay. M. Danesh Mesgaran*[1], E. Jani[2], A. Vakili[1], A. Solaimany[2], and H. Jahani-Azizabadi[1], [1]*Dept. Animal Science, Ferdowsi University of Mashhad, Mashhad, Iran*, [2]*Islamic Azad University*, *Kashmar, Iran*.

The aim of this study was to evaluate the effect of peppermint essential oil (PE) and non-fiber carbohydrates (NFC) including sucrose (SUC) and starch (STA) on gas production parameters of alfalfa hay (AH). Treatments were AH, AH plus PE (40 and 80 µl/g DM), AH supplemented with SUC or STA at 60 and 90 mg/g DM plus PE (0.0, 40 and 80 µl/g DM). Approximately 0.3 g of each sample (n = 4) was placed into a 100 mL glass syringe containing 40 mL of buffered rumen fluid (buffer to rumen fluid was 2:1). Rumen fluid was obtained from 2 rumen cannulated sheep (body weight = 45.5 ± 2 kg) before the morning feeding and strained through 4 layers of cheesecloth. Animals were fed 1.5 kg DM alfalfa hay and 0.4 kg DM concentrate (165 g CP/ kg DM) per head/ day. Syringes were incubated at 39°C and the volume of gas produced were recorded at 2, 4, 8, 12, 24, 36, 48, 72 and 96 h. Data were fitted to an exponential equation of $P = b\ (1\text{-}e^{-ct})$, where b is the volume of gas produced, c is the fractional rate constant of gas production (/h), t is the incubation time (h) and P is the volume of gas produced at time t. The gas production parameters of the supplemented samples were compared with AH as control using Dunnett's test at $P < 0.05$. The parameters for AH were b = 72 mL and c = 0.07/h. Supplementation of AH with PE reduced the volume of gas produced, however, peppermint essential oil caused to reduce ($P < 0.05$) the volume of gas produced from the samples of AH supplemented with the NFC sources. The rate constant of gas produced (c) from AH was significantly ($P < 0.05$) increased by the adding of the NFC and PE (except PE as 80 µL/g DM, which had no significant effect on c). The fractional rate constant was significantly increased when PE as 40 µL/g DM was added to the AH supplemented with the SUC and STA (0.13 and 0.10, respectively). However, at 80 µL/g DM of PE, c was significantly decreased ($P < 0.05$) for those treatments (0.06 and 0.05, respectively). It was concluded that PE at the both applied rates had a potential to alter the fermentability of AH and AH supplemented with the NFC sources.

Key Words: essential oil, gas production, peppermint

M350 Effect of fennel (*Foeniculume vulgare*) essential oil on in vitro gas production parameters of alfalfa hay supplemented with sucrose or starch. M. Danesh Mesgaran*[1], E. Jani[2], A. Vakili[1], H. Jahani-Azizabadi[1], and A. Solaimany[2], [1]*Dept. Animal Science, Ferdowsi University of Mashhad, Mashhad, Iran*, [2]*Islamic Azad University*, *Kashmar, Iran*.

The aim of the present study was to evaluate the effect of fennel essential oil (FE) on gas production parameters of alfalfa hay (AH) and AH supplemented with sucrose (SUC) or starch (STA). Treatments were AH, AH plus FE (40 and 80 µL/g DM), AH supplemented with SUC or STA at 60 and 90 mg/g DM plus FE (0.0, 40 and 80 µL/g DM). Approximately 0.3 g of each sample were placed in a 100 mL glass syringe containing 40 mL of buffered rumen fluid as 2: 1 (n = 4). Rumen fluid was obtained from 2 rumen canullated sheep (body weight = 45.5 ± 2 kg) before the morning feeding and immediately strained through 4 layers of cheesecloth. Animals were fed 1.5 kg DM alfalfa hay and 0.4 kg DM concentrate (165 g CP/ kg DM) per head per day. Syringes were incubated at 39°C and the volume of gas produced were recorded at 2, 4, 8, 12, 24, 36, 48, 72 and 96 h. Statistical analysis was conducted using SAS (1999) procedure. The gas production data were fitted to an exponential equation of $P = b(1\text{-}e^{-ct})$, where b is the volume of gas produced, c is the fractional rate constant of gas production (/h), t is the incubation time (h) and P is the volume of gas produced at time t. The gas production parameters of the supplemented samples were compared with AH as control using Dunnett's test at $P < 0.05$. Supplementation of AH with FE, at both rates applied, reduced the volume of gas produced ($P < 0.05$; 72, 52 and 54 mL/0.3 g DM, respectively), but increased the fractional rate constant of gas production ($P < 0.05$; 0.07, 0.12 and 0.10, respectively). In addition, FE particularly as 40 µL/g DM, reduced ($P < 0.05$) the volume of gas produced from the AH samples supplemented with both SUC and STA. The rate constant of gas produced (c) from AH supplemented with SUC and STA at both levels (0.09 and 0.08/h, respectively) was increased ($P < 0.05$) by the adding of FE as 40 and 80 µL/g DM (0.13 and 0.09/h, respectively). It might be concluded that FE, as 40 or 80 µL/g, caused an alteration in the fermentation potential of AH alone or supplemented with the NFC sources used.

Key Words: essential oil, gas production, fennel

M351 Effect of individual and mixed natural tree extracts on in vitro ruminal fermentation profiles in sheep. F. S. Jiménez-Peralta[1], A. Z. M. Salem*1,4, H. Ammar[2], M. Ronquio[3], and P. B. Albarrán[1], [1]*Autónoma del Estado de México*, *Centro Universitario UAEM-Temascaltepec, Estado de México, C.P. 51300, México*, [2]*Ecole Supérieure d'Agriculture de Mograne*, *Zaghouan, 1121 Mograne, Tunisia*, [3]*Universidad Autónoma del Estado de México*, *Facultad de veterinaria, Toluca, Mexico*, [4]*Alexandria University*, *Department of Animal Production, Faculty of Agriculture (El-Shatby), Egypt*.

Extracts of 2 tree leaves species [*Salix babilónica* (SB) and *Leucaena leucocephala* (LL)] and their mixture (SBLL, 1:1, v/v) rich in secondary metabolites (ESM, 10 g DM/80 mL of solvent), were in vitro evaluated on ruminal fermentation pattern in 4 levels of 0, 0.6, 1.2, and 1.8 mL extract/g DM of TMR (50:50 forage:concentrate diet). Animals used for the extraction of rumen liquid (RL) for the in vitro incubations were allocated into 2 experimental groups (8 animals/group): control (CG) and treated (TG) group. Animals of CG were fed daily on TMR, while those of TG were fed on the same TMR and drenched a daily oral dose of SBLL (30mL/animal) for 60 d. Concentrations of secondary metabolites (SM) in terms of total phenolics (TP), saponins (SAP) and aqueous fraction (AF, lectins, polypeptides and starch) were examined in each tree extract and gas production was recorded at different incubation times (2, 4, 6, 8, 10, 12, 24, 48 and 72 h) of TMR with different extracts levels. Short chain fatty acids (SCFA), in vitro organic matter degradability (IVD) and metabolizable energy (ME)) were estimated. As compared with SB, extracts of LL had higher TP, SAP and AF (i.e., 24, 14 and 116 versus 15, 6 and 74 g/kg DM, respectively). For both animal groups, increasing the extracts dose until 1.8mL/g DM improved ($P < 0.05$) the ruminal fermentation activities of TMR with increasing the extracts dose until 1.8mL/g DM in ether TG or CG, probably due to a higher extracts -soluble sugars. However, higher fermentation activities were observed in SB than LL and SBLL extracts. Ruminal fermentative activities of TMR were reduced by more than 50% in TG versus to CG during all the incubation times, except the first 2 h. In conclusion, administration of SBLL during 60 d to animals did not enhance the ruminal fermentation activities of TMR in sheep. Individual extracts-rich in secondary metabolites at 1.8mL/g DM, in particular SB extracts, had the most potential on ruminal microorganism's activities and may serve as an alternate to antibiotics and ionophores as a growth promoter of weaned lambs.

Key Words: extracts, secondary metabolites, in vitro fermentation, sheep

M352 Medium-term orally administration of extracts impacts on in vitro rumen fermentative activity of some tree leaves in sheep. A. Z. M. Salem*[1,4], F. S. Jiménez-Peralta[1], H. Ammar[2], R. R. Rojo[1], L. M. Camacho[3], and D. Cardoso-Jiménez[1], [1]*Universidad Autónoma del Estado de México, Estado de México*, *Centro Universitario UAEM-Temascaltepec, Estado de México, C.P. 51300, México*, [2]*Ecole Supérieure d'Agriculture de Mograne*, *Zaghouan, 1121 Mograne, Tunisia*, [3]*Universidad Autónoma de Guerrero*, *Facultad de veterinaria, México*, [4]*University of Alexandria*, *Department of Animal Production, Faculty of Agriculture (El-Shatby), Egypt*.

Four tree leaves species (i.e., *Celtis pallid*, *Ficus trigonata*, *Fraxinus excelsior* and *Prunus domestica*) collected during the dry season were used to explore medium-term effects of *Salix babilónica* and *Leucaena leucocephala* extract (SBLL, 1:1 v/v) rich in secondary compounds (ESC, 10g dry leaves/80 mL of solvent) on fermentative activity in the rumen of sheep. Sixteen crossbreed male (Katahdin × Pelibuey) sheep were fed on a TMR (18%CP) and used as a source of rumen liquor. Eight animals were fed the TMR with a daily oral dose of 30mL/animals/d of SBLL for 60 d and used as the treated group (TG), whereas the other sheep were not received extract and always fed the same TMR and used as the control group (CG). The objective was to investigate if adaptation to ESC at the rumen level may develop in response to regular consumption of secondary compounds (SC), resulting in an enhanced ability to digest tree leaves. Gas production was recorded at 2, 4, 6, 8, 10, 12, 24, 48 and 72 h after incubation of leaves samples. Differences in the fermentative activity (short chain fatty acids (SCFA), in vitro organic matter degradability (IVD) and metabolizable energy (ME)) were examined in batch cultures inoculated with rumen fluid obtained on d 60 from both groups of sheep. Gas production and other fermentative parameters (i.e., SCFA, IVD and ME) of the 4 leaves species were reduced by more than 50% in TG versus CG during the all incubation times, except the first 2 h. The magnitude of this effect may be due to direct negative impact of SC in the orally dose on ruminal microorganisms activities or the indirect impacts of SC on saliva production composition. Highest fermentation activities ($P < 0.05$) were in *P. domestica* while the lowest values ($P < 0.05$) were in *F. excelsior*. This effect may be due to the different SC concentrations as well as ADF and NDF composition in leaves samples. In conclusion, administrations of SBLL to animals do not enhance the ruminal fermentation activities and gas production kinetics of tree leaves species. *P. domestica* demonstrated a higher ruminal digestion than other tree species.

Key Words: extracts, in vitro fermentation, sheep

M353 Effect of cumin essential oil on in vitro gas production parameters of alfalfa hay, barley grain and sugar beet pulp. M. Sadjadian, M. Danesh*, A. R. Vakili, H. Jahani, and J. Amini, *Ferdowsi University of Mashhad*, *Mashhad, Iran*.

The objective of the present study was to evaluate the effect of cumin essential oil (CEO) on in vitro gas production parameters of alfalfa hay (AH), barley grain (BG) or sugar beet pulp (BP). Samples of AH, BG, and BP were provided as untreated or treated with CEO (400 mL/g DM). In vitro incubations were carried out using 0.3 g of each sample (4 replicates) which was placed in a 100 mL glass syringe containing 40 mL buffered rumen fluid (ratio of buffer to rumen fluid was 2:1). Rumen fluid was obtained from 2 ruminally cannulated sheep (body weight = 45.5 ± 2 kg), before the morning feeding, and immediately strained through 4 layers of cheesecloth. Animals were fed 1.5 kg DM alfalfa hay and 0.4 kg DM concentrate (165 g CP/ kg DM) per head per day. Syringes were then incubated at 38.6°C and the volume of gas produced was determined at 2, 4, 8, 12, 24, 36, 48, 72 and 96 h after the incubation. The gas production data were fitted using an exponential equation of $P = b \times (1–e^{-ct})$, where b is the volume of gas produced, c is the fractional rate constant of gas production (/h), t is the incubation time (h) and P is the volume of gas produced at time t. Statistical analysis was conducted using SAS (1999) software. Results demonstrated that the gas production parameters of the feed samples (Table 1) were significantly different ($P < 0.05$). In addition, results of the present study indicate that the gas production parameters of the feed samples were significantly altered when CEO was included in the medium. Cumin essential oil caused a significant ($P < 0.05$) decrease of c parameter of BG and BP. While, when cumin was added to the AH and BP samples, the b parameter was decreased (Table 1).

Table 1. Gas production parameters of alfalfa hay, barley grain and sugar beet pulp as untreated or treated with cumin essential oil as 400 mL/g DM

	Treatments						
Gas production parameters	AH	BG	BP	AH+CEO	BG+CEO	BP+CEO	SEM
b (ml/0.3 g)	49.6^{d}	98.7^{b}	84.0^{c}	20.4^{f}	105.6^{a}	44.9^{e}	2.34
c (/h)	0.06^{b}	0.04^{c}	0.09^{a}	0.06^{b}	0.02^{d}	0.06^{b}	0.004

Key Words: cumin, essential oil, gas production

M354 Influence of two browse extracts-rich secondary compounds and their mixture on lamb feed intake and growth performance. A. Z. M. Salem*1,4, H. P. Mejia[1], H. Ammar[2], M. Ronquio[3], J. L. Tinoco[1], R. Rojo[1], and A. M. Garcia[1], [1]*Universidad Autónoma del Estado de México*, *Centro Universitario UAEM-Temascaltepec, Estado de México, C.P. 51300, México*, [2]*Ecole Supérieure d'Agriculture de Mograne*, *Zaghouan, 1121 Mograne, Tunisia*, [3]*Universidad Autónoma del Estado de México*, *Departmento de Nutricion Animal, Facultad de Veterinaria, Toluca, Mexico*, [4]*University of Alexandria*, *Department of Animal Production, Faculty of Agriculture (El-Shatby), Egypt*.

Thirty-two crossbreed male (Katahdin × Pelibuey) lambs (3–4 mo old, average LW 24 ± 0.3kg) were used to study effects of daily oral administration of the extracts-rich secondary compounds (ESC, 10g dry leaves/80 mL of solvent) of either 2 browse species namely *Salix babilónica* (SB) and *Leucaena leucocephala* (LL) or their mixtures (SBLL) during 60 d lamb feed intake and growth performance. Lambs were randomly assigned into 4 groups (8 animals per group) in a factorial design: received no ESC (Control –CTR), and the other 3 groups were submitted to a treatment with ESC (30mL) of either SB, LL or SBLL (1:1 v/v) during the experimental period. Feed intake (FE) was recorded daily while the body weight of lambs was recorded every 20 d among the experimental period: 20 (P1), 40 (P2), and 60 d (P3). Animals of different groups were fed ad libitum on a total mixed ration (18% CP) that was formulated to meet all nutrient requirements for finishing lambs. Oral administration of ESC improved average daily gain (ADG), feed conversion (FC) and economic efficiency (EE) during all the experimental periods, without changing in FE. A gradually improvement in growth performance (ADG and FC) of ESC treated lambs was observed from P1 to P3, versus CTR lambs. Generally, growth performance of SB and LL lambs was better ($P < 0.05$) than SBLL lambs. The cost of one kg DG (i.e., EE) was reduced ($P < 0.05$) by 20.2, 13.3 and 12.88% with ESC administration of SB, LL and SBLL, respectively. This effect may be due to an adaptation of ruminal microorganisms to plant secondary compounds in extracts. Results of our present study revealed that daily administration of ESC, particularly of SB, improved lamb performance rather than LL or SBLL.

Key Words: extracts and secondary compounds, growth performance and feed intake, lambs

M355 Effect of polyclonal antibody preparation on ruminal microbial diversity population in cattle fed three different energetic sources. W. Otero[1], C. Marino*[2], M. Stradiotto[4], C. Barreto[3], V. Pellizari[3], M. Arrigoni[2], and P. Rodrigues[1], [1]*University of Sao Paulo, FMVZ*, *Pirassununga, Brazil*, [2]*University of Sao Paulo State, FMVZ*, *Botucatu, Brazil*, [3]*University of Sao Paulo, ICB II*, *Sao Paulo, Brazil*, [4]*University of Sao Paulo, FZEA*, *Pirassununga, Brazil*.

Nine ruminally fistulated cows were used to test an avian-derived polyclonal antibody preparation (PAP) against specific ruminal bacteria *Streptococcus bovis*, *Fusobacterium necrophorum*, *Clostridium aminophilum*, *Peptostreptococcus anacrobius* and *Clostridium sticklandii*. The experimental design was a 3 × 3 Latin square replicated 3 times with a factorial arrangement of treatments 3 × 3 regarding 2 rumen modifiers, monensin (MON) and PAP plus control group and 3 energy sources. The energetic sources utilized were dry-grounded corn grain (CG), high moisture corn silage (HMCS) and citrus pulp (CiPu). The ruminal content was collected in the d 21 of each trial at 4 h after feeding for the analysis of microbial ruminal diversity by the denaturing gradient gel electrophoresis. Data were submitted to variance analysis by GLM procedure, which separated the effects of interaction between feed additive and energy source, effect of feed additive, effect of energy source as well as effects of period and animal inside the square. Mean effects were separated by Duncan test. Differences were declared at $P < 0.05$. It was observed energetic source effect ($P = 0.0470$) for number of bands amplified in DGGE for *Archaea* community. Animals receiving CiPu demonstrated an increase of 1.56 band (52%) compared with animals receiving CG. Those fed HMCS did not differ between the other 2 groups. For the total sum of bands amplified in DGGE, energetic source effect was observed. The group fed HMCS had more amplified bands than the group fed CG. The group fed CiPu did not differ from the other 2 groups. In general lines, in the present experiment, it was not possible to assign that there was a pattern in the structures of amplification by *Bacteria* and *Archaea* communities of the ruminal content of animals treated with 2 different rumen modifiers or 3 distinct energetic sources.

Table 1. Number of amplified bands obtained by DGGE for *Bacteria*, *Archaea* and sum of *Bacteria* and *Archaea* communities obtained with treatments composed by different energetic sources

	Energy sources					
Variable	CG	HMCS	CiPu	Mean	SEM	Prob.
Bacteria	5.94	9.11	5.94	7.00	0.6400	0.1106
Archaea	3.00^{B}	3.56^{AB}	4.56^{B}	3.70	0.3809	0.0470
Sum	8.94^{B}	12.67^{A}	10.50^{AB}	10.70	0.7123	0.0741

Key Words: denaturing gradient gel by electrophoresis, ionophore, passive imunization

M356 Effect of polyclonal antibody preparation on ruminal protozoa population in cattle fed three different energetic sources. W. Otero[1], C. Marino*[2], M. Stradiotto[4], C. Barreto[3], V. Pellizari[3], M. Arrigoni[2], and P. Rodrigues[1], [1]*University of Sao Paulo, FMVZ*, *Pirassununga, Brazil*, [2]*University of Sao Paulo State, FMVZ*, *Botucatu, Brazil*, [3]*University of Sao Paulo, ICB*, *Sao Paulo, Brazil*, [4]*University of Sao Paulo, FZEA*, *Pirassununga, Brazil*.

Nine ruminally fistulated cows were used to test an avian-derived polyclonal antibody preparation against specific ruminal bacteria *Streptococcus bovis*, *Fusobacterium necrophorum*, *Clostridium aminophilum*, *Peptostreptococcus anacrobius* and *Clostridium sticklandii*. The experimental design was a 3 × 3 Latin square replicated 3 times with a factorial arrangement of treatments 3 × 3 regarding 2 feed additives (monensin and PAP) plus control group and 3 energy sources. The energy sources utilized were dry-grounded corn grain (CG), high moisture corn silage (HMCS) and citrus pulp (CiPu). Sample collection for quantitative protozoa analysis were performed at 19 d of each period at 0 and 4 h after morning meal collected my manual scanning of rumen floor. Data were submitted to variance analysis by GLM procedure, which separated the effects of interaction between feed additive and energy source, effect of feed additive, effect of energy source as well as effects of period and animal inside the square. Mean effects were separated by Duncan test. Differences were declared at $P < 0.05$. Relative counting of *Entodinium* was influenced by the type of energy source at 0 h ($P = 0.0091$) and 4 h ($P = 0.0026$). Animals treated with CG and HMCS showed higher values of these protozoa when compared with animals receiving CiPu but do not differ between them. It was observed feed additive effect for *Isotricha* ($P = 0.1008$) at 4 h. The group treated with PAP showed great values for relative counting compared with CON. The MON group did not differ from the others 2. Also, it was observed energy source effect for *Isotricha* at 0 h ($P = 0.0008$) and 4 h ($P = 0.0001$), where the animals fed CiPu showed greater relative counting than animals fed HMCG and CG that did not differ between them. The utilization of PAP and the addition of CiPu resulted in an increase of total and relative counting of Isotricha which indicate an effect on ruminal microbial population.

Table 1. Absolute ($\times 10^3$/mL) and relative (%) counting of protozoa obtained with the treatments composed by different feed additives and energy sources

	Feed Additive			Energy source				
Variable	CON	MON	PAP	CG	HMCS	CiPu	Mean	SEM
General Count (x10^3/mL)	140.5	143.5	268.7	190.1	226.3	136.3	184.2	37.70
Isotricha								
0 h	9.87^{b}	8.93^{b}	21.73^{a}	6.80^{B}	6.67^{B}	27.07^{A}	13.51	3.06
4 h	6.46^{b}	8.68^{ab}	12.51^{a}	3.97^{B}	3.84^{B}	19.84^{A}	9.22	1.97
Entodinium								
0 h	123.5	123.1	239.2	175.2	209.6	100.9	161.9	36.47
4 h	87.1	81.5	83.7	89.2^{A}	89.4^{A}	73.7^{B}	84.1	2.50

Key Words: additive, passive immunization, ruminant

M357 Effects of ethanol extracts of two specific mixtures of herbs and spices on in vitro rumen microbial fermentation. N. Narvaez*[1], Y. Wang[1], T. A. McAllister[1], and C. Benchaar[2], [1]*Agriculture and Agri-Food Canada*, *Lethbridge Research Centre, Alberta*, [2]*Agriculture and Agri-Food Canada*, *Dairy and Swine R&D Centre, Sherbrooke, Quebec*.

Two in vitro batch culture experiments were conducted to assess the effects of ethanol extracts of 2 different combinations of herbs and spices (ApexRuminant and ApexCalf; Nutri-Ad, Elgin, IL) on rumen microbial fermentation. The treatments were control (no additive), monensin (10 µg/mL), ethanol extract of ApexRuminant (ARe, Exp. 1) and ethanol extract of ApexCalf (ACe, Exp. 2) both supplied at 125, 250, 500, 1000 and 2000 µg/mL. Production of total gas (GP), volatile fatty acids (VFA) concentration, microbial protein (MN), and true dry matter disappear-

ance (TDMD) were determined after 24 h of incubation. Data were analyzed as a completely randomized design and polynomial contrasts were used to determine linear and quadratic dose-effects. Significance was declared at $P \leq 0.05$. In both experiments, monensin increased propionate proportion but decreased GP, TDMD, MN synthesis, total VFA production (mmol/g DM), molar proportions of acetate, butyrate, and branched-chain VFA (BCVFA), and the acetate:propionate ratio (A:P). Addition of ARe at levels up to 500 μg/mL and ACe up to 1000 μg/mL did no cause substantial modifications of rumen fermentation, whereas at higher doses it resulted in different effects that in most cases inhibited rumen fermentation. These effects were dose-dependent and entailed both linear and quadratic trends. When supplied at 1000 or 2000 μg/mL, ARe reduced GP, TDMD, and total VFA production, but increased butyrate and BCVFA proportions, whereas at 2000 μg/mL, ARe supply increased MN and A:P ratio. Addition of ACe at 2000 μg/mL reduced GP, TDMD, but increased MN without altering VFA production or A:P ratio. Results from this study suggest that the active compounds of Apex mixtures are ethanol soluble and exhibited antimicrobial activity at high doses with greater inhibitory effects exerted by ARe compared with ACe on ruminal microbial fermentation.

Key Words: plant extract, rumen fermentation, ethanol extract

M358 Assessment of the effects of two herbs and spices mixtures and their ethanol extracts on in vitro rumen microbial fermentation. N. Narvaez*[1], Y. Wang[1], T. A. McAllister[1], and C. Benchaar[2], [1]*Agriculture and Agri-Food Canada*, *Lethbridge Research Centre, AB,Canada,* [2]*Agriculture and Agri-Food Canada*, *Dairy and Swine R&D Centre, Sherbrooke, QC, Canada.*

An in vitro batch culture experiment was conducted to determine the effects of 2 specific mixtures of herbs and spices (ApexRuminant: AR and ApexCalf: AC; Nutri-Ad, Elgin, IL) and their ethanol extracts (ARe; ACe) on rumen microbial fermentation. Treatments were control (no additive), monensin (10 μg/mL), AR, AC, ARe or ACe, supplied at 250, 500, 1000 and 2000 μg/mL. Production of total gas, volatile fatty acid (VFA) and ammonia N (NH_3-N) concentrations, and apparent dry matter disappearance (ADMD) were determined after 48 h of incubation. Data were analyzed as a completely randomized design and according to a 2 × 2 × 4 factorial to determine the effects of the type of product and the method of extraction. Polynomial contrasts were also used to determine linear and quadratic dose-effects. Significance was declared at $P \leq 0.05$. Compared with the control, monensin reduced ADMD, NH_3-N concentration, total VFA production (mmol/g DM), and acetate:propionate (A:P) ratio. Addition of AR and ARe linearly reduced gas production, ADMD, VFA but linearly increased the A:P ratio. Addition of AC and ACe did not alter gas production, but linearly reduced ADMD and VFA production. The A:P ratio from ACe linearly increased but a quadratic response was observed with AC, being lowest at 500 μg/mL. Compared with AC and ACe, the addition of AR and ARe resulted in lower ADMD, NH_3-N concentration, VFA production, but higher A:P ratio. Addition of AR and AC had higher NH_3-N concentration, but lower ADMD and A:P ratio than ARe and ACe. Considering the type of product (ApexRuminant vs. ApexCalf) and preparation method (no extraction vs. ethanol extraction), ApexRuminant and ethanol extracts (ARe and ACe) exerted greater effects on rumen fermentation than ApexCalf and no extraction. These effects became statistically significant at the supplementation levels of 1000 and 2000 μg/mL.

Key Words: plant extract, ethanol extraction, in vitro rumen fermentation

M359 Use of pine sawdust (*Pinnus patula*) as a fiber source in lamb finishing rations. E. C. Guerra-Medina[1], O. D. Montañez-Valdez*[2], M. A. Cobos-Peralta[3], and M. Pérez-Sato[4], [1]*Centro Universitario de la Costa Sur de la Universidad de Guadalajara*, *Autlán, Jalisco, México*, [2]*Centro Universitario del Sur de la Universidad de Guadalajara*, *Ciudad Guzmán, Jalisco, México*, [3]*Colegio de Postgraduados*, *Montecillo, Texcoco, México*, [4]*Benemérita Universidad Autónoma de Puebla*, *Puebla, Puebla, México*.

Rations for sheep include 5 to 40% of fibrous sources that can be used as cereal straws, alternate sources of oak (*Quercus ilex*) or pine (*Pinnus patula*) sawdust have been used; however its effectiveness has not been researched in depth. With the objective of using an alternative source of fiber in diets for sheep in feedlots, 2 treatments were assessed for 4 periods of 14 d each. There were 2 treatments, one with 30% pine sawdust (SD) and another with 30% corn straw (CS). The variables evaluated were average daily gain (ADG), dry matter intake (DMI), ruminal pH, concentration of volatile fatty acids, and concentration of ammonia. A Completely Randomized Design was used and the data were analyzed using the procedure of repeated measurements. The ADG (246.07 g d^{-1}), concentration of propionic acid (27.3 mol/100 mol), and the average ruminal pH (6.28) was higher ($P < 0.05$) in the SD treatment, while the average concentration ammonia was higher ($P \leq 0.05$) in the CS treatment (33.6 m*M*). There no were differences in DMI ($P \leq 0.05$) between treatments. The results indicate the possibility of using until 30% of pine sawdust as a source of fiber in diets for sheep in feedlots.

Key Words: fiber substitute, average gain, ruminal fermentation

M360 Effect of an inoculum and additive on in situ nutrients digestibility of sugar cane silage. J. A. Reyes-Gutiérrez[1,2], O. D. Montañez-Valdez*[1], R. Rodríguez-Macías[2], M. A. Ruiz-López[2], E. Salcedo-Pérez[2], and M. R. Rodriguez-Ramirez[3], [1]*Centro Universitario del Sur de la Universidad de Guadalajara*, *Ciudad Guzmán, Jalisco, México*, [2]*Centro Universitario de Ciencias Biológicas y Agropecuarias de la Universidad de Guadalajara*, *Las Agujas, Jalisco, México*, [3]*Instituto Nacional de Investigaciones Agricolas y Pecuarias*, *Tecomán, Colima, México*.

The objective of this study was to evaluate the effect of adding an inoculum and an additive handmade in sugar cane silage (SCS) on the in situ digestibility of DM, OM and ruminal pH. Four Holstein cows fitted with rumen cannula (BW 650 ± 50 kg) were randomly assigned to a 3 × 3 Latin square and they were housed in individual pens. Each period was 15 d, 10 for adaptation to experimental diets and 5 to collect samples. The treatments were: T1) sugar cane silage; T2) sugar cane silage with 1% inoculum and 1% additive; T3) sugar cane silage with 3% inoculum and 1% additive. The inoculum consists of 10.0% molasses, 1.0% of yogurt, 5.0% chicken manure, urea 0.5% and 83.0% water and the additive was formulated with 1.0% urea, 0.1% ammonium sulfate and 0.25% phosphorus. There were differences ($P \leq 0.05$) among treatments on the in situ digestibility of DM and OM and ruminal pH (Table 1).The ruminal pH was higher in T1 (7.15) and T2 (6.91) and lower in T3 (6.52). T3 showed higher percentages of DM and OM compared with T2 and control, these results could be explained because the inoculums improve predigestion of nutrients from the sugar cane during the ensiling process. The use of an inoculums and additive on cane sugar silage changes the ruminal pH and disappearance of DM and OM

Table 1. Coefficients of digestibility in situ of DM and OM of experimental materials (%)

Component	T1	T2	T3	SEM
Dry Matter				
96[1]	56.60c	59.99bc	67.11a	1.15
72	52.29b	51.04b	58.22a	0.89
48	51.45b	51.31b	53.79ab	1.08
36	44.08b	49.42a	47.46a	0.66
Organic Matter				
96	47.43b	60.21a	63.16a	2,35
72	56.66b	44.65c	64.28a	0.90
48	45.87c	53.80b	61.90a	1.50
36	47.50c	49.77c	60.30a	1.06

[a,b,c]Different letters in the same row differ ($P < 0.05$).

[1]Hours of incubation.

Key Words: sugar cane, digestibility, additive

M361 The effects of cinnamaldehyde and garlic extract on feed intake and nutrient digestibility by lambs. T. M. Norvell*, B. M. Nichols, T. J. McDonald, M. M. Harbac, and J. A. Paterson, *Department of Animal and Range Sciences, Montana State University*, *Bozeman*.

Three lamb experiments were conducted to evaluate the effects of a commercially available feed additive containing cinnamaldehyde and garlic (CG) on DM intake, DM, NDF and N digestibilities. Experiment one was a 3 × 3 Latin square to determine individual DMI. Twenty-one ewe lambs were randomly assigned to 3 treatments (7 ewes/treatment) in a GrowSafe facility which measures individual feed intake. Diets consisted of 85% ground grass hay and 15% supplement. Dietary treatments were control (no CG), 70 ppm CG, and 140 ppm CG. For each period, individual DMI was measured for 10-d with no adaptation to diets. Average DMI was similar ($P = 0.82$) for the 3 treatments (average = 2.3 kg/d). For Exp. 2, 24 wether lambs were placed in individual metabolism crates and randomly assigned to treatments to measure nutrient digestibility. Wethers were again fed increasing levels of CG. Diets consisted of 77% ground grass hay and 23% supplement. Treatments compared were control (no CG) and diets with 20, 40, or 80-ppm dietary CG. Wethers were fed diets at 3.3% of BW for 10-d of adaptation followed by 6-d fecal collection. The CG did not change DM ($P = 0.99$), NDF ($P = 0.90$) or N digestibilities ($P = 0.82$). Experiment 3 was designed as a 2 × 2 factorial arrangement of treatments using 24 wethers housed in individual metabolism crates. Main effects evaluated were 85% roughage (grass hay) vs. 85% concentrate (corn), and 0 vs. 80 ppm dietary CG. Wethers were offered diets at 2.7% of BW for 18-d of diet adaptation followed by 5-d of feces collection. There were no CG × forage level interactions and CG did not change DM ($P = 0.69$), NDF ($P = 0.33$), or N digestibilities ($P = 0.46$). Average DMI was greater ($P < 0.05$) for the 85% forage diets compared with 85% concentrate diets. Results indicate that at the levels offered, CG did not negatively affect DMI and had no affect on nutrient digestibility.

Key Words: cinnamaldehyde, garlic, feed intake

M362 Interaction of rumen pH, cinnamaldehyde and eugenol mixture and capsicum oleoresin on in vitro fermentation pattern and methane production. D. Bravo[1], S. Calsamiglia*[2], N. D. Pyatt[3], and P. H. Doane[3], [1]*Pancosma*, *Geneva, Switzerland*, [2]*Universitat Autonoma de Barcelona*, *Spain*, [3]*ADM Research*, *Decatur, IL*.

A 2 × 3 factorial arrangement of treatments was used to investigate the interaction between 2 sources of rumen inocula and inclusion of plant extracts on in vitro rumen fermentation and methane. Plant extracts were control (no extract) a mixture of eugenol and cinnamaldehyde (CIE, XT 6965, Pancosma,250 mg/L) or an oleoresin of capsicum (CAP, XT 6933, Pancosma, 250 mg/L). Rumen inocula was obtained from either dairy cows (50:50 forage:concentrate diet, pH 7.0) or beef cattle (10:90 forage:concentrate diet, pH 5.0). Each treatment was tested in triplicate and repeated in 2 periods. Fifty milliliters of a 1:1 ruminal fluid-to-buffer solution were introduced into polypropylene tubes supplied with 0.5 g of DM of DDGS and incubated for 24 h at 39°C. Samples were collected for ammonia N, VFA concentrations and methane analysis. Results were analyzed using SAS, and significant differences declared at $P < 0.05$. The beef-type fermentation resulted in lower total VFA (155.3 mM, −16%), acetate (45.4 mol/100mol, −25%) and butyrate (6.8 mol/100mol, −29%) proportions, reduced acetate to propionate ratio (1.26, −53%), ammonia-N (16.0 mg N/dL, −15%) and methane (18.7 µL/L, −48%) concentrations, and higher propionate proportion (36 mol/100mol, +61%). Using beef inocula, inclusion of CIE increased total VFA (+12%) and the proportion of propionate (+24%), and decreased methane (−18%) concentration. When dairy rumen inocula was used, CIE increased propionate proportion (+25%) and decreased acetate proportion (−8%), the acetate to propionate ratio (−25%), and methane production (−38%). For both inocula environments, CAP had little effect, agreeing with earlier research where the main effect for CAP being reported for DMI and feeding behavior. These results indicated that the mixture CIE reduced methane production in vitro, and that the effect was larger in a dairy-type environment without addition of CAP, compared with the beef-type environment.

Key Words: essential oils, methane, in vitro

M363 Influence of condensed tannin supplementation on intake, ruminal and total digestibility, rate of digestion, and urinary excretion of urea and total nitrogen of beef steers fed high concentrate diet. R. Mezzomo*[1], P. V. R. Paulino[1], S. C. Valadares Filho[1], J. P. I. S. Monnerat[1], G. S. Viana[1], M. G. Machado[1], J. C. M. Lima[1], T. S. Martins[1], P. Lencioni[2], and D. Grandini[3], [1]*Universidade Federal de Viçosa*, *Viçosa, MG, Brazil*, [2]*Silva Team*, *Buenos Aires, Argentina*, [3]*Nutron*, *Itapira, SP, Brazil*.

This trial was conducted to evaluate the effect of condensed tannin (TN) associated or not with a true protein source on intake, ruminal and total digestibility, ruminal digestion rate and urinary nitrogen excretion in beef steers fed high concentrate diet (87% of DM). Four crossbred steers (407 kg BW) fitted with rumen cannula were assigned to a 4x4 latin square design, arranged in a 2x2 factorial arrangement. Steers were fed a basal diet based on cracked corn, whole cottonseed, sugar-cane bagasse, mineral mixture and one out of 4 supplements: soybean meal with condensed tannin (SMT); soybean meal without condensed tannin (SM); condensed tannin without soybean meal (TN) and a treatment without both soybean meal and condensed tannin (BS). Quebracho extract were used as tannin source, included to provide 4 g of tannin/100 g of diet DM and all diets were formulated to be isonitrogenous. Intake of DM and nutrients was not affected ($P > 0.10$) by TN supplementation. However, there was an effect ($P < 0.10$) of TN supplementation on ether extract digestibility. A smaller ($P < 0.10$) excretion of urinary urea nitrogen (71.94 vs. 53.62 g) and total nitrogen (86.43 vs. 74.07 g) was observed in the animals supplemented with TN. Serum urea nitrogen concentration did not differ ($P > 0.10$) among treatments. There was an interaction ($P < 0.10$) between condensed tannin and soybean mean on ruminal digestibility and digestion rate of crude protein (CP).

When soybean meal was provided in the diet TN caused a reduction on CP ruminal digestibility from 46.92 to 33.46%, leading to a smaller digestion rate of CP. No differences in DM passage rate were observed ($P > 0.10$) among treatments. Urinary urea nitrogen and total nitrogen excretions were higher in the animals supplemented with soybean meal. The use of condensed tannin as an additive in cattle fed high concentrate diet using soybean meal as true protein source decreases the digestion rate and ruminal degradability of crude protein without affecting feed intake.

Key Words: feedlot, protein, RUP

M364 Effect of Copaiba (*Copaifera* sp.) oils on in vitro rumen fermentation of coastcross hay. R. C. Araujo*[1], A. V. Pires[1], A. L. Abdalla[2], M. R. S. R. Peçanha[2], and A. S. Morsy[2], [1]*ESALQ, Universidade de São Paulo*, *Piracicaba, SP, Brazil*, [2]*CENA, Universidade de São Paulo*, *Piracicaba, SP, Brazil*.

Copaiba oils have antimicrobial properties and are obtained from the trunk of *Copaifera* sp. trees. A randomized complete block design was used to determine the effects of *C. reticulata*, *C. multijuga*, and *C. langsdorfii* oils on rumen fermentation of coastcross (*Cynodon* sp.) hay by using an in vitro gas production (GP) system. Treatments were control (CTL), pure monensin at 3 µM (MON), and 75 or 150 µL of *C. reticulata*, *C. multijuga*, or *C. langsdorfii* oil. In each flask (160 mL), 0.5 g of hay (91.3% DM) was incubated with 50 mL of medium and 25 mL of rumen fluid at 39°C for 24h. Replicates were n = 6 for GP and n = 3 for all other variables. Two inocula (from 3 lambs each) were used as source of variation. PROC Mixed of SAS was used and differences declared when $P < 0.05$. By GC/MS analysis, major secondary compounds in oils were *C. reticulata* – trans-caryophyllene (50.2%) and α-humulene (8.1%); *C. multijuga* – trans-caryophyllene (21.9%), α-trans-bergamotene (11.4%), and β-bisabolene (9.1%); *C. langsdorfii* – trans-caryophyllene (56.5%) and α-humulene (9.4%). MON decreased GP (117.5 vs. 103.7 mL), CH_4 production (13.0 vs. 9.8 mL), CH_4 to gas ratio (0.1100 vs. 0.0943), and truly degraded dry matter (TDDM; 57.4 vs. 50.9%) when compared with CTL. MON did not affect total SCFA and C_2 concentrations, but increased C_3 concentration (12.3 vs. 14.0 mM) and decreased C_4 concentration (8.6 vs. 7.5 mM) when contrasted with CTL. All Copaiba oils at 150 µL had lower GP than CTL. However, TDDM was reduced by all Copaiba oils in both doses. The CH_4 production and CH_4 to gas ratio did not differ between *Copaifera* sp. oils and CTL. Total SCFA, C_2, and C_3 concentrations, as well as C_2 to C_3 ratio were also not influenced by *Copaifera* sp. oils. The only exception was *C. reticulata* oil at 75 µL, which showed a greater C_3 concentration than CTL (12.3 vs.13.0 mM). All treatments showed similar results for ammonia concentration. Results indicate that *Copaifera* sp. oils decreased in vitro DM degradability with minimal effects on fermentation profile of coastcross hay.

Key Words: methane, plant extracts, plant secondary compounds

M365 Effects of garlic oil on methane production, microbial growth and diet fermentation in Rusitec fermenters. M. D. Carro*[1,2], M. L. Tejido[1,2], C. Saro[1,2], and M. J. Ranilla[1,2], [1]*Dept. Producción Animal, Universidad de León*, *24071 León, Spain*, [2]*Instituto de Ganadería de Montaña (CSIC-ULE)*, *Finca Marzanas, 24346 Grulleros, León, Spain*.

Garlic oil (GAR) has been shown to reduce methane production in the rumen, but little is known about its effects on ruminal microbial growth. Two 15-d incubation runs were conducted with 4 Rusitec fermenters to investigate the effects of GAR on ruminal microbial growth and fermentation of a 50:50 alfalfa hay:concentrate diet. Each fermenter received daily 30 g of diet DM. In each run, 2 fermenters received daily 100 mg of GAR dissolved in 0.7 mL of ethanol (180 mg of GAR / L of fermenter content) and 2 received 0.7 mL of ethanol (control). After 11 d of GAR treatment, the main fermentation parameters were determined during 3 consecutive days. Microbial growth was determined on d 15 using 15N as a microbial marker.

No effect of GAR ($P > 0.05$) was observed on dry matter degradability (61.9 vs. 62.3% for control and GAR, respectively), neutral detergent fiber degradability (44.6 vs. 45.9%) and daily production of total volatile fatty acids (VFA; 100 vs. 103 mmol) and ammonia-N (210 vs. 221 mg). The GAR increased the molar proportion of propionate ($P = 0.02$; 17.5 vs. 14.9%), decreased butyrate proportion ($P < 0.001$; 14.6 vs. 17.2%), and tended to decrease the proportion of acetate ($P = 0.07$; 53.6 vs. 54.5%). Fermenters receiving GAR showed greater ($P < 0.001$) proportions of isobutyrate, valerate and caproate compared with controls. Daily production of methane was reduced ($P < 0.001$) by 10.8% by GAR, resulting in lower ($P = 0.002$) methane/VFA ratios in GAR treated fermenters compared with controls. Microbial growth tended to be greater ($P = 0.09$) in fermenters receiving GAR (247 vs. 237 mg of microbial N/d), but its efficiency was similar in all fermenters ($P = 0.12$; 25.5 vs. 23.0 mg of microbial N / g organic matter apparently fermented). Supplementation of GAR to fermenters was an effective means to reduce methane production without negatively affecting microbial growth, diets degradability or VFA production.

Key Words: garlic oil, methane, Rusitec fermenters

M366 Effect of Copaiba (*Copaifera* sp.) oils on in vitro rumen fermentation of a high-concentrate diet. R. C. Araujo*[1], A. V. Pires[1], A. L. Abdalla[2], L. A. Castilho[2], and R. C. Lucas[2], [1]*ESALQ, Universidade de São Paulo*, *Piracicaba, SP, Brazil*, [2]*CENA, Universidade de São Paulo*, *Piracicaba, SP, Brazil*.

Copaibas (*Copaifera* sp.) are Brazilian trees whose oil extracted from the trunk shows antimicrobial properties. A randomized complete block design was used to determine the effects of *C. reticulata*, *C. multijuga*, and *C. langsdorfii* oils on rumen fermentation of an 80:20 concentrate:forage diet by using an in vitro gas production (GP) system. Treatments were: control (CTL), pure monensin at 3 µ*M* (MON), and 75 or 150 µL of *C. reticulata* (RET75 and RET150), *C. multijuga* (MLT75 and MLT150), or *C. langsdorfii* (LNG75 and LNG150) oil. In each flask (160 mL), 0.5 g of diet (91.4% DM) was incubated with 50 mL of medium and 25 mL of rumen fluid at 39°C for 16 h. Replicates were n = 6 for GP and n = 3 for all other variables. Two inocula from lambs (n = 3 each) adapted to the incubated diet were used as source of variation. The PROC Mixed of SAS was used with differences declared when $P < 0.05$. By GC/MS analysis, major secondary compounds in oils were RET – trans-caryophyllene (50.2%) and α-humulene (8.1%); MLT – trans-caryophyllene (21.9%), α-trans-bergamotene (11.4%), and β-bisabolene (9.1%); LNG – trans-caryophyllene (56.5%) and α-humulene (9.4%). Compared with CTL, MON decreased GP (160.3 vs. 147.5 mL) and CH_4 production (16.3 vs. 13.8 mL) as well as truly degraded dry matter (TDDM; 81.5 vs. 77.9%). MON did not affect total SCFA and C_2 concentrations, but increased C_3 concentration (17.9 vs. 21.3 m*M*) and decreased C_2 to C_3 ratio (2.67 vs. 2.21) when compared with CTL. MLT75 (164.8 mL), LNG75 (167.7 mL), and LNG150 (165.5 mL) had greater GP than CTL (160.3 mL). No effects were observed for all oils on CH_4 production, CH_4 to gas ratio, and TDDM. Compared with CTL, LNG150 showed greater total SCFA (89.9 vs. 98.7 m*M*) and

C_2 (48.0 vs. 53.9 m*M*) concentrations. RET75, RET150, and LNG150 showed greater C_3 concentration (19.1, 19.3, 18.9 m*M*, respectively) when contrasted with CTL (17.9 m*M*). All oils did not affect C_2 to C_3 ratio. Copaiba oils affected rumen fermentation of a high-concentrate diet without effects on methanogenesis. *C. langsdorfii* oil at 150 µL showed the most positive effects by increasing total SCFA concentration.

Key Words: methane, plant extracts, plant secondary compounds

M367 Effects of supplemental poultry fat on calves grazing bermudagrass pasture. J. G. Powell*, T. J. Wistuba, and E. B. Kegley, *University of Arkansas*, *Fayetteville*.

Bermudagrass is a warm season perennial found throughout the southeastern US If fertilized, bermudagrass can contain adequate crude protein for growing cattle, but energy is often limiting for maximal growth rates. Supplementing grain will increase energy intake; although at high rates of supplementation grain can cause decreased forage intake. The objective of this experiment was to evaluate the effect of adding poultry fat to a grain supplement on growth performance of calves grazing bermudagrass; the supplemental fat could make a more energy dense, beneficial, supplement or alternatively the added fat could impair rumen fiber digestion and thus reduce forage intake. Sixty calves (228 ± 3.2 kg, 30 heifers and 30 steers) were obtained from a single source. Calves were stratified by sex and weight and assigned randomly to 6 2.4-ha pastures. Pastures were assigned randomly to receive 1 of 2 treatments. The 2 treatments were corn-soybean meal supplements with 0 or 5% poultry fat. Supplements were formulated to be isonitrogenous (17% CP, DM basis). Calves were offered 1.1 kg/d of the appropriate supplement for the 140-d trial. Calves were weighed and forage availability in the pastures was measured at 28-d intervals. Cattle growth and forage availability were analyzed using the mixed procedures of SAS with pen as the experimental unit. Pregnancy data were analyzed using the GENMOD procedures of SAS with heifer as the experimental unit. Supplemental poultry fat did not affect final BW (337 vs. 336 kg, $P = 0.76$) or ADG ($P = 0.86$). No differences were detected in available forage due to dietary treatment (treatment × day interaction, $P = 0.43$). After the trial, heifers were kept as a single group, fed a common diet, and bred. There was no effect of supplemental fat during the growing phase on the number of heifers that became pregnant (53 vs. 43%, $P = 0.72$). Adding 5% poultry fat to the grain supplement fed to growing cattle grazing bermudagrass had no impact on growth.

Key Words: growing cattle, poultry fat, bermudagrass

M368 Studying the effect of different direct fed microbials on rumen fermentation in vitro. D. Barrau, M. Quintino Cintora, and N. D. Walker*, *Lallemand Animal Nutrition*, *Montreal, QC, Canada*.

Direct-fed microbials (DFMs) are commonly used in the beef feedlot industry to improve host health and productivity. The aim was to study the effect on rumen fermentation of a live yeast DFM Levucell SC (LSC), and 2 bacterial DFM products; one containing *L. buchneri* (MLB); the other a mixture of *L. buchneri* and *L. acidophilus*, (MLB+LA) with incubations which had no added DFM. Rumen contents were removed before feeding from 3 steers fed a finishing diet (70% high moisture corn, 15% DDGs, 10% alfalfa hay) and pooled. Strained contents (SRF) were mixed with anaerobic buffer (1:1) and used to set up triplicate batch incubations containing either glucose, corn starch or ground corn, +/− the test DFMs. Bacterial DFMs were added at a final cfu/ml of 1 × $10e^{05}$, yeast at 1 × $10e^{06}$. At 0, 3, 6, 9 and 24 h, gas production and pH were measured and samples removed for VFA and lactate analysis. To determine the effect of the 3 DFMs on fiber digestion, the %DM and %NDF disappearance of samples of wet (WDG) and dry Distillers grains (DDG) (+/− solubles), wet corn gluten (CG), alfalfa hay (AH) and the mixed ration (MR) the animals were fed, was measured using the Daisy fermentor. Incubation jars, including a control (no addition) were set up by mixing SRF with anaerobic buffer (1:4). Each DFM was added to a jar along with filter bags containing a known amount of each substrate. Triplicate bags were removed at 0, 3, 6, 12 and 24h and analyzed for fiber content. All incubations were repeated on 2 different days. Compared with control, all 3 DFMs reduced the accumulation of lactate from corn starch at 9 and 24h ($P < 0.008$) and significantly reduced lactate accumulation from ground corn at 6 h ($P < 0.05$). No effect of the DFMs on gas production or pH was seen. The effects on fiber digestion were DFM, substrate and time dependent. MLB significantly increased %NDFd of DDGs at 6 and 12h and MR at 3 and 24h ($P < 0.05$). LSC increased %DMd and %NDFd of CG by 24 h ($P < 0.05$). All 3 DFMs increased %NDFd of WDGS ($P < 0.05$) in the later part of the incubation. No significant effect was observed on the other substrates tested. To conclude, DFMs may help reduce lactate accumulation and improve fiber digestion.

Key Words: DFM

M369 Effect of a commercial microbial inoculant (Promote) on corn silage and animal performance. C. J. Fruge*, F. M. LeMieux, W. A. Storer, and T. H. Shields, *McNeese State University*, *Lake Charles, LA*.

An experiment was conducted to evaluate the efficacy of a commercial microbial inoculant (Promote) for corn silage and the subsequent effect on heifer performance. The 3 experimental treatments were: 1) no inoculant (control), 2) inoculant (100,000 CFU per gram of corn silage), and 3) inoculant (50,000 CFU per gram of corn silage). Promote was applied to corn silage as a liquid suspension during the ensiling process in horizontal poly bags. Silage samples were collected at d 0, 7, 14, 21, and 61 relative to ensiling. Samples were analyzed (Analab, Fulton, IL) for chemical composition for each treatment. Levels of lactic acid increased while pH decreased in both treatments of inoculated silage. A growth study with developing heifers, (n = 225) average initial wt 261 kg, was initiated at d 135 post ensiling. After a 14 d acclimation to feeding, heifers were randomly allotted (n = 75) to receive one of the 3 treatments as the forage component of their diet. Heifers were weighed on d −14, 0, 21, 55, and 86 to obtain ADG. Heifers consuming diets treated with Promote had increased ($P < 0.01$) ADG during the first month. Subsequently, heifers receiving the untreated silage excelled. Overall ADG between heifers receiving treatments 1 and 2 became similar ($P > 0.1$) by d 86 and were greater than ($P < 0.01$) heifers receiving treatment 3.

Key Words: silage, inoculant, heifer

M370 Effects of Fibrozyme on in vitro ruminal digestion and fermentation of a corn and wet distillers-based finishing beef diet with and without monensin. J. M. Tricarico, M. A. Witt, and J. S. Jennings*, *Alltech, Inc.*, *Brookings, SD*.

Two in vitro ruminal fermentation experiments were conducted to analyze the effects of a fibrolytic enzyme (Fibrozyme, Alltech Inc.) dose on digestibility of a corn and wet distillers-based finishing diet with or without monensin. Diets were a conventional finishing diet containing monensin at 50 µg/g of substrate (CONV) or a natural finishing diet with no monensin (NAT). The diet substrate (0.5g) was weighed in an Ankom bag and placed in a sealed 200 mL glass bottle. Bottles were flushed with

CO_2 and 100 mL of a 20% rumen fluid 80% buffer solution was added to begin the 72 h incubation period. Rumen fluid was collected from a single Holstein cow, receiving a common dairy TMR. During Exp. 1, the CONV and NAT diets with and without Fibrozyme at 0, 0.6, and 1.2 mg/mL of inoculum were compared. Fibrozyme was then applied to the NAT diet at 0, 0.6, 1.2, and 1.8 mg/mL of inoculum in Exp. 2. Enzyme by diet interactions occurred ($P < 0.05$) for true DM (TDMD) and NDF digestibility (NDFD) in Exp. 1. Fibrozyme increased TDMD (87.4, 88.7, and 89.1%) and NDFD (26.1, 33.7, and 36.1%) linearly ($P < 0.05$) in the CONV diet but only the highest dose increased TDMD (86.0 vs. 87.0%) and NDFD (30.3 vs. 35.4%) in the NAT diet. After elevating the dose further in the NAT diet (Exp. 2), the increases in TDMD (86.0 vs. 89.0 and 89.1%) and NDFD (25.8 vs. 41.8 and 42.3%) were similar for 1.2 and 1.8 mg/mL of supplemental Fibrozyme inclusion. In addition, 1.8 mg/mL of supplemental Fibrozyme increased ($P < 0.05$) final culture pH (6.51 vs. 6.56) and reduced butyrate molar proportions (0.183 vs. 0.173). Fibrozyme inclusion also tended ($P = 0.06$) to increase the fractional rate of degradation linearly (0.065, 0.073, 0.077, and 0.079 h-1). These results are consistent with our hypothesis that Fibrozyme will increase digestibility in finishing feedlot diets with a lower effective dose of Fibrozyme in the presence of monensin.

Key Words: fibrolytic enzyme, digestibility, finishing diet

M371 Influence of condensed tannin supplementation on protein efficiency, microbial protein yield, nitrogen balance and ruminal fermentation characteristics in beef steers fed high concentrate diet. R. Mezzomo*[1], P. V. R. Paulino[1], M. S. Duarte[1], L. S. Moura[1], L. H. P. Silva[1], E. San Vito[1], L. D. A. Rufino[1], C. Cabral[2], D. Grandini[3], and S. C. Valadares Filho[1], [1]*Universidade Federal de Viçosa*, *Viçosa, MG, Brazil*, [2]*Silva Team*, *Buenos Aires, Argentina*, [3]*Nutron*, *Itapira, SP, Brazil*.

This trial was conducted to evaluate the effects of condensed tannin (TN) associated or not with a true protein source on protein efficiency, microbial protein yield, nitrogen balance and ruminal fermentation characteristics (RFC) in beef steers fed high concentrate diet (87% of DM). Four crossbred steers (407 kg BW) fitted with rumen cannula were assigned to a 4x4 latin square design, arranged in a 2x2 factorial arrangement. Steers were fed a basal diet based on cracked corn, whole cottonseed, sugar-cane bagasse, mineral mixture and one out of 4 supplements: soybean meal with condensed tannin; soybean meal without condensed tannin; condensed tannin without soybean meal and a treatment without both soybean meal and condensed tannin. Quebracho extract were used as tannin source, included to provide 4 g of TN/100 g of diet DM and the diets were formulated to be isonitrogenous. The nitrogen balance indicated that the use of TN improved the efficiency of nitrogen utilization ($P < 0.10$), however, no differences were observed when soybean meal was added to the diet ($P > 0.10$). There was an interaction ($P < 0.10$) between condensed tannin and soybean mean supplementation on the flux of rumen undegradable protein (RUP), metabolizable protein (MP) and on the ratio MP:CP. In the presence of soybean meal the addition of TN increased the flux of RUP (302.24 to 416.02 g/d), MP (540.23 to 671.03 g/d) and improved the ratio MP:CP (58.69 to 46.54). Microbial protein yield and microbial efficiency did not differ among treatments ($P > 0.10$). There was no effect of TN supplementation ($P > 0.10$) on ruminal pH, VFA and ammonia (N-NH3) concentration. N-NH3 increased and ruminal pH decreased with the inclusion of soybean meal ($P < 0.10$) in the diet. The utilization of condensed tannin as an additive in cattle fed high concentrate diet using soybean meal as true protein source implies in positive effects on efficiency of N utilization, increasing the flux of metabolizable protein.

Key Words: Quebracho extract, feedlot, RUP

M372 Effects of supplementing an exogenous proteolytic enzyme on growth performance in growing beef steers. J. M. Vera[1], C. T. Noviandi*[1], Arief[2], J.-S. Eun[1], and D. R. ZoBell[1], [1]*Department of Animal, Dairy, and Veterinary Sciences, Utah State University*, *Logan,* [2]*Faculty of Animal Science, Andalas University*, *Padang, West Sumatra, Indonesia*.

An exogenous proteolytic enzyme (EPE) has been previously found to increase in vitro NDF degradability of dried distillers grains with solubles (DDGS). To further investigate the effects of EPE, 48 Angus crossbred growing beef steers (292 ± 25.2 kg BW) were used to assess the growth performance when fed a DDGS-based TMR diet without or with an EPE supplementation in a completely randomized design. The growing TMR diet consisted of 13.6% alfalfa hay, 50.3% corn silage, 30.7% DDGS, and 5.4% feedlot supplement (DM basis). The EPE contained 38,622 U/g protease activity with negligible fibrolytic activities. The EPE was diluted with water and added at a rate of 0.52 g/kg DM TMR as it was mixing for the group of EPE treatment. Four animals were placed in each pen, and 6 pens allocated to each treatment. All steers were adapted to the TMR diet for a 2-week period before start of the trial. Feed was offered for ad libitum consumption once daily at 0800 h with free access to water. Feed intake was measured weekly, and individual BW of steers was recorded on 2 consecutive days at the beginning of trial and wk 4 and 8. The experiment lasted 56 d, and data were analyzed using the MIXED procedure of SAS. There were no significant differences ($P > 0.10$) for final BW (398 vs. 401 kg), BW gain (107 vs. 108 kg), and ADG (1.90 vs. 1.93 kg/d) between control and EPE treatment, respectively. Furthermore, EPE supplementation did not affect DM intake (10.5 vs. 10.0 kg/d) and gain to feed ratio (0.191 vs. 0.199). Therefore, supplementation of an EPE product at the dose rate used in this study did not alter growth performance of growing beef steers fed a DDGS-based TMR diet.

Key Words: exogenous proteolytic enzyme, growing beef steers, growth performance

M373 Effects of zinc and chlortetracycline supplements on growth performance, blood metabolites, carcass characteristics, and claw health in young Holstein bulls. H. Fagari-Nobijari[1], H. Amanlou[1], M. Dehghan-Banadaky*[2], and M. H. Shahir[1], [1]*University of Zanjan*, *Zanjan, Iran*, [2]*University of Tehran*, *Karaj, Tehran, Iran*.

This study conducted to evaluate the effects of supplementing finishing diet with zinc and/or chlortetracycline on growth performance and claw health of calves. Holstein bulls (n = 212; initial BW = 375.5 ± 18.4 kg) were randomly allocated to one of 4 treatments in a completely randomized design as a 2 × 2 factorial experiment for 56 d. Dietary treatments include: 1) the basal diet (control); 2) basal diet plus 150 mg of Zn/kg of DM as ZnSO4; 3) basal diet plus chlortetracycline (200 mg/animal/d; CTC); and 4) basal diet plus 150 mg of Zn/kg of DM + CTC (200 mg/animal/d). Animals received fresh total mixed ration for ad libitum. DMI was measured daily. BWs were recorded and blood samples were collected on d 0, 28, and 56. Liver samples were taken on d 56. Ultrasound measurements of backfat thickness (UFAT), rump fat thickness (URPFAT), and longissimus muscle area (ULMA) were made on d 56. All claws of animals were examined every 2 weeks to identify claw lesions. Data were statistically analyzed using the repeated measures option in Proc Mixed of SAS. Zn supplement decreased ADG, G:F, and apparent DM digestibility ($P < 0.01$); however, DMI was not influenced. Dietary CTC improved G:F on d 28 to 56 and decreased DM digestibility, but it did not affect ADG and DMI. Dietary CTC increased plasma total protein and urea nitrogen. Zinc supplementation decreased ULMA. The supplementation of CTC decreased UFAT and URPFAT.

Serum concentration of Zn, Cu, plasma total protein, albumin, alkaline phosphatase, and Zn concentration of liver were affected by the interaction of CTC × Zn. The prevalence of lameness was 14.15% with the highest odds ratio (OR) for lameness in control and Zn supplemented groups (OR = 7.2, 2.53, respectively). In summary, CTC supplementation did not improve ADG and G:F in bulls, however it affected carcass characteristics and improved claw health. Supplemental Zn decreased ADG and G:F and did not decrease lameness.

Key Words: zinc, chlortetracycline, young bulls

M374 The use of copper and chlortetracycline supplements for improving of growth performance, carcass characteristics and claw health in young Holstein bulls. H. Fagari-Nobijari[1], H. Amanlou[1], M. Dehghan-Banadaky*[2], and A. Shabani[3], [1]*University of Zanjan*, *Zanjan, Iran*, [2]*University of Tehran*, *Karaj, Tehran, Iran*, [3]*Tabriz Islamic Azad University*, *Tabriz, Iran*.

Two hundred 12 young Holstein bulls (initial body weight = 375.4 ± 17.1 Kg) were allotted to one of 4 treatments in a completely randomized design as a 2 × 2 factorial experiment for 56 d. treatments include: 1) the basal diet (control); 2) basal diet plus 30 mg of Cu/kg of DM as CuSO4; 3) basal diet plus chlortetracycline (200 mg/animal/d; CTC); and 4) basal diet plus 30 mg of Cu/kg of DM + CTC (200 mg/animal/d). Animals received a fresh total mix ration for ad libitum. DMI was measured daily. The body weights were recorded and jugular blood samples were collected on d 0, 28 and 56. Ultrasound measurements of backfat thickness (UFAT), rump fat thickness (URPFAT), and longissimus muscle area (ULMA) were made on d 56. All claws of young bulls examined every 2 weeks for identifying claw lesions. Data were statistically analyzed using the repeated measures option in Proc Mixed of SAS. Copper supplementation with or without CTC improved average daily gain, gain:feed and it might also influenced carcass characteristics ($P < 0.05$). Serum cholesterol decreased with Cu supplementation. Serum urea nitrogen tended to decrease by CTC supplementation ($P < 0.1$) and serum Ca tended to increase by supplemental of Cu ($P < 0.1$). Cu supplementation decreased UFAT and UPRFAT; however, it increased ULMA. Interaction of Cu × CTC affected UPRFAT ($P > 0.03$); also, UFAT tended to decrease by interaction of Cu × CTC ($P < 0.1$). Supplemental CTC had no effect on ultrasound carcass characteristics. Hip height was similar between treatments. The prevalence of lameness and skin and interdigital space disorders (ID) were high in Cu supplemented bulls compared with CTC group (OR = 2.97 and 1.94, respectively). The prevalence of white line disorders, heel erosion, and sole disorders statistically were not significant. In summary, supplemental Cu may improve carcass characteristics and growth performance of finishing bulls, but it may not prevent lameness. However, lameness decreased when Cu supplementation was used with CTC.

Key Words: copper, chlortetracycline, young bulls

M375 Chlortetracycline supplementation affected carcass characteristics and claw health in young Holstein bulls. H. Fagari-Nobijari[1], M. Dehghan-Banadaky*[2], S. H. Hosseini-Sabeghi[3], H. Amanlou[1], and A. Shabani[4], [1]*University of Zanjan*, *Zanjan, Iran*, [2]*University of Tehran*, *Karaj, Tehran, Iran*, [3]*Ghaemshahr Islamic Azad University*, *Ghaemshahr, Iran*, [4]*Tabriz Islamic Azad University*, *Tabriz, Iran*.

One hundred and 6 young Holstein bulls (initial BW = 376 ± 19.5 kg) were randomly allocated to 2 treatments in a completely randomized design for 56d. Treatment groups received 1) the basal diet with no supplemental chlortetracycline (control) and 2) basal diet plus chlortetracycline (100 mg/animal/d; CTC). Animals received fresh total mix ration for ad libitum allowing 10% orts. Group dry matter intake was measured daily. The Body Weights were recorded and Jugular blood samples were collected on d 0, 28 and 56. Ultrasound measurements of backfat thickness (UFAT), rump fat thickness (URPFAT), and longissimus muscle area (ULMA) were made on d 56. All claws of animals examined every 2 weeks for identifying claw lesions. Chlortetracycline supplementation tended to decrease average daily gain (ADG) ($P = 0.2$) but gain:feed (G:F) did not differ ($P = 0.48$). Also, URPFAT was not affected by treatments ($P = 0.2$). However, CTC tended to decrease UFAT ($P = 0.07$). Statically, young bulls supplemented with CTC did not increase ULMA vs. unsupplemented animals ($P = 0.3$). Supplemental CTC improved serum concentrations of Cu ($P = 0.04$) and Zn ($P = 0.004$) and also, decreased cholesterol ($P = 0.05$) than control. There was no difference between treatments on concentration of plasma IGF-I ($P = 0.4$). The prevalence of lameness was 19.81%. Lameness was most frequently observed in the control group (OR = 4.08). The prevalence of skin and interdigital space disorders (ID) was the greatest cause of lameness in the present study (52.38% of whole lameness) and was higher in control than the other group (OR = 5.17; 42.85% of whole lameness). Statistically, the prevalence of sole disorders (SD), white line disorders (WD), and heel erosion (HE) were not different ($P = 0.56$, 0.33, and 0.56, respectively). In summary, supplemental CTC may decrease growth performance in finishing bulls, however, it may successfully prevent lameness and may alter fat metabolism.

Key Words: chlortetracycline, claw health, young bulls

M376 Effect of chestnut tannins supplement on milk production traits of dairy sheep on pasture. A. Nudda*[1], G. Battacone[1], A. Fenu[1], M. Decandia[2], M. Sitzia[2], M. Acciaro[2], and G. Pulina[1], [1]*Dipartimento di Scienze Zootecniche, University of Sassari*, *Sassari, Italy*, [2]*Agricultural Research Agency of Sardinia - AGRIS Sardegna*, *Sassari, Italy*.

The use of tannins in grazing ruminants reduces OM digestibility in the rumen and increases protein escape. This is particularly desirable when animals graze on grass with a high content of soluble protein, because tannins can reduce the production of ammonia in the rumen and increase the protein available for intestinal digestion. The present study aimed to investigate the milk productive response of dairy ewes, grazing on pasture composed by 70% of *Medicago polymorpha* (27.5% dry matter, DM; 44.3% NDF, 29.5% ADF, 18.3% CP, on a DM basis) and 30% of *Lolium rigidum* (39.6% DM; 58.3% NDF, 31.2% ADF, 9.4% CP, on a DM basis), to the supplementation of concentrate (300 g/d; 87.1% DM; 29.4% NDF, 16.9% ADF, 17.6% CP, on a DM basis) containing 3 levels of commercial chestnut hydrolyzable tannin (0, 6 and 12%, on a DM basis; T0, T6 and T12, respectively). Thirty-six 2- to 4-yr-old Sarda ewes (12 per experimental group), in mid lactation (90–120 DIM), and grazing on pasture were used in this one-month trial. Daily milk production was recorded and daily milk samples were collected for analysis of fat, protein, lactose, SCC and urea. Data were analyzed by ANOVA including tannin level and sampling as fixed factors and their interaction. Tannin level did not influence milk yield and milk fat and protein concentration. Lactose was higher in T12 than in T0, being T6 intermediate. The urea content was not modified by the addition of tannin to the diet. The SCC was lowered by the inclusion of tannin in the diet. These results showed that the dose of tannins used did not modify the productive performance of dairy sheep on pasture.
Research supported by the Ministero dell′Istruzione dell′Università e della Ricerca (Project PRIN 2008).

Key Words: dairy sheep, tannins, milk

M377 The estimation of rumen fungi growth on maize stubble treated with steam and sodium hydroxide by using of quantitative competitive polymerase chain reaction. M. Chaji* and T. Mohammadabadi, *Department of Animal Science, Ramin (Khuzestan) Agricultural and Natural Resources University*, *Ahwaz (Molassani), Khuzestan, Iran*.

This experiment was conducted to evaluate the effect sodium hydroxide (NaOH) and steam on growth of rumen anaerobic fungi on maize stubble (MS) using quantitative competitive polymerase chain reaction (QC-PCR) assay. Rumen fungi were isolated from pre-incubated wheat straw in the rumen of fistulated sheep and then grown by Joblin (1981) method. These isolates were used (1:9) as a source of fungi inoculums in serum bottles containing fungi culture medium, 1 g maize stubble (as untreated or treated with 45 g/ kg DM NaOH, steam at 130°C and 120 min, and or $NaOH^+$steam; UMS, T1MS, T2MS and T3MS, respectively) and 1 mL antibiotic solution at 39°C (3 times sub culturing). Total genomic DNA was isolated from pure culture samples using guanidine thiocyanate-silica gel method. A universal PCR primer pair GAF (F): 5′-GAG GAA GTA AAA GTC GTT AAC AAG GTT TG-3′ and GAF (R): 5′-GAA ATT CAC AAA GGG TAG GAT GAT TT-3′ was used to amplify a specific region of 18S rDNA from rumen anaerobic fungi. Standard control DNA was constructed to use in the QC-PCR and was shown to amplify under the same reaction condition and the same amplification efficiency as the target DNA. The relative intensities of PCR products that were used to compare fungal biomass, was quantified by Image J 1.29x and the data was analyzed using the GLM procedure of SAS for a completely randomized design. The result showed that growth of rumen anaerobic fungi in the medium containing MS treated with NaOH and steam (+0.24, +0.19, respectively) was greater than untreated MS (−0.61) and the highest fungi growth was for medium containing MS treated with $NaOH^+$steam (+0.63) ($P < 0.05$). Therefore it is appears that rumen anaerobic fungi growth and in vitro maize stubble degradation increased by NaOH and steam treatments.

Key Words: maize stubble, rumen fungi, steam

M378 The in vitro fermentation of sesame straw processed with alkali by rumen isolated bacteria. T. Mohammadabadi* and M. Chaji, *Department of Animal Science, Ramin (Khuzestan) Agriculture and Natural Resources University*, *Ahwaz (Molassani), Khuzestan, Iran*.

The aim of this study was to determine rumen bacteria fibrolytic activity by using disappearance of DM and NDF in rumen isolated bacteria culture containing sesame straw (SS) as untreated and or treated with sodium hydroxide (NaOH). The experimental samples were including; untreated SS and SS treated with 30, 40 and 50 g/kg DM NaOH; USS, N1SS, N2SS and N3SS, respectively. Rumen fluid collected from 4 fistulated sheep, centrifuged (1000 rpm, 10 min), and supernatant was used to grow bacteria in medium containing fungicides (benomyle: 500 ppm/mL medium and metalaxyle: 10 mg/ml medium) under anaerobic conditions at 39°C for 24 h. These isolates were then used as a source of inoculum for culturing bacteria in a serum bottle containing 45 mL of culture medium and 1 g of experimental sample under anaerobic conditions (using 3 times subculture) for 12, 24, 48, 72 and 96 h. The residual substrates of each bottle were then filtered and used to determine disappearance of DM and NDF. Data of DM and NDF disappearance were analyzed as a completely randomized design using the general linear model procedure of SAS (1990). The result showed disappearance of DM after 96 h incubation by rumen isolated bacteria will be 67.3, 78.3, 86.3 and 92.1 g/100 g for untreated SS and treated with 30, 40 and 50 g/k g DM NaOH, respectively ($P < 0.05$). The highest increase of NDF disappearance after 96 h incubation was for SS treated with 50 g/kg DM NaOH (452.3 mg/g DM) that fallowed by SS treated with 40 and 30 g/kg DM NaOH (420.2 and 383.3 mg/g DM, respectively) ($P < 0.05$). Therefore, it appears that the growth and fibrolytic activity of rumen isolated bacteria on sesame straw is influenced by sodium hydroxide content.

Key Words: sesame straw, sodium hydroxide, rumen bacteria

M379 Synergism between cellulolytic and non-cellulolytic rumen bacteria on different fibrous substrates: Study in semi-defined cultures. J. Chiquette* and K. Lauzon, *Agriculture Canada*, *Sherbrooke, Quebec, Canada*.

The objective was to investigate the occurrence of synergistic fibrolysis when cellulolytic bacteria are cocultured with non-cellulolytics in a semi-defined medium in vitro. Cellulolytic bacteria were *Fibrobacter succinogenes* GC5 and *Ruminococcus flavefaciens* NJ and the non-cellulolytics were *Prevotella bryantii* 25A and *Prevotella ruminicola* 19189. Timothy hay and alfalfa hay were used as substrates to measure NDF disappearance with time (3 and 7 d). Each bacterial population was quantified by real-time PCR when in monoculture or when cocultured on the different substrates. Cellulolytic bacteria were grown at 37°C

for 72 h in basal medium containing 1% (w/v) Avicel (NJ) or 0.3% cellulose filter paper (GC5). Non-cellulolytic bacteria were grown in basal medium containing 0.5% (w/v) cellobiose as a sole carbon source until the end of the log phase (12h). The OD-adjusted inocula were added in monocultures (0.2 mL) or in cocultures (0.2 mL each for cellulolytics and non-cellulolytics) to tubes containing 10 mL of basal medium with 100 mg of each substrate. After 7 d of incubation, a greater disappearance of timothy NDF was observed when *R. flavefaciens* was cocultured with *P. ruminicola* (18.2%) or *P. bryantii* (18.1%) compared with the monoculture of *R. flavefaciens* (16.4%) ($P \leq 0.05$). Similarly, when *F. succinogenes* was cocultured on timothy hay with *P. ruminicola*, NDF disappearance was greater (26.9%) compared with the monoculture of *F. succinogenes* (24.3%) ($P \leq 0.05$). *P. ruminicola* was in greater number when cocultured with NJ or GC5 on timothy hay ($P \leq 0.05$). *P. bryantii* tended to be in greater number ($P \leq 0.15$) when cocultured with *R. flavefaciens*. There was no synergistic fibrolysis between the 2 bacterial groups on alfalfa hay. These results demonstrated that synergistic fibrolysis was substrate dependent and was accompanied by increased populations of the non-cellulolytic bacteria.

Key Words: synergism, fibrolysis, rumen

M380 Effects of chemical treatments on in situ ruminal degradation of canola straw in Holstein cows. M. Ghiasvand, M. Dehghan-Banadaky*, and K. Rezayazdi, *Department of Animal Sci., Campus of Agriculture, University of Tehran*, *Karaj, Tehran, Iran*.

This study was conducted to evaluate the effects of different chemical treatments on canola straw including: T1 urea (3% of DM); T2 urea and molasses (urea 3% and molasses 2% of DM); T3 ammonium hydroxide (3% of DM); T4 sodium hydroxide (5% of DM); T5 sodium hydroxide and hydrogen peroxide (NaOH 5% and H2O2 2% of DM); and T6 water (2.5 L/ Kg DM). All treatments received 2.5 L water/ kg DM of canola straw. Chopped straw treated in double plastic bags at room temperature for 21 d then samples of each treatment collected and used for in situ nylon bags procedure. Three nonlactating, ruminally cannulated Holstein cows were used for the in situ experiment. Samples incubated in rumen for 0, 3, 6, 12, 24, 48, 72 and 96 h. Bags residual analyzed for dry matter (DM) and neutral detergent fiber (NDF) to calculate ruminal disappearance of nutrients. Data were fitted to the nonlinear regression equation: $D(t) = a + b(1 - e^{-ct})$ where D is percentage disappearance of DM or NDF at time t, a the soluble fraction and b the less rapidly degradable fraction which disappears at the constant fractional rate c per time t. Fraction of a for DM and NDF in T4,5 were greater than other treatments. Ruminal degradation rate (c) of DM and NDF were significantly faster in treated compared with untreated straw, but T4 and 5 increased degradation rates and degradability compared to other treatments. Although T4 and T5 had similar actions, T4 is prefer because of less chemical material usage and cost.

Key Words: canola straw, chemical treatments, ruminal degradation

M381 Effect of rice bran extracts on fermentation, protein, dry matter and organic matter digestibility in rumen in vitro. D. Srichana*[1] and S. Kondo[2], [1]*Department of Agricultural Technology, Faculty of Science & Technology, Thammasat University*, *Pathumtani, Thailand*, [2]*Faculty of Medicne, Thammasat University*, *Pathumtani, Thailand*.

Rice bran consists of γ-oryzanol which has ferulic acid, a phenolic compound as a component. Phenolic compounds have been known to change rumen fermentation. Hence this study was conducted to investigate the effect of rice bran extracts on rumen fermentation end products and protein, dry matter and organic digestibility in batch culture. The experiment was performed at 39°C for 24 h. Culture flasks containing 3 g of dairy cow diet were added with 120 mL mixture of rumen fluid and buffer (1:3). The extraction of Sangyot rice bran (SYE) and Hom Mali rice bran (MLE) using 95% ethanol had been carried out. Seven treatments of the 2 extracts were prepared at concentrations of 0.05, 0.5, 5 mg/ml and the control (without the extract). They were subsequently arranged in CRD and added to the culture flasks in triplicate. The results showed that ammonia concentration was decreased ($P < 0.05$) by SYE 5 mg/ml (6.23 m*M*) and it was increased ($P < 0.05$) by MLE 5 mg/L (11.54 m*M*) when compared with the control (9.38 m*M*). The obtained results were parallel with the results of protein digestibility which was decreased ($P < 0.05$) by SYE 5 mg/mL (39.89%) and increased ($P < 0.05$) by MLE 5 mg/mL (49.11%) when compared with the control (48.04%). Dry matter and organic matter digestibility was decreased ($P < 0.05$) by SYE 5 mg/mL (51.95 and 50.23%, respectively) when compared with the control (61.11 and 60.33%, respectively). The rest and the control were not significantly different ($P > 0.05$). The highest OD was MLE 5 mg/mL (2.77) followed by the OD of SYE 5 mg/mL (2.56). Both were higher ($P < 0.05$) than the OD of the control (2.27). The lowest concentrations of acetic acid and propionic acid (49.99 and 24.12 m*M*, respectively) were detected when treated with SYE 5 mg/mL. Butyric acid concentrations of all the treatments were not significantly different ($P > 0.05$) ranging from 10.62 to 14.09 m*M*. In conclusion, SYE 5 mg/ml decreased the digestibility of protein, dry matter and organic matter whereas MLE 5 mg/L enhances the highest growth of rumen microbes. None of the extracts were able to increase propionic acid concentration in batch culture.

Key Words: rice bran extract, rumen, batch culture

M382 The effect of sewage irrigation on mineral composition and in vitro digestibility of forage sorghum. E. Yosef*[1], J. Miron[1], E. Zukermann[2], M. Nikbachat[1], and D. Ben-Ghedalia[1], [1]*ARO Israel*, *Bet-Dagan Israel*, [2]*Extension Service-Ministry of Agriculture*, *Bet-Dagan, Israel*.

Sorghum is common summer forage cultivated in Israel, and due to lack of summer rainfalls it needs irrigation. Use of sewage water irrigation increased in Israel due to regional droughts and the necessity to eliminate the excess urban waste water. The purpose of this study was to evaluate the effect of secondary-treated sewage water irrigation on the composition and in vitro digestibility of forage sorghum strain FS5 grown for summer and sequential autumn harvests. The irrigation treatments were sewage (S) vs. flood (F) water at a level of 1890 m^3 /ha during summer growth and a level of 2400 m^3/ha during sequential autumn growth. Each treatment consisted of 5 replicate plots and sampled by manual harvesting at the soft dough stage of maturity. The conductivity of S and F water was 1.41 and 0.81 ds/m, respectively. The plant morphology, crop yields and NDF content were not affected by type of water irrigation; however, yields and plant protein content were significantly lower in autumn cut than in summer cut for both treatments. The S treatment had no significant effect on DM digestibility in vitro of both harvests (62.9% vs. 61.5% for 1st cut and 60.7% vs. 59.1% for 2nd cut). The NDF content of autumn cut was higher and dry matter and NDF digestibility lower as compared with summer plants. However, in summer harvest, S treatment decreased significantly NDF digestibility as compared with F treatment (43.1% vs. 47.4%). Despite higher mineral concentrations in S water as compared with F water: Na (x 5.4), S (x 2.6), K (x 14), P (x 473), Al (x 5.6), B (x 2.4), Mn (x 24.3), Cu (x 31.9), the mineral content of sorghum plants from both treatments was similar. In autumn cut plants, B and Na contents were by 98% and 109% higher

than in summer cut. In summer plants the nitrate contents were 4 fold higher than in the autumn plants. In this study the minerals content of secondary-treated sewage water were below the critical level that might damage sorghum quality.

Key Words: sorghum forage, digestibility, minerals

M383 Kinetics of degradation assessment and prediction of the fraction of indigestible neutral detergent fiber by-products. J. G. L. Regadas Filho[1], E. S. Pereira*[2], P. G. Pimentel[2], T. S. OLiveira[1], M. R. G. F. Costa[2], and I. S. G. Maia[2], [1]*Universidade Federal de Viçosa*, *MG, Brazil*, [2]*Universidade Federal do Ceará*, *Fortaleza, Brazil*.

The experiment was conducted to estimate the kinetics parameters of ruminal degradation of neutral detergent fiber (NDF) of by-products of cashew (*Anacardium occidentale*; pulp and cashew nut), passion fruit (*Passiflora edulis*), melon (*Cucumis melo*), pineapple (*Ananas comosus* L. Merr), west indian cherry (*Malpighia emarginata*), grape (*Vitis vinifera* L.), annatto (*Bixa orellana* L.) and coconut (*Cocos nucifera*) submitted to the gravimetric technique of nylon bag, and evaluate the prediction equation of indigestible fraction of neutral detergent fiber (iNDF) adopted by the Cornell Net Carbohydrate and Protein System (CNCPS). The feed samples were ground, placed in nylon bags with dimensions of 7 × 14 cm and porosity of 50 micron and incubated in duplicate in the rumen of a heifer, at 0, 3, 6, 9, 12, 16, 24, 36, 48, 72, 96 and 144 h. The incubation residues were evaluated for NDF content and interpreted by a non-linear logistic model. The evaluation process of predicting the indigestible fraction of NDF was carried out through adjustment models of linear regression between values predicted and observed values. There was wide variation in the degradation parameters of NDF from by-products. The rate of degradation of NDF ranged from 0.0267 h^{-1} and 0.0318 h^{-1} for grape and pulp cashew to 0.0884 h^{-1} and 0.0971 h^{-1} for passion fruit and west Indian cherry, respectively. The potentially digestible fraction of NDF (pdNDF) ranged from 4.17 and 14.13% for the melon and grape to 81.91 and 90.67% for cashew nut and coconut respectively. The equation used by CNCPS was able to predict the iNDF of the by-products, however, due to the high value of the mean square prediction error (291.40), such estimative shown inaccurate, being preferred the estimation by biological means.

Key Words: CNCPS, feeds, validation

M384 Plant bioactive screening of vegetation browsed/grazed by goats on Mexican semiarid rangelands. H. M. Cuchillo*[1], D. C. Puga[1], O. A. Navarro[2], and F. R. Perez-Gil[1], [1]*Departamento de Nutrición Animal, INCMNSZ*, *Mexico, Distrito Federal, México*, [2]*Facultad de Química, UNAM*, *Mexico, Distrito Federal, México*.

It is well recognized that plants consumed by ruminants, to cope their nutritional needs, contain a wide range of non-nutrient phytochemicals. Many plant bioactive metabolites are linked to antinutritive properties; however some of them are recognized as beneficial compounds which their significance remain unclear. Thus, we evaluated antioxidant activity (AA), total polyphenols (TP), flavonoids (FV) and hydroxycinnamic acids (HA) of plants browsed/grazed by goats during summer 2008. Direct observation of 2 core animals throughout grazing/browsing time during 3 d was done. Vegetation recollection was performed simulating the goats bites. The assessment included *Aristida adscensionis, Bouteloua curtipendula, B. repens, Chloris virgata, Leptochloa dubia, Lippia queretarensis, Pennisetum ciliare, Rhynchelytrum roseum, Urochloa fasciculata, Acacia farnesiana, A. schaffneri, Mimosa biuncifera, Prosopis laevigata, Celtis pallida, Jatropha dioica, Psilactis brevilingulata, Verbasina serrata, Zalazania augusta, Opuntia affasiacantha, O. amyctaea, O. hytiacantha, O. imbricata. O. robusta, O. streptacanta*, and *O. tomentosa*. Consecutive methanolic extractions in triplicate were realized whether from whole plants, steams, leafs, cladodes, fruits, flowers or a mixture of them. A screening of AA was completed with TLC method against $DPPH^+$ whereas TP was made with Folin-Ciocalteu reagent. FV and HA were determined by HPLC. Results showed that all the extracts displayed AA, though the pronounced effects have a positive relation with TP content. TP, HA and FV were found in higher means on fruits and flowers while the lowest were achieved by stems, cladodes and leaves. TP ranged from 0.077 for *O. hyatacanta* cladodes to 38.20 g of gallic acid/100g for *A. farnesiana* fruits. Besides, fruits of *P. laevigata* reported the top value of caffeic acid while *B. repens* achieved the greatest cinnamic acid mean. Epigallocatequin accounted the highest concentrations in *O. hytiacantha* prickly pears. Further investigations to clarify the possible implications of plant bioactives on animal husbandry and productivity are necessary.

Key Words: grazing, antioxidant activity, plant bioactives

M385 The effects of high pressure steam treatment on some chemical and physical characteristics of sugarcane pith. M. Chaji*[1], A. A. Naserian[2], R. Valizadeh[2], and T. Mohammadabadi[1], [1]*Ramin Agricultural and Natural Resources University*, *Ahwaz, Khuzestan, Iran*, [2]*Ferdowsi University of Mashhad*, *Mashhad, Khorasan Razavi, Iran*.

The nutritional characteristics of the steam treated sugarcane pith were determined by physico-chemical properties. High-pressure steam-treated sugarcane pith was prepared at 19 bar for 3 min (70% moisture) in a Monel pressure vessel (Emamkhomeini Co., Khuzestan-Iran). Functional specific gravity (FSG) was measured by pycnometeric method; a hydration solution prepared from rumen liquor was used. Water holding capacity (WHC) of feedstuffs was measured using filtration method; the samples were filtered through Whatman No. 1 filter paper. The wet sample was weighed after letting water decant for 10 min. WHC was the quantity of water retained by the sample and expressed as mg/ml sample dry matter. A 100 mL glass graduated cylinder was filled with sample and swirled for 15 s., bulk density (BD) was equal to the weight of sample (mg) over the volume occupied (ml). Steam treatment resulted in a significant decrease in NDF, 77 vs. 55%; hemicellulose to cellulose ratio, 0.54 vs. 0.10, and increase degradation of hemicellulose. Using the steam pressure improved the physical properties of sugarcane pith by increasing the BD, 0.20 vs. 0.31 mg/ml and FSG, 0.3 vs. 0.57 g/ml and decreasing WHC, 2.5 vs. 2.1 mL/g. Steam-pressure treatment may improve the nutritional value of sugarcane by-product for ruminants, and also the physical properties might explain some behaviors of the feedstuffs in rumen which are not recognizable by the chemical approach.

Key Words: functional specific gravity, water holding capacity, bulk density

M386 Effects of chemical treatment on the digestibility of corn stover in diets with modified distillers grains with solubles. J. L. Anderson*[1], J. R. Russell[1], D. D. Loy[1], N. A. Pyatt[2], M. J. Cecava[2], and P. H. Doane[2], [1]*Iowa State University*, *Ames*, [2]*Archer Daniels Midland*, *Decatur, IL*.

Two sheep metabolism trials were conducted to investigate the effects of chemical treatment on the DM digestibility of corn stover in diets with modified distillers grains with solubles (MDGS). Chopped corn stover was either untreated (C) or treated with anhydrous ammonia at 3% (NH3) or calcium oxide at 5% (CaO; DM basis) at either a low (27%; LM) or high (36%; HM) moisture concentration and ensiled in 115-l barrels for 6 mo at ambient conditions. Post-ensiling, each stover was

ground through a 2.54-cm screen. In Exp 1, wether lambs (42 kg) were used in a 6 × 6 Latin-square design to evaluate stover silages at 30% (DM basis) in diets with 65% MDGS and 5% of a corn-based supplement. In Exp 2, wether lambs (43 kg) were used in a 7 × 7 Latin-square design to evaluate the effects of stover inclusion level in MDGS diets. The control consisted of 10% corn silage (CS), 40% MDGS, and 50% of a corn-based supplement (DM basis). Treatments consisted of the HM-C or HM-CaO stover silages fed at 10, 20, and 35% of diet DM with the balance of the diet as MDGS (40, 50, and 60%) and a corn-based supplement (50, 30, and 5%) of the DM. Both trials had a 10-d adjustment phase when all diets were limit-fed at 1.5x maintenance for the least digestible diet and a 5-d collection phase when amounts fed were adjusted for orts collected during the adjustment period. Apparent DM digestion (g/d and %; $P < 0.05$) for LM-C, HM-C, LM-NH3, HM-NH3, LM-CaO, and HM-CaO diets were 473, 67.5; 478, 66.1; 572, 70.1; 551, 71.5; 548, 72.3; and 595, 74.3, respectively. In Exp 2, apparent DM digestion (g/d and %; $P < 0.05$) were 760, 83.1; 686, 80.9; 629, 78.4; 593, 74.5; 682, 78.5; 461, 64.1; and 544, 69.1 for the CS, 10% HM-C, 10% HM-CaO, 20% HM-C, 20% HM-CaO, 35% HM-C, and 35% HM-CaO diets, respectively. Treatment with 5% CaO at a high moisture concentration is more effective than anhydrous 3% NH3 in the improvement of corn stover digestibility.

Key Words: corn stover, alkali treatment, digestibility

M387 Partial replacement of corn silage and alfalfa silage with Italian ryegrass silage in diets of high producing dairy cows. J. T. Woolever* and D. K. Combs, *University of Wisconsin-Madison*.

Two experiments were conducted to evaluate milk yield and milk composition when high quality Italian ryegrass silage was used as a source of digestible fiber and digestible energy in rations of high producing dairy cows. In experiment I, 6 pens of 8 animals were randomly assigned to a control diet (n = 3) or a treatment diet (n = 3) in a 6-week crossover design (3 weeks/treatment). In experiment II, 10 pens of 8 animals were assigned to the same control diet (n = 5) or the same treatment diet (n = 5) in a randomized complete block design. In both experiments, control diet consisted of alfalfa silage (25% of diet DM), corn silage (25% of diet DM), high moisture corn (30% of diet DM) and concentrate. Treatment diet included alfalfa silage (16% of diet DM), corn silage (17% of diet DM), ryegrass silage (18% of diet DM), high moisture corn (30% of diet DM) and concentrate. Diets were formulated to be iso-nitrogenous and iso-caloric, but the treatment diet contained less nonfiber carbohydrate (NFC) (46.5% vs. 48.5%) and more NDF (26.9% vs. 24.8%) as a % of DM. Milk yield and milk components were collected over the course of both experiments. In experiment I, cumulative milk yield was unaffected by diet (7,196 kg control vs. 7,003 kg treatment, $P > 0.40$). Pens of cows consuming the ryegrass diet had higher milk fat levels in experiment I (3.75% vs. 3.60%, $P < 0.05$). Cumulative 4% fat corrected milk yield was similar for control and treatment groups (7,321 kg vs. 7,301 kg). Other milk components did not statistically differ between periods or diets. Cumulative milk yield was similar between treatment groups during experiment II (118,842 kg vs. 118,724 kg, $P > 0.98$). Milk composition and 4% fat corrected milk yield did not differ due to treatment in experiment II. Rations including ryegrass silage can produce similar levels of milk and fat corrected milk compared with more traditional high NFC diets containing high levels of corn and alfalfa silages. Including grass in dairy rations appears to be a feasible method to reduce the NFC level of early lactation diets and increase levels of dietary fiber.

Key Words: Italian ryegrass, grass silage, NDF digestibility, NDFD

M388 Effect of a live yeast, *Saccharomyces cerevisiae* I-1077 on in situ ruminal degradation of alfalfa hay and fiber-associated microbes. F. Chaucheyras Durand[1,2], A. Ameilbonne[1,2], N. D. Walker*[1], P. Mosoni[2], and E. Forano[2], [1]*Lallemand Animal Nutrition*, *Blagnac, France*, [2]*INRA*, *Saint-Genes Champanelle, France*.

In ruminants the digestion of plant material is performed by a complex symbiotic relationship of rumen microbiota. However, the chemical composition and the physical structure of the plant material limit the efficacy of degradation. Also, fibrolytic microbial activities may be depressed under certain dietary conditions, as with ruminal acidosis. Our aim was to investigate effects of a live yeast, *S. cerevisiae* I-1077, on in situ ruminal degradation of alfalfa hay under non-acidotic conditions. We also measured the population levels of bacteria and fungi associated to feed particles by qPCR. Three rumen cannulated cows were fed with grass silage and meadow hay. A first period of 4 weeks without yeast (-SC) was followed by a second 4 week-period (+SC) during which the cows received daily 10^{10} cfu of *S. cerevisiae* I-1077. Nylon bags containing 5g of chopped alfalfa hay were incubated in the rumen for 2, 6, 12 and 24 h. Bags were removed from the rumen, washed, dried and residual NDF determined. *F. succinogenes, B. fibrisolvens* and anaerobic fungi were quantified by PCR. The live yeast induced a significant increase in alfalfa DMd and NDFd (Table 1). The rate of degradation was particularly stimulated. The early colonisation of alfalfa particles by anaerobic fungi appeared to be improved; the populations of *B. fibrisolvens* were greatly promoted whatever the incubation time of the bags, whereas *F. succinogenes* populations, which were dominant, were not influenced by yeast supplementation. In conclusion, the daily distribution of *S. cerevisiae* I-1077 significantly improves alfalfa hay degradation in the rumen and affects feed particle associated microbial populations.

Table 1. Effects of *S. cerevisiae* I-1077 on alfalfa hay degradation and particle associated microorganisms

	2		6		12		24	
	-SC	+SC	-SC	+SC	-SC	+SC	-SC	+SC
DMD (%)	13.17	26.98*	17.45	32.6*	29.15	40.7*	41.53	50.84*
NDFD (g/kg NDF)	83.74	211.21*	107.25	237.14*	183.12	261.41*	336.11	363.48
Anaerobic fungi[1]	3.52	3.56	2.29	3.29	3.73	5.82	11.61	10.87
B. fibrisolvens[2]	4.46	4.88*	5.61	6.66*	5.64	6.66*	6.33	7.45*
F.succinogenes[2]	7.32	7.42	8.05	8.04	8.07	8.29	8.28	7.96*

*P-value <0.05.

[1]µg/gDM.

[2]log10 of 16S rDNA copy numbers/g DM.

Key Words: yeast, fiber

M389 Evaluating the effect of an active dry yeast on fiber digestion in vitro and *in situ*. N. D. Walker* and M. E. Quintino Cintora, *Lallemand Animal Nutrition*, *Montreal, QC, Canada*.

The aim was to measure the effect of adding live yeast CNCM I-1077 (LSC) on fiber digestion kinetics by rumen microorganisms in vitro and in situ. For the in vitro studies, rumen contents were removed from 3 fistulated lactating dairy cows fed 50% forage:50% concentrate, DM basis, pooled and strained (SRF). SRF was mixed with anaerobic buffer (1:4) and added to 4 jars (2 control, 2 treatment) containing filter bags with a known weight of substrate and incubated in a Daisy fermentor. LSC was added at 1×10^6cfu/mL incubation. Substrates tested were corn silage (CS), wheat silage (WS), alfalfa silage (AS), grass silage

(GS), alfalfa hay (AH), hay (H) and straw (S). Bags (3) were removed at 0,3,6,12 and 24h and analyzed for %NDFd. Incubations were repeated on 2 different days. In vitro data showed that yeast supplementation significantly increased %NDFd for CS ($P < 0.01$), WS ($P < 0.05$), AS ($P < 0.05$), GS ($P < 0.05$) and AH ($P < 0.05$). At 12h, %NDFd was significantly increased for S ($P < 0.05$), however no significant effect was observed on H. In a second part of the study, nylon bags containing the same samples of CS, WS, AS, AH and H, were placed in the rumen of the donor animals and incubated for 0, 3, 6, 12, 24, 48 and 96h and analyzed for %DM and %NDF losses. At the same time, rumen contents were removed from each animal and used to set up corresponding Daisy fermentors. Due to limitations with the number of fermentor jars, only CS, WS and AS were tested. Animals were then fed LSC (1×10^{10}cfu/day) for 14 d before the measurements were repeated. Applying Mertens and Loften NDF kinetics model to the in situ data demonstrated that LSC significantly ($P < 0.05$) reduced the lag time for all except AS. The extent of fermentable NDF was increased ($P < 0.05$) for all except WS. The fractional rate was increased for AH ($P < 0.05$), WS ($P < 0.01$) and AS ($P < 0.01$) with LSC supplementation, with the rate being doubled for WS and AS. No correlation existed between the in vitro and in situ results at 24 h, however if LSC had increased the rate in vitro it also increased it in situ. All the data shows that supplementation with LSC can have a positive effect on fiber digestion both in vitro and in situ.

Key Words: yeast, fiber

M390 Influence of Rumensin200 and tallow on the rumen parameters and fiber digestion of dairy cows. H. Castillo, M. Rivas*, D. Dominguez, L. Durán, M. Arana, G. Villalobos, and J. A. Ortega, *Universidad Autonoma de Chihuahua*, *Chihuahua, Chihuahua, Mexico*.

The modification of rumen physical-chemical parameters such as pH and oxidation-reduction potential (ORP) by addition of Rumensin200 and tallow to the TMR of dry and lactating cows was investigated. For this experiment, 4 ruminally fistulated Holstein cows were fed rations based on a 90:10 (dry) and 40:60 (lactating) forage to concentrate ratios. Four treatments were randomly assigned in a 4 × 4 Latin square experimental design as follows: TMR (T1), TMR + 2/3.3 g Rumensin 200(dry/lactating), (T2), TMR + 3,2% DM tallow (T3) and TMR + 2/3.3 g Rumensin 200+ 3.3% DM tallow (T4). The cows were fed ad libitum (0800 and 1500 h) in individual stalls and milked twice daily (0400 and 1300 h). Each of 4 experimental periods had 12 d of conditioning, followed by sampling on d 13 and 15. Samples of ruminal content were taken at 0, 1, 2, 4, 8, 12, 18 and 24 h after morning feeding for DM and NDF digestibility evaluation with standard protocols. Oxidation-reduction potential and pH were measured in rumen with a multiparameter electrode. Statistic analysis of data was done using PROC mixed in SAS. Ruminal pH fluctuated considerably during day and showed a quadratic trend for all treatments ($P < 0.05$), producing wide value ranges as follows: T1 = 6.22–7.02, T2 = 6.27–7.02, T3 = 6.22–6.93, and T4 = 6.03–6.95. However, there were not significant differences among treatments and between dry and lactating stages ($P > 0.05$). The oxidation-reduction potential changed significantly between physiological stages and over time ($P < 0.05$), while exhibiting little variation among treatments. Dry matter digestibility and NDF were not different among treatments ($P > 0.05$). This experiment suggested that the addition of Rumensin200 and tallow lowered the ORP to more negative values and showed a significant difference of this parameter between dry and lactating stages.

Key Words: Rumensin, ORP, pH

M391 Nutrient demand interacts with orchardgrass maturity to affect dry matter intake and yields of milk and milk fat. K. L. Kammes* and M. S. Allen, *Michigan State University*, *East Lansing*.

The effect of dry matter intake in the preliminary period (pDMI) on responses to diets containing orchardgrass silage harvested at 2 maturities were evaluated. Fifteen ruminally cannulated Holstein cows were used in a crossover design experiment with a 14-d preliminary period and 2 18-d treatment periods. During the preliminary period, pDMI of individual cows ranged from 22.9 to 33.4 kg/d and 3.5% fat-corrected milk yield ranged from 30.8 to 58.3 kg/d. Treatments were diets containing orchardgrass silage harvested from one field at either 44.9% (EARLY) or 54.4% NDF (LATE) as the sole forage. Both diets contained 22% forage NDF and 27% total NDF. Main effects of maturity and their interaction with pDMI were tested by ANOVA. There was no main effect of treatment for DMI, however, DMI response to grass maturity tended to depend on pDMI ($P = 0.11$). While cows with high pDMI consumed more EARLY compared with LATE, the reverse was observed for cows with low pDMI. Intakes of organic matter (OM), starch, NDF, and nitrogen were greater for LATE compared with EARLY ($P < 0.05$). LATE increased yields of milk, milk protein, lactose, and solids not fat compared with EARLY. Interactions were detected between grass maturity and pDMI for fat-corrected milk and milk fat yield and concentration with a greater benefit for EARLY compared with LATE as pDMI increased. Rumen pool of indigestible NDF (iNDF) was greater for LATE compared with EARLY (3.63 vs. 2.53 kg, $P < 0.001$), which resulted in greater rumen pools of DM, OM, and NDF. Greater rumen pool size of iNDF for LATE was because of greater iNDF fraction of the forage NDF and a longer ruminal turnover time ($P < 0.05$) compared with EARLY. Rates of passage and digestion of potentially digestible NDF were similar for both treatments ($P > 0.10$). Dry matter intake was likely increasingly limited by rumen fill for LATE compared with EARLY as nutrient demand increased. Greater starch intake for LATE compared with EARLY is consistent with greater yield of milk and decreased yield of milk fat.

Key Words: grass maturity, intake, milk production

M392 High total nonstructural carbohydrates timothy enhanced performance of mid-lactation dairy cows. A. F. Brito*[1], G. F. Tremblay[3], A. Bertrand[3], Y. Castonguay[3], G. Bélanger[3], R. Michaud[3], and R. Berthiaume[4], [1]*University of New Hampshire*, *Durham*, [2]*Université Laval*, *Québec, QC, Canada*, [3]*Agriculture and Agri-Food Canada*, *Québec, QC, Canada*, [4]*Agriculture and Agri-Food Canada*, *Sherbrooke, QC, Canada*.

We have previously reported that alfalfa cut at sundown [high total nonstructural carbohydrates (TNC)] and harvested as baleage increased milk yield and microbial protein synthesis in late-lactation cows fed only forage. The current study examines the effects of feeding a timothy-based high-TNC TMR on performance of mid-lactation cows. Diets contained (% of DM): 1) 40% PM-cut timothy baleage and 25% PM-cut timothy silage (High-TNC diet) or 2) 40% AM-cut timothy baleage and 25% AM-cut timothy silage (Low-TNC diet). Both TMR contained a common concentrate (35% on DM basis). The High- and Low-TNC TMR contained respectively (% of DM): 16.8 vs. 16.9 CP, 43.3 vs. 44.1 NDF, and 14.2 vs. 13.3 TNC. Six multiparous (MC) and 10 primiparous cows (PC) averaging 135 DIM were blocked by DIM, milk yield, and parity and randomly assigned to treatments in a crossover design. No signicant diet (TNC) x parity interaction was observed. DMI ($P = 0.02$) and yields of milk fat ($P = 0.01$), milk protein ($P = 0.04$), and milk lactose ($P = 0.05$) were all higher in cows fed the High- vs. the Low-TNC diet. Compared with the Low-TNC diet, the High-TNC diet

increased both milk yield ($P = 0.07$) and 4% FCM ($P = 0.03$). Overall, the high-TNC diet enhanced performance of mid-lactation cows fed 35% of dietary concentrate.

Table 1. Performance of cows fed High- vs. Low-TNC diets

	PC			MC			P	
Item	High-TNC	Low-TNC	SED	High-TNC	Low-TNC	SED	TNC	Parity
DMI, kg/d	18.0	17.2	0.33	20.7	20.0	0.42	0.02	0.02
Milk yield, kg/d	21.4	21.0	0.55	25.7	24.3	0.71	0.07	0.04
4% FCM, kg/d	20.9	20.5	0.41	25.3	23.9	0.53	0.03	0.04
Fat, %	3.85	3.87	0.05	3.88	3.88	0.07	0.74	0.91
Fat, kg/d	0.82	0.81	0.02	1.00	0.95	0.02	0.01	0.05
Protein, %	3.28	3.26	0.02	3.25	3.23	0.03	0.43	0.68
Protein, kg/d	0.70	0.68	0.02	0.83	0.79	0.02	0.04	0.04
Lactose, %	4.50	4.50	0.02	4.38	4.31	0.03	0.13	0.19
Lactose, kg/d	0.96	0.94	0.03	1.13	1.06	0.03	0.05	0.12

Key Words: timothy, dairy cows, TNC

M393 Modification of the Penn State Particle Separator with 3.18- or 4.76-mm perforated steel sieves to measure physically effective fiber. K. W. Cotanch*, J. D. Darrah, C. S. Ballard, and R. J. Grant, *William H. Miner Agricultural Research Institute*, *Chazy, NY*.

The Penn State Particle Separator (PSPS) 3-sieve system was modified in attempts to better predict physical effectiveness factor (pef) of total mixed rations (TMR), corn silage, and haycrop silage with as-is samples on-farm. The PSPS 1.18-mm wire mesh sieve was replaced with either 3.18-mm (40% open area) or 4.76-mm (32% open area) perforated steel sieve. These sieves are identical to those used in the Z-Box system. Samples were sieved according to standard PSPS protocol using 19-mm, 8-mm, and either the 3.18-mm or 4.76-mm sieve. Samples were sieved in 3 replicates by 2 technicians. Samples were: 25 TMR varying in dry matter, forage-to-concentrate ratio, and forage type (dry hay or silage), 12 corn silages, and 12 haycrop silages. Physical effective factor of as-is sample determined with modified PSPS was compared with pef determined with the standard method of dry vertical sieving with RoTap (proportion of DM ≥1.18 mm). Within forage type, mean bias of pef determined using RoTap and PSPS sieve was calculated. The PSPS sieve with the smallest mean bias (expressed as units of pef) and narrowest 95% confidence interval encompassing zero was deemed to most accurately assess pef. Use of 3.18-mm perforated steel sieve in the PSPS reliably predicts pef of as-is corn silage samples, while the 4.76-mm sieve accurately predicts pef of haycrop silage. The 3.18-mm sieve is slightly more accurate than the 4.76-mm sieve at predicting pef of TMR samples. Modification of the PSPS with perforated steel sieves accurately predicts pef of as-is samples.

Table 1. Mean bias and confidence interval of pef determined using RoTap and PSPS sieve

Forage type	n	Sieve (mm)	Mean bias ± SD	Upper 95% CI	Lower 95% CI
Corn silage	12	3.18	0.020 ± 0.012	0.028	0.013
		4.76	–0.045± 0.020	–0.032	–0.058
Haycrop silage	12	3.18	0.138 ± 0.061	0.176	0.099
		4.76	–0.004 ± 0.082	0.048	–0.056
TMR	25	3.18	0.042 ± 0.076	0.073	0.011
		4.76	–0.047 ± 0.065	–0.020	–0.074

Key Words: Penn State Particle Separator, physical effective factor

M394 Effect of the level of forage and monensin on *trans*-18:1 isomers and CLA in milk. R. Mohammed*[1], J. J. Kennelly[1], and J. K. G. Kramer[2], [1]*University of Alberta*, *Edmonton, Alberta, Canada*, [2]*Guelph Food Research Centre*, *Guelph, Ontario, Canada*.

Milk fat *cis*9, *trans(t)*11-conjugated linoleic acid (CLA) is well known for its anti-cancer effects in animal models. This study reports the effect of the level of forage (F), monensin (M) and its interaction (F×M) on t-18:1 isomers and CLA in milk. Forty Holstein cows in mid-lactation were assigned to 4 diets in a 2 × 2 factorial arrangement of treatments. Treatments were 2 levels of forage (60% or high forage, HF and 40% or low forage, LF) and 2 levels of monensin per kg DM (0 ppm or M- and 16 ppm or M+). All diets were supplemented with sunflower seed (3.6% DM). Milk samples were collected at the end of 2nd and 4th week during treatment and again at the end of 2nd and 4th week after monensin-withdrawal. During treatment, milk *t*10–18:1 (% total FAME) was 0.70^{b}, 0.79^{b}, 0.71^{b}, and 1.2^{a}, for HFM+, HFM-, LFM+ and LFM- respectively (SEM = 0.09; *P*-values for F = 0.03, M =< 0.01 and F×M = 0.04). Milk *t*11–18:1 content was 1.2, 1.3, 1.2 and 1.7 for HFM+, HFM-, LFM+ and LFM- respectively (SEM = 0.13; P-values for F = 0.07, M = 0.02 and F×M = 0.08) and CLA content was 0.61, 0.77, 0.70 and 0.98 for HFM+, HFM-, LFM+ and LFM-, respectively (SEM = 0.06; *P*-values for F = 0.02, M <0.01 and F×M = 0.34) during treatment. After monensin withdrawal, the main effects and interaction for milk t10–18:1 was not different. Milk *t*11–18:1 content was 0.94, 1.1, 1.2 and 1.3 for HFM+, HFM-, LFM+ and LFM- respectively (SEM = 0.09; *P*-values for F = 0.02, M = 0.14 and F×M = 0.85) and CLA content was 0.50, 0.64, 0.63 and 0.67 for HFM+, HFM-, LFM+ and LFM-, respectively (SEM = 0.04; *P*-values for F = 0.05, M = 0.02 and F×M = 0.15) after monensin-withdrawal. Conclusions: This study demonstrates the role of low forage diet in enhancing milk CLA and *t*11–18:1. Monensin supplementation at 16 ppm did not favor greater *t*11–18:1 and CLA. However, its presence reduced the shift to *t*10–18:1, particularly for the LF diet. Monensin effects on milk fat *t*10- and *t*11–18:1 did not persistent in the monensin-withdrawal period.

Key Words: forage level, monensin, CLA

M395 Comparison between the Penn State Particle Separator and the Z-Box to estimate the peNDF content of dairy cow rations. A. S. Atzori*, P. Carta, and A. Cannas, *Dipartimento di Scienze Zootecniche, University of Sassari*, *Sassari, Sardinia, Italy*.

Optimal particle size distribution in TMR requires field monitoring. Two field sieving devices to assess physical effective NDF content (peNDF) of dairy cattle rations, the Penn State Particle Separator (PSPS), made by 3 sieves, and the Z-Box (ZB), made by 1 sieve, were compared with a reference method. Samples from 2 different diets for lactating cows (34.1 ± 1 and 39.1 ± 1% of NDF on DM basis for rations 1 and 2, respectively) were collected from the beginning, middle and end of feeding alleys. The ration peNDF (25.3 ± 1 and 28.1 ± 1% of DM) was determined by dry sieving the diets with the laboratory reference method of Mertens (1997). Rations peNDF were hence obtained by sieving the as fed diets using the PSPS (1.5 L sample) and the ZB (0.25 L sample) following the indications of the producers. TMR distribution homogeneity was evaluated measuring the differences in peNDF in the 3 points of the feeding alley. Results were compared with a monofactorial ANOVA. The PSPS and ZB differed in peNDF estimations within diet ($P < 0.01$). The PSPS estimates of peNDF (27.4 ± 1 and 33.6 ± 1% of DM, for rations 1 and 2, respectively) were higher than the laboratory values, but the differences were significant ($P < 0.05$) only for ration 2, the most fibrous. The ZB estimates of peNDF (20.6 ± 1 and 24.6 ± 1% of DM for ration 1 and 2, respectively) were only numerically ($P >$

0.1) lower than the laboratory values. For both devices, increasing the quantity of sieved sample (1.0, 2.0, 3.0 L for PSPS; 0.15, 0.35, 0.45 L for ZB) resulted in increased peNDF concentration. Regarding TMR distribution homogeneity, both PSPS and ZB were able to detect the small differences in peNDF content (<8%) that occurred within feeding alley. The PSPS was also able to detect, due to the use of 3 sieves, large differences (>50%) in homogeneity within feeding alley for large particles (>8 and 19 mm). In conclusion, the 2 field sieving methods tested gave different values of peNDF compared with the reference method. Their accuracy was also affected by dietary NDF concentration.

Key Words: peNDF, PSPS, Z-Box

M396 Effects of methionine analogues on rumen fibrolytic activities and fibrolytic microorganisms. E. Devillard*[1], C. Martin[2], D. Morgavi[2], E. Forano[2], and P. Mosoni[2], [1]*Adisseo SAS*, *03600 Commentry, France*, [2]*INRA de Theix*, *63122 St Genes Champanelle, France*.

Milk performance can be improved by balancing rations with methionine (Met) analogs, HMB and HMBi [2-hydroxy-4-(methylthio)-butanoic acid and its isopropyl ester, respectively]. It has been suggested that all the HMB and part of the HMBi act in the rumen through improving organic matter digestibility and fiber degradation, partially explaining improvements in milk performance. The aim of the present study was to investigate the effects of HMB and HMBi on rumen activities and rumen microbial populations, with a special emphasis on fibrolytic activities and fibrolytic microorganisms. Six rumen-cannulated Holstein cows fed a wheat/hay (50/50) diet were used in 3 × 3 Latin square design with 2 animals per block. Treatments were supplementation or not with HMB or HMBi (14 g equivalent Met per day). Each period of treatment consisted in 3-week adaptation followed by 8 weeks of experimentation. Under our experimental conditions, supplementation with HMB and HMBi had no effect on rumen carboxymethylcellulase and xylanase activities, in sacco degradability of maize grain and maize silage, ammonia and total volatile fatty acid concentrations. However, a decrease in acetate/propionate ratio was observed with both Met analogs ($P < 0.05$) due to a numerical increase in propionate concentration. The concentrations of total protozoa (counted by microscopy), total bacteria and 2 fibrolytic bacteria *Fibrobacter succinogenes* and *Ruminococcus albus* (quantified by qPCR), were not affected by the supplementations. Conversely, the concentration of the fibrolytic bacterium *Ruminococcus flavefaciens* increased by 1.7 fold in the presence of both Met analogs ($P = 0.03$). In addition, *R. flavefaciens* was also found to better colonize maize silage and maize grain with HMBi (2 fold, $P = 0.01$). In conclusion, both Met analogs stimulate *R. flavefaciens* population but only HMBi increases *R. flavefaciens* attachment to feeds. The modes of action of the 2 sources of Met on fibrolytic populations still require further investigation.

Key Words: rumen, methionine, fibrolytic microorganisms

M397 Effect of soybean hulls levels on ruminal parameters of dairy cows grazing elephant grass. J. C. Martinez*[1,3], T. V. Voltolini[4], A. V. Pirez[2], and F. A. P. Santos[2], [1]*São Paulo State University*, *Jaboticabal, São Paulo, Brazil*, [2]*São Paulo University*, *Piracicaba, São Paulo, Brazil*, [3]*University of California*, *Davis,* [4]*Embapa Semi-árido*, *Petrolina, Pernambuco, Brazil*.

The trial evaluated soybean hulls (SH) inclusion on concentrate supplements offered to lactating cows grazing Elephant Grass during the rainy season. Trial was conducted at Animal Sciences Department, USP/ESALQ, Piracicaba/SP-Brazil. Twelve multiparous Holstein (509 kg LW, 90 DIM at trial beginning) were used on a replicated 4 × 4 Latin Square design. Data were analyzed by MANOVA and GLM procedures of SAS (2002). Animals were kept on a 4.6ha pasture area divided in 25 0.2ha paddocks fertilized with 80 kg N ha/month. All concentrates had 19% crude protein (CP) and were soybean and ground corn based. SH substituted 20, 50 and 75% of corn on experimental treatments. The microbial N was analyzed by HPLC, and VFA by photometry. Treatments did not affect ruminal VFA (123.5 m*M*), ammonia (26.9 mg/dL) concentrations, ruminal pH (6.33), and microbial N flux (183.0 g N/day) (Table 1). Results indicate that SH can be utilized as a replacement for corn on lactating cows rations with no effects on rumen fermentation parameters.

Table 1. Ruminal parameters of dairy cows supplied with different levels of soybean hulls

	Treatments					
	Corn	25%SH	50%SH	75%SH	Mean	Pr(t)
C2, mM/mL	71.6	76.4	69	71.2	71.3	.87
C3, mM/mL	37.2	31.8	27.4	31.7	32	0.09
C4, mM/mL	16	15.8	13.4	13.8	14.8	0.32
Iso-C4, mM/mL	1.23	1.33	1.26	1.09	1.23	0.08
C5, mM/mL	1.7	1.62	1.47	1.57	1.59	0.24
Total VFA, mM/mL	130.6	126.7	115.1	121.6	123.5	0.42
NH3, mg/dL	28.5	25.2	27.1	26.7	27	0.12
pH	6.41	6.25	6.31	6.36	6.33	0.27
Microbial N, g of N/day	184	183	183	180	183	0.14

Within rows, means followed by different superscripts are significantly different ($P < 0.05$).

Key Words: volatile fatty acids, ruminal metabolism, tropical pastures

M398 Effects of crude protein levels in the supplementation of dairy cows grazing elephant grass on milk yield and composition. M. A. C. Danes*, F. A. P. Santos, L. J. Chagas, J. R. R. Dorea, and A. M. Pedroso, *University of Sao Paulo*, *Piracicaba, Brazil*.

The experiment was conducted to evaluate the effects of crude protein (CP) levels in grazing dairy cow rations on milk yield and composition. Thirty-one Holstein and crossbred (Holstein × Jersey) cows averaging 120 d in milk (DIM) were fed 3 levels of crude protein in the concentrate supplement for 72 d. Cows were blocked by breed, parity, DIM and milk yield into 11 incomplete groups of 3 cows and randomly assigned to dietary treatments. Concentrates contained fine ground corn, minerals, vitamins and 3 CP levels (8.7, 13.4 and 18.1% DM) were achieved by replacing corn with soybean meal. Grazing management was intensive, with high levels of nitrogen fertilizer and high stocking rate. Cows were allotted to a new paddock every day, after the afternoon milking, and received the concentrate individually twice a day before each milking, at a 1 kg concentrate/3 kg milk ratio. Milk yield was registered weekly, and milk, concentrates and pasture samples were taken weekly. The data were analyzed as an incomplete randomized blocks design. The average crude protein content of the Elephant grass was 18,5% DM. Increasing the CP level of the concentrate had no effect on milk yield, which was 19.5, 19.4 and 19.1 kg/d for 8.7, 13.4 and 18.1% CP concentrate respectively. There was no difference in protein, fat, and casein content of milk among treatments. Milk fat, protein and casein content average values were 3.5%, 3.3% and 2.6%, respectively. Milk urea nitrogen (MUN) increased linearly ($P < 0.01$) from 8.4 to 10.3 and 13.1 mg/dL as the CP level of the supplement increased from 8.7 to 13.4 and 18.1%. Under the conditions of this study, yields of milk and milk protein were not increased by feeding protein supplement for dairy cows grazing highly

fertilized tropical grasses. The linear increase in MUN resulted from an excessive nitrogen (RDP) supply in the diet.

Key Words: grazing dairy cows, protein supplementation, tropical pasture

M399 Effect of soybean hulls levels on performance of dairy cows grazing elephant grass. J. C. Martinez*[1,3], T. V. Voltolini[4], and F. A. P. Santos[2], [1]*São Paulo State University*, *Jaboticabal, São Paulo, Brazil*, [2]*São Paulo State University*, *Piracicaba, São Paulo, Brazil*, [3]*University of California*, *Davis,* [4]*Embrapa Semi-árido*, *Petrolina, Pernambuco, Brazil*.

The trial evaluated soybean hulls (SH) inclusion on concentrate supplements offered to lactating cows grazing Elephant grass during the rainy season. Trial was conducted at Animal Sciences Department, USP/ESALQ, Piracicaba/SP-Brazil. Twelve multiparous Holstein (509kg LW, 90 DIM at trial beginning) were used on a replicated 4 × 4 Latin Square design. Data were analyzed by GLM procedures of SAS (2002). Animals were kept on a 4.6-ha pasture area divided in 25 0,2ha paddocks fertilized with 80 kg N ha/month. All concentrates had 19% crude protein (CP) and were soybean and ground corn based. SH substituted 20, 50 and 75% of corn on experimental treatments. Cows received concentrate according to milk production on a 1:3 basis, fixed at trial beginning, twice daily after each milking. No differences were observed among treatments ($P > 0.05$) for milk production. Treatments did not affect milk fat, protein, lactose, total solids and urea concentrations ($P > 0.05$) (Table 1). As complement, the live weight (LW) (516 kg), body condition score (BCS) (2.2), plasma urea (31.8 mg/dL) and nonesterified fatty acids (NEFA) (358.2 mEq/L) concentrations were not affected by treatments ($P > 0.05$). Results indicate that SH can be utilized as a replacement for corn on lactating cows rations with no effects on milk production and composition, LBW and blood composition.

Table 1. Milk yield and composition of dairy cows feed with different levels of soybean hulls

	Treatments					
	Corn	25%SH	50%SH	75%SH	Mean	Pr>(t)
Milk, kg/day	17.8	17.7	17.4	17.3	17.7	0.50
FCM, kg/day	16.5	16.8	16.6	16.3	16.5	0.92
Fat, %	3.06	3.21	3.22	3.2	3.14	0.80
Fat, kg/day	0.54	0.56	0.56	0.55	0.55	0.93
Protein, %	2.81	2.92	2.78	2.78	2.82	0.70
Protein, kg/day	0.50	0.52	0.48	0.48	0.50	0.54
Urea, mg/dL	15.71	15.94	14.95	14.54	15.78	0.23

Within rows, means followed by different superscripts are significantly different ($P < 0.05$).

Key Words: supplementation, tropical pastures, milk yield and composition

M400 Evaluation of starch digestibility and physico-chemical properties of Monsanto corn hybrids. D. Ngonyamo-Majee*[1], P. Feng[2], J. Hinen[1], G. Hartnell[1], B. Kutzner[1], M. Brandt[1], and M. Stephens[1], [1]*Monsanto Company*, *St. Louis, MO,* [2]*Monsanto Company*, *Ankeny, IA*.

The negative correlation between corn vitreousness vs. starch availability and milk production potential has been widely reported in US and Europe. Two studies were conducted in 2006 and 2007 to determine the variability of Monsanto corn germplasm on kernel physico-chemical properties and their influence on ruminal starch degradability (RSTARCHD). Samples (30 hybrids in 2006 and 44 hybrids in 2007) for both studies were sourced from various Monsanto locations where the particular hybrid background is recommended. The decision to cover diverse germplasm background and different locations ensured we develop a more robust near infrared reflectance (NIR) calibration. The hybrids were all harvested at R6 stage (black layer). The samples were split into 2 sets. One set was used for whole kernel analyses; vitreousness (visual procedure), 1000-kernel weight, density (water displacement procedure) and NIT predictions of starch and protein. The other set was ground through a 6 mm Wiley grinder and processed for determination of in vitro ruminal starch degradability using the Daisy II procedure. Results from these studies showed wide genetic variability on RSTARCHD and physico-chemical traits. Negative correlations were observed between RSTARCHD and kernel protein ($r = -0.79$), density ($r = -0.30$), and vitreousness ($r = -0.42$). A positive correlation was observed with extractable starch ($r = 0.76$). The data generated NIR calibration with RSTARCHD ranging from 50.3 to 66.3% (mean 56.6 ± 3.33%). The calibration statistics were within acceptable range ($R^2 = 0.83$; standard error of calibration = 1.36 and standard error of cross validation = 1.67). We are continuing to expand the calibration with more diverse germplasm and locations.

Key Words: corn starch, rumen degradability, vitreousness

M401 Growth performance of Bluchi female lambs fed by diets containing different levels of date palm leaves. R. Valizade, A. Salahi*, and M. Mahmodi, [1]*Ferdowsi University*, *Mashhad, Iran*.

The objective of present study was to evaluate the effect of diets containing date palm leaves (DPL) fed to Baluchi female lambs in a completely randomize design on growth performance. The study was carried out with 24 female Iranian Baluchi lambs of 4–5 mo of age and average body weight (BW) of 20.48 ± 4.9 kg, and lambs were allocated to 4 dietary treatments in a feedlot condition. All lambs were given a TMR composed of 39% forage (Alfalfa hay (15%), and wheat straw or DPL) and 61% concentrate (corn grain 45%, soybean meal 15%, limestone 0.4%, premix 0.4%, and salt 0.2%). The dietary treatment were 1) wheat straw (24%), 2) wheat straw (16%), DPL (8%), 3) wheat straw (8%), DPL (16%), 4) DPL (24%). The experiment was conducted for 76 d and data were analyzed using the PROC MIXED procedure (repeated measurement) of SAS (version 9.1; SAS Institute Inc., Cary, NC). Average daily feed intake by the lambs in different treatment were 857, 918, 986, and 1035 g/d, respectively. The difference between all means was significant ($P < 0.05$). Lambs fed by 1 dietary treatment were lower average daily body weight gain (g/day) than other groups. Average daily gains of lambs on dietary treatments of 1, 2, 3 and 4 were 106,143, 156, and 165 g/d, respectively. The best feed conversion ratio was also recorded for the lambs on diet containing 24% DPL (6.16 kg feed consumed per kg of weight gain). The obtained data at Feed intake on metabolic weight (69.3, 69.1, 75.6 and 74.5 g/kg W0.75) differed significantly. Ruminal pH (6.64, 6.55, 6.56 and 6.53); ruminal NH3 (13.12, 12.4, 11.12 and 10.38 mg/100mL); blood urea nitrogen (19.27, 20.74, 20.36 and 20.09 mg/dl); blood glucose (71.62, 60.31, 67.2 and 62.6 mg/dl) were into the normal ranges. It was concluded that inclusion of DPL can be beneficial mainly for smallholder farmers during periods of low rainfall and forage scarcity.

Key Words: date palm leaves, Bluchi female lambs, growth performance

M402 Effect of date palm leaves substitution with wheat straw on health and rumen parameter of Saanen dairy goats. A. Salahi*, R. Valizade, A. Naserian, and A. Tahmasbi, *Ferdowsi University*, *Mashhad, Iran*.

This experiment was conducted to determine the effect of date palm leaves (DPL) feeding on the blood parameter of Saanen dairy goat. Nine lactating dairy goats were randomly assigned to treatment in a 3 × 3 Latin squares design. All goats were given a TMR composed of 40% forage and 60% concentrate (corn grain 26%, cotton seed meal 15%, sugar beet pulp 15.5, wheat bran 2%, limestone 0.5%, premix 0.5%, salt 0.5%). The dietary treatment were 1) alfalfa hay (20%), wheat straw (20%) 2) alfalfa hay (20%), DPL (20%) and 3) alfalfa hay (20%), treated (4% urea) and ensiled DPL (20% DM basis). The experiment lasted for 63 d (3 periods of 21 d which 15 d for diet adaptation and last 7 d for data collection). Goats were individually fed twice daily at 07:00 and 15:00. Data were analyzed using General Linear Models procedure of SAS 9.1 for ANOVA to evaluate difference among experimental groups, mean compared with Duncan test. Average dry matter intake by the goats in different treatment were 2055, 2055, and 1794 g/d, respectively. The difference between there means was significant ($P < 0.05$). Ruminal pH (6.43, 6.41, 6.24); ruminal NH3 (23.8, 22.9, 19.00 mg/100 mL); blood urea nitrogen (20.2, 20.2, 18.9 mg/dL); blood glucose (39.1, 38.5, 40.1 mg/dL); blood Cholesterol (79.7, 79.7, 79.1 mg/dL) were into the normal ranges. Although no differences were detected between these figures, the obtained data on blood triglyceride (6.9, 12.2, 9.9 mg/dL) differed significantly. The studied parameters in this experiment support inclusion of DPL into the diets for dairy goats in a dry area with poor vegetation and rainfall.

Key Words: date palm leaves, Saanen dairy goat, blood parameter

M403 Milk production and composition of Saanen dairy goat fed by ration containing date palm leaves. A. Salahi*, R. Valizade, A. Naserian, and A. Tahmasbi, *Ferdowsi University*, *Mashhad, Iran*.

Date palm leaves (DPL) is one of the most abundant agricultural by-products in south of Iran were fed to 9 Saanen dairy goat in a 3 × 3 Latin square design. All goats were given a TMR composed of 40% forage and 60% concentrate (corn grain 26%, cotton seed meal 15%, sugar beet pulp 15.5, wheat bran 2%, limestone 0.5%, premix 0.5%, salt 0.5%).The dietary treatment were 1) alfalfa hay (20%), wheat straw (20%) 2) alfalfa hay (20%), DPL (20%) and 3) alfalfa hay (20%), treated (4% urea) and ensiled DPL (20% DM basis). The experiment lasted for 63 d (3 periods of 21 d which 15 d for diet adaptation and last 7 d for data collection). Data were analyzed using General Linear Models procedure of SAS 9.1 for ANOVA to evaluate difference among experimental groups, mean compared with Duncan test. Average dry matter intake by the goats in different treatment were 2055, 2055, and 1794 g/d, respectively. The difference between the means was significant ($P < 0.05$). Average milk production by the goats in different treatments were 1375, 1389 and 1381 g/d, respectively. The difference among there means as well as other milk constituents (fat, protein, and lactose) was not significant. Although no differences were detected between these figures, the obtained data on BUN (11, 11, 15.5 mg/dL) differed significantly. Total solid of the milk produced by goats in different treatments were 10.34, 10.63, and 10.8%, respectively. Total cell counts of the milk samples were 241, 314, and 537cell per mL, respectively. The difference among there means also was not significant. It was concluded that DPL can be fed to such animals without any adverse effects.

Key Words: date palm leaves, Saanen dairy goat, milk parameter

M404 Effects of an alfalfa feeding strategy in the first week postpartum on feed intake and ketogenic status in transition cows. M. Larsen* and N. B. Kristensen, *Faculty of Agricultural Science, Aarhus University*, *Tjele, Denmark*.

Feeding additional forage fiber to fresh cows is believed to secure good rumen function. Thirteen multiparous Holstein cows were used in a randomized block design to study the effects of an alfalfa feeding strategy to postpartum transition dairy cows on dry matter intake (DMI) and ketogenic status. At calving, cows were randomly assigned to 1 of 2 ad libitum fed total mixed diets: a control lactation diet (CTRL) or an alfalfa haylage lactation diet (ALFA) for the first week postpartum. From wk 2 to 4 postpartum, all cows were fed CTRL. The CTRL was composed of (dry matter basis) 35% corn silage, 25% grass-clover silage, 20% rolled barley and 20% concentrate mix. The ALFA diet was composed of 50% CTRL diet and 50% alfalfa haylage. Forage NDF was 19.1% in CTRL and 30.1% in ALFA. Blood was sampled at 14 d prepartum and at 4, 15, and 29 d in milk (DIM). The statistical model included block, treatment, DIM and treatment × DIM, where DIM within cow was considered as a repeated measure. In the first week postpartum, DMI was unaffected by treatment ($P = 0.41$) and averaged 10.5 and 11.5 ± 0.8 kg/d with ALFA and CTRL, respectively. A carry over effect of ALFA was observed during wk 2 to 4 postpartum, where DMI was lower ($P < 0.01$) for cows previously fed AFLA as compared with CTRL (14.4 and 16.4 ± 0.4 kg/d, respectively). The orts percent was higher ($P < 0.01$) with ALFA in the first week postpartum, but did not differ ($P = 0.40$) in wk 2 to 4 postpartum. Milk yield was unaffected by treatment ($P = 0.30$). Blood plasma glucose concentration decreased more ($P = 0.04$) from prepartum to 4 DIM with AFLA as compared with CTRL. Concomitantly, plasma concentrations of acetoactetate+acetone and β-OH-butyrate as well as their ratio tended to increase more ($P = 0.06$ to $P = 0.11$) from prepartum to 4 DIM with AFLA as compared with CTRL. In conclusion, the tested alfalfa haylage feeding strategy did not induce greater DMI in postpartum transition cows. The results showed that high forage feeding strategies for fresh cows increase the risk for hyperketonemia.

Key Words: transition, feed intake, forage fiber

M405 Milk production efficiency improves with addition of an exogenous fibrolytic enzyme to a total mixed ration. L. Holtshausen*[1], Y.-H. Chung[1], H. Gerardo-Cuervo[2], M. Oba[2], and K. A. Beauchemin[1], [1]*Agriculture and Agri-Food Canada*, *Lethbridge, Alberta, Canada*, [2]*University of Alberta*, *Edmonton, Canada*.

Ruminant response to feed enzymes remains variable despite it being well researched in the last couple of decades. This study aimed to determine whether addition of Econase RDE (AB Enzymes, Germany) to a TMR improves productivity of early-lactation dairy cows. Sixty Holstein dairy cows (46 ± 10 DIM) were blocked by parity and randomly assigned to one of 3 treatments for a 10-wk period: 1) Control diet (CTL; no enzyme), 2) Low enzyme (LE; CTL with 0.5 mL Econase RDE/kg TMR DM) and 3) High enzyme (HE; CTL with 1.0 mL Econase RDE/kg TMR DM). Endoglucanase and xylanase activity for Econase RDE was 722 and 2604 nmol/mg enzyme product, respectively. The CTL diet had 21% alfalfa silage, 21% barley silage, 11% alfalfa hay and 47% concentrate (DM basis). Twenty-four hour in situ DM, NDF and ADF degradation of alfalfa and barley silage, with and without enzyme, were determined using 6 cannulated cows. Cows on the CTL diet had a higher DMI ($P < 0.01$) than cows on the HE diet and tended ($P = 0.09$) to have a higher DMI than cows on the LE diet. Fat corrected milk yield and milk composition did not differ. Cows on the HE diet had a greater FCM production efficiency than CTL cows ($P < 0.01$), with that of LE

cows being intermediate and not different from CTL cows ($P = 0.31$). Enzyme addition did not improve in situ DM or NDF degradation of alfalfa or barley silage, but there was a tendency ($P = 0.10$) for greater ADF degradation of alfalfa silage. Greater FCM production efficiency with dietary addition of exogenous fibrolytic enzymes might in part be a result of greater ADF degradation of some feedstuffs, particularly alfalfa.

Table 1. Performance of early-lactation dairy cows and in situ degradation of feedstuffs with the addition of an exogenous fibrolytic enzyme

Item	CTL	LE	HE	SE	P (trt)
DMI, kg/d	24.5	22.9	22.2	0.58	0.02
3.5% FCM yield, kg/d	36.5	36.1	36.3	0.66	0.90
Milk fat, %	3.29	3.19	3.26	0.057	0.44
Milk protein, %	2.95	3.01	3.03	0.027	0.14
FCM Efficiency, kg FCM/kg DMI	1.50	1.58	1.67	0.041	0.02

	Barley		Alfalfa			
24h Degradation	CTL	Enz	CTL	Enz		
DM	46.1	47.7	68.8	70.0	1.14	0.20
NDF	19,4	20.9	26.7	28.7	1.77	0.34
ADF	31.9	32.2	36.6[a]	40.7[b]	1.63	0.21

[a,b]$P = 0.10$.

Key Words: feed enzymes, production efficiency, dairy cow

M406 Effect of different sources of pectin feedstuffs on chewing activities in early lactating Holstein cows. M. Kordi*, A. Naserian, R. Valizade, and A. Tahmasbi, *Ferdowsi University*, *Mashhad, Iran*,

Eight primiparous early lactating Holstein cows (60 ± 23 d postpartum, weighing 530 ± 60 kg) were assigned into a duplicated 4 × 4 Latin square design for evaluation of different pectin feedstuffs on intake and chewing activities of lactating dairy cows with 4 3-wk periods. Cows were allocated into 4 diets whit 1)10% barley grain, 2)10% sugar beet pulp, 3)10% wheat bran and 4) 10% dried citrus pulp . Each experimental period was 21 d including 14 d adaptation period and 7 d collecting samples. Chewing behavior observations were visually recorded every 5 min for 24 h. The time spent for each animal observation was not more than 5 s. Eating, ruminating, and total chewing times were determined and expressed as minutes per day. Time (expressed in minutes) expended in each activity was calculated by the number of observations recorded multiplied by 5. Total chewing time was considered as the sum of eating and ruminating times. Eating, ruminating, and total chewing times were also expressed as minutes per kg of DM and NDF intakes. Chewing activities data are shown in Table 1).There were no differences ($P > 0.05$) in the daily intake of DM (kg/d). Eating behavior as minutes per Kg of DMI were not affected by treatments ($P > 0.05$) but there were significant differences in eating behavior as minutes per kg of NDFI ($P < 0.05$). Similarly there were significant differences on ruminating and total chewing activities between treatment diets ($P < 0.05$). These data suggest that, the addition of sources of pectin feedstuffs at 10% levels (dry matter basis) of the dairy cow ration instead of cereal grain; will decrease the cost of milk production without any negative effect on chewing activities.

Table 1. Effects of treatments on chewing activities of lactating dairy cows.

	Treatment				
	T1	T2	T3	T4	SEM
DMI (kg/day)	19.34	19.63	19.74	18.7	0.34
Eating					
min/d	380.63	390.63	373.13	378.13	11.205
min/kg DMI	19.75	19.89	18.92	20.58	0.73
min/kg NDFI	63.1[ab]	59.04[ab]	56.31[b]	64.34[a]	2.30
Ruminating					
min/d	510.63[a]	460[b]	452.5[ab]	490b	16.12
min/kg DMI	26.36[a]	23.46[b]	22.97[b]	26.28[a]	0.803
min/kg NDFI	84.23[a]	69.61[b]	68.36[b]	83.44[a]	2.45
Chewing					
min/d	891.25 [a]	850.63[ab]	824.38[b]	857.5[ab]	15.1
mink/g DMI	46.11[a]	43.35[ab]	41.82[b]	46.32[a]	1.05
min/kg NDFI	147.32[a]	128.65[b]	124.48[b]	147.04[a]	3.26

Key Words: chewing activities, lactating Holstein cow, pectin feedstuffs

M407 Effect of different sources of pectin feedstuffs on blood metabolites in early lactating Holstein cows. M. Kordi*, A. Naserian, R. Valizade, and A. Tahmasbi, *Ferdowsi University*, *Mashhad, Iran*.

This experiment was conducted to determine the effect of different sources of pectin feedstuffs on blood metabolites in early lactating Holstein cows. Eight primiparous early lactating Holstein cows (60 ± 23 d postpartum, weighing 530 ± 60 kg) were assigned into a duplicated 4 × 4 Latin square design with 4 3-wk periods. Cows were allocated into 4 diets whit 1)10% barley grain, 2)10% sugar beet pulp, 3)10% wheat bran and 4) 10% dried citrus pulp . Each experimental period was 21 d including 14 d adaptation period and 7 d collecting samples. Blood samples were collected from the jugular vein 2h after the morning feeding. Blood serum was collected after centrifuged at 1,500 × *g* for 20 min, frozen at – 40°C, and later analyzed for glucose, urea N, cholesterol, triglyceride, alkaline phosphate and albumin. Blood metabolites data and DMI are shown in Table 1.There were no differences ($P > 0.05$) on daily intake of DM (kg/d) (Table 1). Similarly, no treatments effects were observed blood metabolites (Table 1). These data suggest that, the addition of sources of pectin feedstuffs at 10% levels (dry matter basis) of the dairy cow ration instead of cereal grain; will decrease the cost of milk production without any negative effect on DMI and blood metabolites.

Table 1. Blood metabolites of dairy cows

	Treatment				
Item	T1	T2	T3	T4	SEM
DMI (kg/day)	19.34	19.63	19.74	18.69	0.348
Glucose (mg/dL)	55.8	53.8	54.1	53.5	22.902
Blood urea nitrogen (mg/dL)	24.37	25.62	25.87	26.25	0.786
Cholesterol (mg/dL)	186.25	186.88	193.88	185.63	8.142
Triglyceride (mg/dL)	9.25	10.625	10.625	12.87	2.69
Alkaline phosphate (U/L)	68.25	75.5	69.25	71.87	4.212
Albumin (g/dL)	4.23	4.25	4.28	4.22	0.047

Key Words: barley, lactating Holstein cow, pectin feedstuff

M408 Effects of forage family (alfalfa vs. orchardgrass) on apparent ruminal synthesis of niacin and vitamin B6 in lactating dairy cows. M. Seck*[1,3], J. A. Voelker Linton[2], M. S. Allen[2], P. Y. Chouinard[3], and C. L. Girard[1], [1]*Agriculture and Agri-Food Canada*, *Sherbrooke, Quebec, Canada*, [2]*Department of Animal Science, Michigan State University*, *East Lansing,* [3]*Departement de sciences animales, Universite Laval*, *Quebec, Quebec, Canada*.

Effects of forage family on apparent ruminal synthesis and post-ruminal supply of niacin (B3) and vitamin B6 were evaluated using 8 ruminally and duodenally cannulated lactating Holstein cows. The experiment was a crossover design with 2 15-d treatment periods and a preliminary period in which dry matter intake (pDMI) of a diet intermediate in composition between the treatment diets was measured. Treatment diets were formulated to contain 23% forage NDF and contained as sole forage, alfalfa (AL, 43% NDF) or orchardgrass (OG, 48% NDF) silages. Intakes of B3 and B6 were greater ($P \leq 0.01$) for AL than OG (B3: 2337 vs. 847 ± 87 mg/d; B6: 75 vs. 55 ± 4 mg/d) but AL decreased ($P \leq 0.03$) duodenal flows of B3 and B6 compared with OG (B3: 1702 vs. 2508 ± 175 mg/d; B6: 46 vs. 82 ± 11 mg/d for B6). Ruminal synthesis of B3 and B6 was greater ($P \leq 0.01$) for OG compared with AL (B3: 1661 vs. −635 ± 139; B6: 27 vs. −28 ± 9 mg/d). Intakes of B3 and B6 increased with pDMI for AL but not for OG (pDMI × T, $P \leq 0.01$) but duodenal flow of B3 tended to increase with pDMI to a greater extent for OG than for AL (pDMI × T, $P = 0.09$). With increasing pDMI, B3 degradation in the rumen increased for AL but synthesis increased for OG (pDMI × T, $P \leq 0.01$). No interactions between pDMI and treatments were observed for B6 duodenal flow or ruminal synthesis ($P > 0.6$). B3 intake was correlated negatively with ruminal synthesis ($r = -0.9$, $P < 0.01$) and flow ($r = -0.52$, $P = 0.04$) while B6 intake and synthesis were correlated negatively ($r = -0.48$, $P = 0.06$). Mean ruminal pH was correlated negatively with ruminal synthesis ($r = -0.76$, $P \leq 0.01$) and flow ($r = -0.68$, $P \leq 0.01$) of B3 (not B6). Microbial nitrogen flow (g/d) was correlated positively with ruminal synthesis ($r = 0.48$, $P = 0.06$) and flow ($r = 0.6$, $P \leq 0.01$) of B6 (not B3). Forages from different families (alfalfa vs. orchardgrass) altered ruminal fermentation which affected ruminal synthesis and supply of vitamins B3 and B6 to dairy cows.

Key Words: dairy cow, niacin, pyridoxine

M409 Effect of the volatile fraction from silage and forage:concentrate ratio on ruminal degradation of fresh chopped or ensiled sugarcane. J. L. P. Daniel*[1], L. G. Nussio[1], R. C. Amaral[1], S. G. Toledo Filho[1], J. R. Lima[1], E. Cabezas[1], and O. C. M. Queiroz[2], [1]*University of São Paulo, "Luiz de Queiroz" College of Agriculture*, *Piracicaba, SP, Brazil*, [2]*University of Florida*, *Gainesville*.

The objective of this study was to determine whether volatile fermentation end products from silage and forage:concentrate ratio affect the in situ ruminal degradation of fresh chopped or ensiled sugarcane. We hypothesized that ethanol present in the volatile fraction from silage could increase ruminal degradation, and high-concentrate diet could decrease it. Sugarcane was mechanically harvested at 21.5 degrees brix and ensiled in 200 L plastic buckets (experimental silos) without adding any additive. Samples obtained before and after 90 d of storage, were dried at 60oC in a forced air oven, ground at 5 mm, and used to prepare Dacron bags, in triplicate, keeping the ratio 10–20 mg of sample per cm2 of the bag. Six Nelore beef steers were randomly assigned in a replicated 3 × 3 Latin square design with 14-d periods. Steers were fed ad libitum once daily at 0800 h. Dietary treatments were balanced to be isonitrogen content: 75D – 75% sugarcane silage without volatile fraction (dried at 60oC and re-hydrated) and 25% concentrate, 75W – 75% wet sugarcane silage and 25% concentrate, and 40W – 40% wet sugarcane silage and 60% concentrate (DM basis). On d 11 of each period, at feeding time, all bags were positioned into the ventral sac of the rumen during 24 h. Rumen pH was measured each 2 h during 24 h on d 13. Dry matter degradation (DEG24) was determined as the difference between sample and residue weights. Fresh and ensiled sugarcane were compared. DEG24 of fresh sugarcane (55%) was higher ($P < 0.01$) than that of ensiled sugarcane (39%). It was not detected effect ($P = 0.13$) on DEG24 across dietary treatments (averages: 75D = 48%, 75W = 47%, 40W = 45% of DM). Rumen pH was lower ($P < 0.01$) for the high-concentrate diet (75D: 6.65, 75W: 6.71, 40W: 6.33), however, all diets kept favorable rumen environment for digestion. The volatile fraction present in sugarcane silage did not improve the ruminal degradation of DM.

Key Words: volatile organic compounds, ethanol, rumen pH

M410 Performance of lactating crossbreed cows on tropical pasture fed by supplements with soybean meal and Optigen or urea. D. C. Abreu*[1], R. P. Lana[1], A. S. Oliveira[1], F. A. Barbosa[2], F. L. Andrade[1], P. T. Silva[1], and F. A. C. Neto[3], [1]*Universidade Federal de Viçosa*, *Viçosa, MG, Brasil*, [2]*Universidade de Brasília*, *Brasília, DF, Brasil*, [3]*Colorado State University*, *Fort Collins*.

Sources of nonprotien nitrogen (NPN) are attractive because of their low cost relative to vegetable proteins. Urea is the most commonly used NPN source but is rapidly hydrolysed to ammonia within the rumen and may therefore be used inefficiently by the rumen microbes. This study investigated the performance and nutrient utilization response of crossbreed lactating dairy cows to the substitution of soybeans by 2 sources of non-protein nitrogen. Twenty one crossbreed Holstein-Zebu cows (second or third parity; BW = 499 ± 60,63 kg; DIM = 167 d) grazing *Brachiaria decumbes* pastures were distributed in a 3 × 7 incomplete Latin squares design. Three periods, with 21 d each (samples collected on last 7 d of with period). Within herd, cows were fed by pasture source (ad libitum) and concentrated supplement isonitrogenous with 24% of crude protein, on DM basis (Table 1). The control diet contained a conventional N source (soybean meal; SBM) and others NPN as urea and Optigen. Daily milk production was condensed to weekly averages. Data was analyzed by repeated measures using PROC-MIXED of SAS. There was no effect ($P > 0.05$) of difference source of protein (SBM vs. NPN); interaction of source of NPN and level of NPN; source of NPN (urea vs. Optigen) and level of NPN. For crossbreed Holstein-Zebu cows on tropical pasture, the urea or Optigen can be supplemented and add until 6% of DM of concentrated, without difference in the performance of lactating crossbreed cows.

Table 1. Composition of ingredients of supplement (%, DM basis)

	Source of NPN						
Ingredients, %	control diet	Urea, %			Optigen, %		
		2	4	6	2	4	6
Corn grain	58.50	69.00	79.50	90.00	69.00	79.50	90.00
Soybean meal (SBM)	37.50	25.00	12.50		25.00	12.50	
Urea		2.00	4.00	6.00			
Optigen					2.00	4.00	6.00
Mineral/ supplement mix	4.00	4.00	4.00	4.00	4.00	4.00	4.00

Key Words: nonprotein nitrogen, Optigen, crossbreed dairy cows

M411 Modeling degradation characteristics and nutrient availability of anthocyanidin accumulating Lc-Alfalfa and alfalfa selected for a low initial rate of degradation in dairy cows. A. Jonker*[1,2], M. Gruber[2], Y. Wang[3], and P. Yu[1], [1]*Department of Animal and Poultry Science, College of Agriculture and Bioresources, University of Saskatchewan*, *Saskatoon, SK, Canada*, [2]*Saskatoon Research Centre, Agriculture and Agri-Food Canada*, *Saskatoon, SK, Canada*, [3]*Lethbridge Research Centre, Agriculture and Agri-Food Canada*, *Lethbridge, AB, Canada*.

Protein efficiency of dairy cattle eating alfalfa might be improved by introducing a gene that stimulates the accumulation of anthocyanidin in alfalfa forage. The objective of this study was to determine nutrient availability in the rumen and small intestine of newly developed anthocyanidin accumulating Lc-alfalfa populations by a modeling approach. Three winter hardy alfalfa varieties Rangelander, Rambler and Beaver were crossed with 3 transgenic T0 Lc-alfalfa populations 88–19, 88–09 and 88–01, respectively. The 3 phenotypic purple Lc-progeny used in this study were compared with AC Grazeland (selected for a low initial rate of degradation; LIRD). Alfalfa samples were collected at a vegetative pre-bud stage during the growing season of 2008 (AAFC, Saskatoon, SK, Canada). Data from wet chemical analysis and an in situ trail was used as input for the Dutch 2007 DVE/OEB protein system and VEM energy system to determine nutrient availability from tested alfalfa populations for dairy cows. The results were analyzed in a CRD using the contrast statement in Proc Mixed of SAS. The Lc-alfalfa populations had an average anthocyanidin concentration of 163.4 µg/g DM. The Lc-alfalfa had a lower ($P < 0.05$) undegradable NDF fraction and tendency for a higher ($P < 0.10$) rumen degradable CP and rumen degradable CHO and rumen degraded protein balance compared with LIRD-alfalfa. Total intestinal digestible protein (70.0 vs. 61.9 g/kg DM) tended to be higher ($P < 0.10$) and net energy for lactation was higher ($P < 0.05$; 1.50 vs. 1.42 Mcal/kg) in Lc-alfalfa compared with LIRD-alfalfa. In conclusion, Lc-alfalfa accumulated anthocyanidin and had a higher nutrient availability for the animal for milk production than LIRD-alfalfa.

Key Words: anthocyanidin-accumulating alfalfa, protein and energy models, dairy cattle

M412 Influence of reconstituted and silage sorghum grain on site and extent digestion in finishing cattle. U. A. González[1,3], M. González[1], A. Plascencia[2], and L. Corona*[3], [1]*Universidad Autónoma del Estado de México*, *Toluca, Estado de México,México*, [2]*Universidad Autónoma de Baja California*, *Mexicali, BC, México*, [3]*Universidad Nacional Autónoma de México*, *Cd. Universitaria, DF, México*.

Five calves (average BW: 190 ± 30 kg) with cannulas in the rumen and proximal duodenum were used in a 5 × 5 Latin square design to evaluate the influence of reconstituted and ensiling sorghum grain on nutrient digestion with the following treatments: 1) DCC (dry cracked corn); 2) RCS (reconstituted cracked sorghum); 3) DWS (dried whole sorghum); 4) RWS (reconstituted whole sorghum); and 5) DCS (dry cracked sorghum). The diets contained 73% of grain (% DM). Ruminal digestion of OM was greater ($P < 0.01$) for DWS and RWS (60 ± 1%) compared with others treatments. The higher ($P < 0.005$) ruminal starch digestion was for DWS and RWS (64 and 65% respectively), while N digestion was greater ($P < 0.0004$) for RWS (48%) compared with RCS (40%). Post-ruminal digestion of OM was higher ($P < 0.0001$) for RCS (71%) and starch digestion was greater ($P < 0.05$) for RCS (82%) compared with the other treatments. Total tract digestion of OM was greater ($P < 0.05$) for RCS and RWS (87 and 83%) compared with DCC, RWS and RCS (78 ± 1%); total starch digestion was greater ($P < 0.05$) for RCS (93%) respect to DCC, RWS and DCS (87 ± 1%), and lower for DWS (83%). The ruminal pH was higher ($P < 0.0453$) for DWS compared with RCE and RWS. DCC had the lowest ($P < 0.0084$) ruminal proportion of acetic acid respect to RCS and DCS. Propionic acid production was higher ($P < 0.0235$) for DCC on RCS and DCS. Butyric acid production showed the lowest proportion ($P < 0.021$) for DWS respect RCS and RWS. The ratio acetate: propionate was lower ($P < 0.0085$) for DCC respect the rest of the treatments. The energy values calculated by replacement for RCS, DWS, RWS and DCS corresponded to 4.58, 3.77, 4.14 and 3.71 ED Mcal/kg, respectively. We concluded that the method of processing before restore cracked (RCS) and reconstituted sorghum (RWS) improve their nutritional value due to increase post-ruminal digestion of starch and N.
Funded by: DGAPA-PAPIIT IN206006

Key Words: cattle, digestion, reconstituted sorghum

M413 Effect of germinated and ensiling sorghum grain on digestion and ruminal fermentation by feedlot cattle. F. Rodríguez[1], S. E. Buntinx[1], M. E. Ortega[2], and L. Corona*[1], [1]*Universidad Nacional Autónoma de México*, *Cd. Universitaria, DF,México*, [2]*Colegio de Posgraduados*, *Montecillo, Edo. de México, México*.

Five steers (average BW: 400 kg) with cannulas in the rumen and proximal duodenum were used in a 5 × 5 Latin square design to evaluate the influence of sorghum grain germinated and ensiling on nutrient digestion and ruminal fermentation . Treatments consisted of a basal finished diet containing 73% sorghum grain(% DM basis) as: 1) DCS (dry cracked sorghum-0h reconstituted); 2) RWS (reconstituted whole sorghum-24h); 3) GS2 (germinated sorghum 2d-48h); 4) GS4 (germinated sorghum 4d-96h); and 5) GS6 (germinated sorghum 6d-144h). The grain germinated and ensiling was reconstituted to 30% moisture, germinated for 2, 4, 6 d and ensiling for 21d. Post-ruminal digestion of OM was lower (5%,$P < 0.01$) for GS2 than for GS6 and for starch was higher (29.5%$P < 0.10$) for germinated treatments respect to DCS. Geminated tended to increase (linear effect, $P < 0.10$) post-ruminal starch digestion. Total tract digestion was higher for SG6 respect to SG2 for OM (7.22% $P < 0.05$), starch (3.76, $P < 0.10$) and nitrogen (4.06%, $P < 0.05$). DE Mcal/kg was higher ($P < 0.05$) for SG6 (3.72) than for SG2 (3.50). The ruminal pH was lower ($P < 0.10$) for DCS (6.24) respect to GS2, GS4 and GS6 (6.6, 6.5, 6.4 respectively). Germinated treatments increased ($P < 0.1$) molar proportion of acetate (6.73%) and decreased ($P < 0.05$) molar proportion of butyrate. Germinated tended to increase (linear effect, $P < 0.10$) molar proportion of acetate. Germinated increased post-ruminal starch digestion and SG6 had the higher total tract digestion for OM, starch, N and DE value.
Funded by: DGAPA-PAPIIT IN206006

Key Words: cattle, germinated, reconstituted sorghum

M414 Performance of beef heifers finished at pasture in tropical conditions and supplemented with sunflower crushed seeds, in dry season. S. L. N. Cerilo*, R. H. de Tonissi e Buschinelli de Goes, H. L. Lima, K. A. de Souza, A. F. Marquez, T. da Cunha Cornélio, K. A. Guimarães Nogueira, D. de Faria Pereira, E. R. de Oliveira, and A. M. de Araújo Gabriel, *Universidade Federal da Grande Dourados*, *Dourados, MS, Brasil*.

To evaluate the partial substitution of soybean meal for sunflower crushed seeds in the performance of Nellore Heifers, at pastures of *B. humidicula* during the dry season, we used 24 animals, with initial body weight (BW) of 310 kg, with body condition score (BC) of 2.25, divided into paddocks of 3000 m^2, in a completely randomized design. Supplements evaluated were supplied collectively at 0.8% BW/animal/day consisting of corn, soybean meal and mineral, with 20% CP; the soybean

meal was replaced in the proportions of 0, 20, 40, and 60% for sunflower crushed seeds. The estimated ether extract of the supplements were 2.5, 4.7, 7.0, 9.2%, respectively. The animals were weighed every 21 d and monitored for BC (1–5). The average daily gain of animals showed a quadratic response (ADG = 0.2416+0.012x-0.0002x^2, r^2 = 0.99), and the replacement levels of 20 and 40% showed higher daily gains, 0.411 and 0.440 kg/day, while the levels of 0 and 60% had average of 0.242 and 0.320 kg/day. The inclusion of sunflower crushed seeds improved daily gain ($P < 0.10$) (average of 0.390 kg/day), this corresponds to an increase by 60% compared with supplementation with only corn and soybean meal. The efficiency of the use of concentrates (kg gain/kg of supplement) was greater for supplements containing sunflower crushed seeds, 12.26, 13.42 and 9.87% for the replacement levels of 20, 40 and 60% of soybean meal; the supplement without sunflower crushed seeds was efficient to 7.31%, these values can be related to the inclusion of sunflower crushed seeds into the concentrate, changing the energy density. The animal's BC improved with the sunflower crushed seeds, where the animals supplemented had the best initial (2.2, 2.5 and 2.2) and final (4.0, 4.0 and 3.7) body condition, for substitution levels of 20, 40 and 60%. The animals supplemented with corn and soybean, were initial and final body conditions of 2.1 and 3.6. Partial substitution of soybean meal with sunflower crushed seeds improves daily gain and body condition of animals on finishing systems on pasture.

Key Words: supplement, concentrated efficiency, daily gain

M415 Ingestive behavior of grazing Nellore steers supplemented with increased levels of energetic concentrate. J. R. R. Dorea, F. A. P. Santos, A. L. Marra, L. R. D. Agostinho Neto, D. C. Balestrin, M. A. C. Danes*, V. N. Gouvea, and A. M. Pedroso, *University of Sao Paulo*, *Piracicaba, Brazil*.

The objective of this trial was to evaluate the ingestive behavior of grazing Nellore steers receiving increased levels of energetic concentrate during rainy season. Eight rumen canulated Nellore steers averaging 380 kg of initial body weight, were randomly assigned to 1 of 2 complete 4x4 Latin squares. Each of the 4 experimental periods lasted 18 d, with 17 d for adaptation and 1 d for data collection. The grass pasture was *Brachiaria brizantha*, cv. Marandu. Pastures were rotationally grazed using a height-based management, on which 25 cm was the entrance height into the paddocks, that were left when a 15 cm post grazing residue was reach. The treatments were 3 levels of energetic supplementation (0.3, 0.6 and 0.9% BW, DM basis), based on fine ground corn and monensin (20 ppm/animal/d), plus a control treatment, with no supplementation. The concentrate was individually fed once daily, in the morning, and the animals had free access to a mineral premix. Ingestive behavior was determined by visual observation of individual animals, during 24 h, 5 min intervals, totaling 288 observations. Parameters evaluated were grazing, rumination and resting periods. The data was tested with *t*-test at 5% probability. There was a linear decrease ($P < 0.05$) in grazing time as the level of the supplementation increased. There was no difference among treatments for ruminating and resting periods. The energetic supplementation of animals grazing a high quality pasture can increase even more the substitution effect, what can result in decreased grazing time.

Table 1. Ingestive behavior of beef steers under increased level of energetic supplementation during rainy season

	Levels of concentrate (%BW)				P-value	Contrast		SEM[1]
	0	0.3	0.6	0.9	Treatment	L	Q	
Grazing time[2]	441	385	372	363	*	*	ns	9.82
Ruminating time[2]	395	399	358	378	ns	ns	ns	9.38
Resting time[2]	441	515	548	551	ns	ns	ns	16.37

[1]Standard error of the mean.

[2]Minutes; ns = not significant, * = $P < 0.05$.

Key Words: beef cattle, ingestive behavior, supplementation

M416 The effect of rumen protozoa of water buffalo and cow on fiber digestion in vitro. S. Jabbari*, M. Eslami, M. Chaji, T. Mohammadabadi, and M. Bojarpour, *Department of Animal Science, Ramin (Khuzestan) Agriculture and Natural Resources University*, *Ahwaz (Molassani), Khuzestan, Iran*.

The objective of this study was to compare the in vitro digestibility of wheat straw by rumen protozoal populations of water buffalo and Holstein cows. There is no information about the fibrolytic activity of rumen protozoa of water buffalo of Khuzestan in Iran. In vitro digestibility of dry matter (DM) and neutral detergent fiber (NDF) was measured by procedure of Tilley and Terry (1963). Rumen fluid was obtained from 2 buffalo and cows, which fed 30:70 concentrate: forage (corn grain, barley grain and wheat bran: sugarcane silage, corn silage, alfalfa hay and wheat straw). To preparing rumen protozoa, rumen fluid was added to antibiotic solution (streptomycin sulfate, penicillin G and chloramphenicol, 0.1 mg/ml each) and fungicides (benomyle: 500 ppm/ml medium and metalaxyle: 10 mg/ml medium), then was mixed with McDougall buffer in a ratio 1:4. After gasifying with CO2, tubes were incubated at 39°C. After 48 h the fermentation, 6 mL of HCl solution (20%) and 5 mL pepsin solution were added and the incubated for 48 h simulating post-ruminal degradation. After incubation, the residual substrates of each tube were filtered and used to determine disappearance of DM and NDF. Data of DM and NDF disappearance were analyzed as a completely randomized design using the general linear model procedure of SAS. The results of this experiment indicated that the DM digestibility of wheat straw by rumen protozoal population of buffalo was higher than that by rumen protozoa population of cows (25.2 and 21.13 g/100 g, respectively) ($P < 0.05$). Neutral detergent fiber digestibility of wheat straw was 16.7 and 10.3 g/100 g for protozoal population of buffalo and cows, respectively ($P < 0.05$). The DM and NDF digestibility by rumen protozoa from buffalo was 1.19 and 1.62 folds of the rumen protozoa from cows, respectively. Therefore, rumen protozoa of Khuzestan water buffalo have higher fiber breakdown compared with cows under the same diet.

Key Words: fiber digestion, buffalo, rumen protozoa

M417 The degradation of alfalfa treated with enzyme and or sodium hydroxide by rumen anaerobic fungi. T. Mohammadabadi* and M. Chaji, *Department of Animal Science, Ramin (Khuzestan) Agriculture and Natural Resources University*, *Ahwaz (Molassani), Khuzestan, Iran*.

This experiment was conducted to investigate the effect of rumen fungi on degradation of alfalfa treated with enzyme (30 g/kg DM) or sodium hydroxide (45 g/ kg DM) by using disappearance of dry matter (DM) and neutral detergent fiber (NDF) and chitin content in pure culture of

rumen anaerobic fungi for 12 d. Treatments were: untreated alfalfa and treated with sodium hydroxide (NaOH) (45 g/ kg DM), enzyme (30 g/kg DM) and or NaOH +enzyme. Rumen fluid was collected from 2 fistulated Holstein steers and centrifuged (1000 rpm, 10 min), then supernatant was used to grow fungi in medium containing antibiotic solution (streptomycin sulfate, penicillin G and chloramphenicol, 0.1 mg/ml each) under anaerobic conditions at 39°C for 24 h, by Joblin (1981) method. These isolates were used (1:9), as a source of inoculum for culturing fungi in a serum bottle containing 45 mL of culture medium and 1g of experimental sample under anaerobic conditions (using 3 times subculture) for 12, 24, 48, 72 and 96 h. The residual substrates of each bottle were then filtered and used to determine the DM and NDF concentrations. The chitin content of each medium was determined as described by Chen and Johnson (1983). The result showed disappearance of dry matter after 12 d incubation by rumen fungi will be 43.2, 58.3, 60.3 and 63.3 g/100 g DM for untreated alfalfa and treated with NaOH, enzyme and or $NaOH^{+}$enzyme, respectively. Sodium hydroxide and enzyme caused to increase disappearance of NDF and chitin content, and the highest increase was for medium containing alfalfa treated with $NaOH^{+}$enzyme (168.6 mg/g DM and 5.96 g/kg DM, respectively) ($P < 0.05$). Therfore, it appears that the degradation of alfalfa by rumen fungi is influenced by NaOH and enzyme treatments.

Key Words: rumen fungi, sodium hydroxide, enzyme

M418 Exchanging tropical fiber sources on intake and ingestive behavior of feedlot rations in beef cattle. R. S. Goulart*, V. P. Santos, G. B. Muraro, J. L. P. Daniel, R. C. Amaral, S. G. Toledo Filho, E. H. Cabezas, L. G. Nussio, and A. V. Pires, *University of São Paulo–ESALQ*, *Piracicaba, SP, Brazil*.

Forage and nonforage tropical fiber sources were evaluated in a 5 × 5 Latin square trial using Nelore steers within five 19-d periods (10-d adaptation followed by 9-d data collection). The 5 diets were composed of fiber sources: 20% NDF from corn silage (CS) (50.2% NDF); and 4 diets containing 10% NDF from corn silage added with 10% NDF from each of the following sources: sugarcane (SC) (46.8% NDF), sugarcane bagasse (SCB) (81.0% NDF), soybean hulls (SH) (75.1% NDF) and high oil – cottonseed meal (HOCM) (49.2% NDF). Steers were fed once daily in the morning and allowed ad libitum access to feed in tie stall pen. Data from the Latin squares were analyzed using Mixed procedures of SAS. Greater DM intake (9.26 kg/d) was observed for the diet which contained 20% NDF as CS ($P < 0.05$) compared with diets containing SC (8.85 kg/d) or SCB (6.86 kg/d). No differences in DM intake was observed between HOCM diets (9.62 kg/d) and CS diets. However, steers fed SH diet (8.44 kg/d) consumed less ($P < 0.05$) than CS. Steers fed SC or SCB diets showed greater capacity ($P < 0.01$) in stimulating rumination (50.0 and 62.3 min/kg DM, respectively) when compared with CS (42.5 min/kg DM), SH (26.7 min/kg MD) or HOCM diets (38.9 min/kg DM) for the same inclusion of NDF (% DM). This variation in feeding behavior affected the amount of acid produced in rumen fermentation of each treatment. Greater pH ruminal was observed for SC (6.21) and SCB (6.30) ($P < 0.01$) compared with CS (6.08) and SH (6.04). Thus, dietary NDF concentration alone from tropical roughage sources were not correlated to ruminal pH. Even though, it might provide a useful tool for exchanging roughages in diets, these results suggested that this fraction should not be considered exclusively as a predictor for estimate DM intake and ingestive behavior. Further studies involving physical and chemical traits from tropical roughage sources are on the way.

Key Words: roughage source, dry matter intake, Nelore steers

M419 Effect of levels of fiber and corn grain processing in diets for finishing Zebu cattle. R. Carareto*, F. A. P. Santos, G. B. Mourão, A. M. Pedroso, C. Sitta, W. Angolini, and B. Correa, *University of Sao Paulo*, *Piracicaba, São Paulo, Brazil*.

The objective of this trial was to compare 3 levels of grass hay and 2 types of corn grain processing in high concentrate diets for finishing feedlot cattle. Ninety-two Nellore bulls with an average initial SBW of 400 kg were used in a 63-d feeding trial after a 21 d period for adaptation to high concentrate diets. Animals were blocked by SBW and randomly allotted to 16 pens. Experimental diets were isonitrogenous and contained (%DM) 10% to 0% hay, 53.6 to 63.6% corn grain, 35% wet corn gluten feed, 1.4% of mineral mix with monensin.
Treatments were: 1) fine ground corn and 10% hay, 2) fine ground corn and 5% hay, 3) fine ground corn and 0% hay, 4) cracked corn and 0% hay. Data were analyzed based on a randomized complete blocks design, with pens as the experimental units, using the Proc. Mixed of SAS (1999) version 9.2 for Windows. Dry matter intake (DMI) and ADG were lower for treatments without hay ($P < 0.05$) (Table 1). Feed efficiency (DMI/ADG) was not affect by treatments ($P > 0.05$) (Table 1). Although the DMI and ADG were lower, the finishing Nellore bulls performance was not affected by treatments.

Table 1. Dry matter intake (DMI), average daily gain (ADG) and feed efficiency (DMI/ADG) of finishing Nelore bulls fed 4 different diets

Variables	T1	T2	T3	T4	Standard Error	Pr>F
ADG (kg /day)	1.55	1.51	1.30	1.36	0.0800	0.032
DMI (kg DM/day)	10.32	10.26	8,79	9.00	0.3729	0.0002
DMI/ADG	6.65	6.80	6.75	6.67	0.2365	0.9827

Key Words: Nelore, finishing, feedlot

M420 Influence of daily ingestion of alfalfa treated with quebracho tannins on in vitro fermentative activity of some browse species. H. Ammar[1,2], S. López[2], A. Z. M. Salem*[3,4], and J. S. González[2], [1]*Ecole Supérieure d'Agriculture de Mograne*, *Dept. Production Agricole, 1121-Zaghouan, Tunisia*, [2]*Instituto de Ganadería de Montaña (CSIC-Universidad de León)*, *24346 León, Spain*, [3]*Universidad Autónoma del Estado de México*, *Centro Universitario UAEM-Temascaltepec, Estado de México, C.P. 51300, México*, [4]*Alexandria University*, *Department of Animal Production, Faculty of Agriculture (El-Shatby), Egypt*.

Leaves from 4 shrub species (*Erica australis*, *Cistus laurifolius*, *Quercus pyrenaica*, and *Rosa canina*) collected from the mountain of Leon (northwestern Spain) were used to test the medium-term effects of the intake of quebracho condensed tannins on the fermentative activity in the rumen of sheep. Leaves from all shrubs were sampled at 3 different maturity stages (spring, summer and autumn). Eight Merino rumen cannulated sheep fed chopped alfalfa hay were used. Four sheep were given alfalfa hay treated with 50 g quebracho/kg DM for 60 d (group Q), whereas the other animals were always given untreated alfalfa hay and used as the control group (C). Differences in the fermentative activity were examined in vitro in batch cultures inoculated with rumen fluid obtained on d 60 from both groups of sheep. In vitro dry matter digestibility (IVD) and gas production kinetics from leaves and flowers of all shrub species were determined. Except for the flowers of *C. laurifolius*, IVD was higher ($P < 0.05$) when rumen fluid from Q sheep was used. Likewise, a significant effect of inoculum source on the dry matter disappearance after 144 h of incubation was observed for the flowers of *E. australis*. For the same substrate, the inoculation with rumen fluid from Q sheep resulted in a higher gas production at 24 h and faster fractional

gas production rates. The differences were generally statistically significant ($P < 0.05$) in most comparisons and the magnitude of this effect was greater when material with higher tannin contents was incubated (leaves of *E. australis* and *C. laurifolius*). In conclusion, rumen fluid from sheep fed a diet supplemented with condensed tannins showed a higher fermentative activity to degrade tannin-rich browse. This could be due to the appearance and proliferation of tannin-tolerant bacterial species or to the induction of changes in the existing bacteria to enhance their tolerance to these phenolic compounds.

Key Words: shrub, in vitro digestibility and gas production, sheep

M421 Productive characteristics and chemical composition of elephant grass (*Pennisetum purpureum Schum,* cv. Mineiro) submitted to chemical and organic fertilization. T. S. Oliveira*[1], J. C. Pereira[1], R. A. M. Vieira[4], J. G. L. Regadas Filho[1], and E. F. Aguiar[2], [1]*Universidade Federal de Viçosa*, *Viçosa, Minas Gerais, Brazil*, [2]*Universidade Federal do Vale do Jequitinhonha e Mucuri*, *Diamantina, Minas Gerais, Brazil*, [3]*Universidade Estadual de Montes Claros*, *Janaúba, Minas Gerais, Brazil*, [4]*Universidade Estadual do Norte Fluminense Darcy Ribeiro*, *Campo dos Goytacazes, Rio de Janeiro, Brazil*.

The objectives of this work were to study the effect of chemical (CF) and organic (OF) fertilization on the forage DM production and chemical composition characteristics of elephant grass and to estimate the total net energy for lactation (NEL) and the total digestible nutrients (TDN). Two elephant grass stocking piles were formed and 2 fertilization systems were used. The plant was evaluated in relation to height, age, DM ha-1 production (DMP), DM content and leave: stem ratio. Except for the age, the other values were analyzed in relation to the plant height. Based on the plant age, DM ha day-1 production and growth rate (GR) were calculated. As for elephant grass nutritive values (chopped forage), the experiment was carried out in a completely block (6 periods) randomized design and 3 replicates per forage (CF and OF) per block. Data of CP, NDF, ash, Ca, P, Mg and K were evaluated by F test, at 5% of probability. Based on the NDF contents, the NEL and TDN of the elephant grass from the 2 fertilization systems were estimated. The best plant performance at field was for the elephant grass submitted to organic fertilization, which was higher in water content, growth rate and forage DM ha day-1 production. Also in the nutritive value aspect, the elephant grass submitted to OF showed higher chemical composition values, which were indicatives of better nutritional quality. In this forage, higher contents of CP (17.26%), ash (26%) and P (36.88%) and smaller of NDF (3.96%) were observed in relation to the elephant grass submitted to CF. In the conversion of NPK fertilizer in forage DM, the elephant grass submitted to OF was 41.38% smaller than elephant grass submitted to CF. The elephant grass cultivated under organic fertilization was harvest with higher frequency and with better nutritional quality.

Key Words: elephant grass, chemical fertilization, organic fertilization

M422 Effects of condensed tannins supplementation in a lactating dairy TMR diet on ruminal fermentation in continuous culture, maintained at high and low pH. C. M. Dschaak*, C. M. Williams, J.-S. Eun, and A. J. Young, *Department of Animal, Dairy, and Veterinary Sciences, Utah State University*, *Logan*.

We investigated whether supplementing a water-soluble Quebracho extract would be beneficial to improve the rumen ecosystem by examining effects of ruminal pH on ruminal fermentation. The Quebracho extract contained approximately 75% condensed tannins (CT; Chemtan Company Inc., Exeter, NH), and the CT was supplemented to a barley-based high concentrate, lactating diet at 6% of dietary DM. A dual-flow continuous culture system consisting of 4 fermentors was used in a 4 × 4 Latin square with dietary treatment arranged as 2 × 2 factorial (high and low pH vs. without CT and with CT). High ruminal pH (HpH) was maintained with normal artificial saliva, while low ruminal pH (LpH) was achieved by diluting 60% of the normal artificial saliva with water. The ruminal pH averaged 6.2 and 5.9 to the HpH and the LpH, respectively. The diet used consisted of 33% alfalfa hay, 7% corn silage, 40% rolled barley grain, and 20% concentrate mixture. The 4 treatments were: 1) TMR with HpH and without CT; 2) TMR with HpH and with CT; 3) TMR with LpH and without CT; and 4) TMR with LpH and with CT. Filtered ruminal contents were allowed 5 d of adaptation to the treatments followed by 3 d of data collection. Culture pH decreased with CT supplementation in the HpH, however pH was not affected in the LpH. Methane production increased ($P < 0.01$) in the HpH, but decreased in the LpH due to CT supplementation. Ammonia-N concentration ($P < 0.01$) decreased with CT supplementation regardless of type of ruminal pH. Total VFA increased ($P = 0.02$) with CT supplementation in the HpH, but was not affected in the LpH. Molar proportion of acetate increased ($P = 0.02$) in the HpH, whereas CT supplementation did not affect acetate proportion in the LpH. Propionate proportion was not affected by CT supplementation in the HpH and the LpH. The supplementation of CT in the HpH resulted in positive impacts on microbial production, as was seen in increased VFA and decreased ammonia-N. However, CT supplementation in the LpH had no benefit on ruminal fermentation.

Key Words: condensed tannins, continuous culture, ruminal pH

M423 Milk fatty acid composition of grazing dairy cows supplemented with soy and fish oils. G. M. Martínez[1], G. A. Gagliostro*[2], D. A. Garciarena[1], V. I. Cejas[3], M. A. Rodríguez[3], R.A Castañeda[3], and M Balán[4], [1]*INTA EEA Salta*, *Salta, Argentina*, [2]*INTA EEA Balcarce*, *Balcarce. Buenos Aires, Argentina*, [3]*INTI Lácteos*, *San Martín, Buenos Aires, Argentina*, [4]*Prodeo SRL*, *Chivilcoy, Buenos Aires, Argentina*.

The effect of feeding soy oil (SO, 55.5% C18:2) or a residue of SO extraction (SOR, 61% oil, 55.9% C18:2) combined or not with fish oil (FO, 9.89% EPA, C20:5 n3 and 20.64% DHA, C22:6 n3) on milk fatty acid (FA) profile was studied on 32 grazing dairy cows (115 ± 28 DIM) in a 2x2 factorial arrangement. Oils were mixed with corn silage (CS) immediately before feeding. Treatments (DM basis) were: SO = 72.63% CS, 2.79% urea and 24.58% SO; SO-FO = 68.42% CS, 2.63% urea, 5.79% FO and 23.16% SO; SOR = 62.95% CS, 2.42% urea and 34.63% SOR and SOR-FO = 59.77% CS, 2.30% urea, 5.06% FO and 32,87% SOR. Concentrate (7.3 kg/cow/d) and pasture (8.4 kg/cow/d) were also consumed. Milk samples were obtained before (basal) and then once a week after oils feeding during 35 d. A factorial arrangement with repeated measures over time adjusted by covariable was used. Factor A compared SO vs SOR and factor B examined the effect of FO. Comparisons between basal and final milk FA were tested by the Student t-Test for paired observations. Concentration of C4:0, C6:0 and C8:0 resulted higher in SOR treatments. C14:0 (g/100g FA) was lower ($P < 0.03$) in SO (9.15) compared with SOR (10.17). Compared with basal (12.52 g/100g FA) SO-FO showed the most important reduction in C14:0 (−3.55 g/100g FA). The atherogenicity index of milk (2.29 to 2.59) was reduced (1.43) without differences between treatments. Basal concentrations of 10t C18:1 (0.28 to 0.31 g/100g FA) were increased particularly with SO (4.55 g/ 100 g FA) instead of SOR (3.9 g/ 100 g FA). SO-FO showed the highest 10t C18:1 concentration (5.27 g/100g FA). Increase of 11t C18:1 (VA) over basal (2.56 g/100g FA) resulted higher in SO-FO (+3g/100g FA) followed by SOR-FO (2.91 and +2.84), SO (2.78 and +1.36) and SOR (2.54 and +1.06 g/100g FA). Concentrations

(g/100g FA) of 9c, 11t CLA averaged 3.23 (SO-FO), 2.95 (SOR-FO), 2.43 (SO) and 2.19 (SOR) resulting higher ($P = 0.01$) in FO treatments FO (3.14 vs 2.31) without interaction between FO and sources of supplementary C18:2. After supplementation, the CLA/11t C18:1 ratio decreased in all treatments. The SOR may successfully replace SO to modulate milk FA composition.

Key Words: soy oil residue, fish oil, conjugated linoleic acid

M424 Does the in situ ruminal degradation of feeds vary with the finishing ration fed to beef cattle? Y. L. Li*[1,2] and W. Z. Yang[1], [1]*Agriculture and Agri-Food Canada, Research Centre*, *Lethbridge, AB, Canada*, [2]*Feed Research Institute, Chinese Academy of Agricultural Sciences*, *Beijing, China*.

An in situ study was conducted to determine degradation of feeds in the rumen of beef cattle fed finishing diets that varied with the amounts of silage, barley grain and wheat DDGS. This study was part of the measurements in a metabolic study. Eight ruminally fistulated Angus heifers were assigned in a replicated 4 × 4 Latin square design with 4 diets that consisted of barley silage, barley concentrate, and wheat DDGS in ratios of 15:85:0, 10:65:25, 5:65:30 and 0:65:35, respectively, for control, low, med and high DDGS. Five grams of the barley silage (chopped), barley grain (temper-rolled) and wheat DDGS (as fed) fed to the cattle were incubated in situ in the rumen of 8 heifers for 0, 2, 4, 6, 12, 24 and 48 h in the first 2 periods of the study. The model $y = a+b(1-e^{-ct})$ was fitted to determine degradation kinetics of DM, NDF and CP, where y is nutrient degraded, a is soluble fraction, b is slowly degradable fraction, c is degradation rate constant, t is incubation time. Effective degradability (ED) was determined by $ED = a+[bc/(c+k)]$, where k = 0.06/h. For barley silage, soluble fraction of DM decreased quadratically ($P = 0.01$). The slowly degradable fraction of DM tended to linearly ($P = 0.06$) decrease, and that of CP quadratically ($P = 0.05$) decreased with increasing amount of DDGS in the diets. For barley grain, the kinetic parameters of DM, NDF and CP were generally not affected by the diets except for the ED of NDF which was greater ($P = 0.01$) for med DG (48%) than for the other 3 diets. Finally, for wheat DDGS, the degradation kinetics and ED of DM, NDF and CP were overall not affected. The results suggest that the effects of finishing diet fed to cattle on in situ ruminal degradation kinetics vary with type of feed and nutrient measured; in situ ruminal degradation of wheat DDGS was the least affected by the diets fed to cattle among 3 feeds evaluated.

Key Words: In situ ruminal degradation, wheat DDGS, beef cattle

M425 Performance of grazing dairy cows supplemented with soy and fish oils. G. M. Martínez[1], G. A. Gagliostro*[2], and D. A. Garciarena[2], [1]*INTA EEA Salta*, *Salta, Argentina*, [2]*INTA EEA Balcarce*, *Balcarce, Buenos Aires, Argentina*.

Feeding soy oil (SO) or a residue of oil extraction (SOR) combined or not with fish oil (FO) may be an inexpensive way to increase vaccenic and conjugated linoleic acids in milk. Production responses of dairy cows fed SO (55.5% C18:2), SOR (61% oil; 55.9% C18:2) and FO were examined on 32 grazing dairy cows (115 ± 28 DIM) in a DCA with a 2x2 factorial arrangement over a 35 d period. Oils were mixed to corn silage (CS) defining 4 treatments: SO = 72.63% CS, 2.79% urea and 24.58% SO; SO-FO = 68.42% CS, 2.63% urea, 5.79% FO and 23.16% SO; SOR = 62.95% CS, 2.42% urea and 34.63% SOR and SOR-FO = 59.77% CS, 2.30% urea, 5.06% FO and 32,87% SOR. Concentrate (7.3 kg) and pasture (8.4 kg) were also consumed. Results were analyzed as a factorial arrangement with repeated measures adjusted by covariable. Factor A compared SO vs SOR and factor B examined the effect of including FO. Within treatments, comparisons between pre- and final records were performed using the Student t-Test for pairwise observations. Intake of ration (kg DM/cow/d) was lower ($P < 0.01$) in SO-FO (2.14) and SOR-FO (2.30) compared with SO (2.66) and SOR (2.78). Pre-trial milk yield, milk fat and milk protein contents averaged 26.6 kg/v/d, 35.7 and 34.4 g/kg, respectively. After 35 of oil supplementation milk yield (SO-FO:-3,18, SO:-2.90, SOR-FO:-1.97 and SOR:-1,62 kg/cow/d) and milk fat content (SOR: −9.9, SOR-FO: −9.1, SO-FO: −9 and SO: −6,9 g/kg) decreased ($P < 0.01$), but milk protein content remained unaffected. FCM was also depressed. Milk yield (kg/cow/d) resulted higher ($P < 0.002$) in SOR treatments (23.9) compared with that including SO (22.9). Milk fat content (AxB, $P < 0.10$) was higher ($P < 0.05$) in SO (29.1g/kg) compared with SO-FO (26.1), SOR (26) and SOR-FO (2.61). FCM resulted higher ($P < 0.03$) for treatments without FO (19.75 vs 19.0 kg/cow/d). Yield of FCM (AxB, 0.07) was depressed by SO-FO (18.5 kg/cow/d) compared with SO (19.9), SOR (19.6) and SOR-FO (19.5). Milk fat secretion (g/cow/d) resulted higher in SO (698) compared with SO-FO (631) and SOR (622) without differences between SO and SOR-FO (640). A lower depression of milk yield and milk fat content was observed feeding the SOR supplement.

Key Words: soy oil, milk yield, milk composition

M426 Effect of production system on metabolic and endocrine responses of grass fed cows. L. D. Kaufmann[1], A. Münger[1], H. A. van Dorland[2], R. M. Bruckmaier[2], and F. Dohme*[1], [1]*Agroscope Liebefeld-Posieux, Research Station ALP*, *Posieux, Switzerland*, [2]*University of Bern Vetsuisse Faculty, Veterinary Physiology*, *Bern, Switzerland*.

We previously reported that energy expenditure was higher in dairy cows on pasture compared with those offered the same grass in a free-stall barn. Aiming to better understand these differences, the metabolic and endocrine profile and feed intake of the dairy cows fed grass of the same quality either on pasture (P) or in the barn (B) were investigated. Fourteen dairy cows (milk yield: 44 ± 2.7 kg/d) were randomly assigned to a crossover study. The 2 experimental periods lasted 2 wk each and consisted of an adaptation and a data collection period of 1 wk each. The P cows grazed on pasture whereas B cows had ad libitum access to grass from the same paddock, fed in a free-stall barn. All cows were supplemented with a cereal-based concentrate to meet their predicted nutrient requirements. Concentrate was offered in the barn at 0630 and 1630 h using weighing troughs. Grass intake and nutrient digestibility were estimated by the double alkane technique. Milk metabolites were analyzed and BW was recorded daily during the collection periods. On each day of the collection period, blood was taken at 0530 h from one cow of each treatment group. Samples were centrifuged and stored at −20°C until further analysis. As expected, grass quality was similar in both treatment groups (CP, 179 g/kg DM; NDF, 407 g/kg DM). Daily grass (15.6 kg DM) and concentrate intake (6.4 kg DM) did not differ ($P > 0.05$) and therefore no differences ($P > 0.05$) were observed in total DM, OM and NDF intake between treatments. Digestibility of OM (81.6%) and NDF (78.9%) were similar ($P > 0.05$) in both experimental groups. Milk acetone concentration (1.13 mg/kg) was unaffected ($P > 0.05$) while milk urea level tended ($P = 0.06$) to be lower in P cows (186 mg/kg) compared with B cows (208 mg/kg). Neither blood metabolites (albumin, BHBA, cholesterol, glucose, NEFA, total protein, triglycerides, and urea) nor IGF-1, T3, and T4 differed ($P > 0.05$) between treatments. In conclusion, the analyzed blood traits as well as the nutrient intake do not help explaining the observed differences in energy expenditure of grazing cows compared with cows fed the same grass in the barn.

Key Words: dairy cows, metabolic and endocrine profile, pasture

M427 Production of dairy cows fed varying levels of total mixed ration and pasture. A. Quilaguy-Ayure, G. A. Gagliostro*, D. A. Garciarena, L. Antonacci, and C. A. Cangiano, *INTA EEA Balcarce*, *Balcarce, Buenos Aires, Argentina*.

Nine dairy cows were offered combinations of total mixed ration (TMR) and pasture (P) in a triplicated 3 × 3 Latin square design with 3 partial mixed rations (PMR) targeted at (1) 75% TMR and 25% P, (2) 50% TMR and 50% P and (3) 25% TMR and 75% P. All cows were also fed the TMR-100% diet. TMR was composed (DM) by corn silage (36%), concentrate (49%), soybean meal (6.5%), soybean grain (6.5%) and feather meal (2%). Data were analyzed by a model that included treatment, square and period as fixed effects and cow within square as random effect. Differences between the TMR-100 and the other treatments were stated using the t-Test for paired observations. The actual proportions of TMR and P were (1) 79:21, (2) 58:42 and (3) 33:67. TMR intake (kg DM/cow/d) was 20.32, 13.44 and 7.06 for (1), (2) and (3) treatments, respectively ($P < 0.01$). Reducing the proportion of TMR increased ($P < 0.01$) pasture consumption (5.27, 9.77 and 14.49 kg DM/cow/d) and reduced ($P < 0.01$) total DM intake (25.59, 23.21 and 21.55 kg/cow/d for 1, 2 and 3, respectively). Total DM intake (kg/cow/d) for TMR-100 was higher (28.23, $P < 0.03$) compared with PMR treatments. Total DM intake (% of BW) was similar between TMR-100 (4.42%) and PMR-79 (4.26%), but higher ($P < 0.01$) to PMR-58 (3.82%) and PMR-33 (3.06%). Yields (kg/cow/d) of milk (31.2) or 4%FCM (26.8) did not differ between PMR. Milk production (kg/cow/d) in TMR-100 (32.1) was higher ($P < 0.01$) than PMR-58 (30.7) and 4%FCM did not differ between TRM and PMR treatments. Milk fat content (g/kg) was similar between TMR-100 (28.5) and TMR-79% (29.6) but lower ($P < 0.02$) to TMR-58% (31.3) and TMR-33% (32). Milk protein content (g/kg) resulted higher ($P < 0.02$) in TMR-100% (33.7) compared with TMR-79% (33.2). Milk fat secretion (0.954 kg/cow/d) did not differ. Milk protein yield (kg/cow/d) was similar between PMR diets (1.03) but lower ($P < 0.04$) to TMR-100% (1.07) for TMR-58 and TMR-33. Feed efficiency (kg milk/kg DM) had a tendency ($P < 0.08$) to increase from 1.13 to 1.42 with increased pasture levels in PMR diets. For cows producing between 32 to 30 kg of milk, decreasing the pasture TMR ratio in the diet did not show a clear production benefit.

Key Words: intake, pasture, partial mixed ration

M428 Effect of different pectin rich by products on feed intake, milk production and composition and ruminal pH of lactating dairy cows. M. Kordi*, A. Naserian, R. Valizade, and A. Tahmasbi, *Ferdowsi University*, *Mashhad, Iran*.

Eight primiparous early lactating Holstein cows (60 ± 23 d postpartum, weighing 530 ± 60 kg) were assigned into a duplicated 4 × 4 Latin square design for evaluated of different pectin rich by products on feed intake, milk production and composition and ruminal pH of lactating dairy cows with 4 3-wk periods. Cows were allocated into 4 diets whit 1)10% barley grain, 2)10% sugar beet pulp, 3)10% wheat bran and 4) 10% dried citrus pulp . Each experimental period was 21 d including 14 d adaptation period and 7 d collecting samples. Milk yield recorded daily and milk samples were taken from each milking times during the last 3 d of each period. Milk samples were subjected to analysis for CP, lactose, fat and SNF. The dry matter intake (DMI), NDFI, milk yield and composition and ruminal pH are presented in the Table 1. There were no differences ($P > 0.05$) in the daily intake of DM (kg/d), and milk yield and composition, among treatments (Table 1). Similarly, there were no significant differences in ruminal pH among treatment diets ($P > 0/05$). The NDF intake was significantly different among treatments ($P < 0.05$). These data suggest that, the addition of sources of pectin feed stuffs at 10% levels (dry matter basis) of the dairy cow ration instead of cereal grain; will decrease the cost of milk production without any negative effect on dairy cows performance.

Table 1. Dry matter intake, NDF intake, milk production and composition, and ruminal pH of dairy cows

	Treatment				
Item	T1	T2	T3	T4	SEM
DMI (kg /day)	19.34	19.63	19.74	18.69	0.122
NDF intake(kg/d)	6.05b	6.61a	6.63 a	5.8 8 b	0.110
Ruminal pH	6.25	6.36	6. 3	6.26	0.071
Milk yield (kg /day)	28.68	28.3	28.81	27.37	0.201
Milk composition (%)					
Protein	3.1	3.03	3.16	3.12	0.046
Lactose	4.92	5.01	5.15	4.98	0.057
Fat	3.14	3.44	3.36	3.34	0.07
SNF	8.27	8.3	8.56	8.36	0.099

Key Words: barley, lactating dairy cow, pectin rich byproducts

M429 Modification of the Z-Box system for assessing particle distribution of forages and total mixed rations. K. W. Cotanch*[1], C. S. Ballard[1], J. W. Darrah[1], L. M. Klaiber[1], R. J. Grant[1], and K. Yagi[2], [1]*W. H. Miner Agricultural Research Institute*, *Chazy, NY*, [2]*Zen-Noh National Federation of Agricultural Co-operative Associations*, *Tokyo, Japan*.

The Z-Box has been proven to be an accurate on-farm tool for determining the physical effectiveness factor (pef) of silage-based TMR, corn silage, and haycrop silage. It would be advantageous to consultants and dairy producers to modify the Z-Box to measure particle distributions in addition to pef. The objective of this studywas to select perforated steel screens for the Z-Box to provide particle size distributions similar to the Penn State Particle Separator. Twenty-five kg samples of corn silage (CS, n = 12), haycrop silage (HCS, n = 12), and total mixed ration (TMR, n = 41) were sub-sampled and processed using the Penn State Particle Separator (PSPS) and Z-Box following the accepted methodology for both systems. Three replications of each sample were processed by 3 technicians. For the Z-Box, samples were processed sequentially working from the smallest to largest screen (3.18, 4.76, 6.35, 12.70, and 15.88-mm) following the standard Z-Box vertical-shaking method.. The Z-Box method for assessing particle distribution was evaluated for accuracy within forage type by calculating the mean bias of particle distributions determined using PSPS and various Z-Box screens. The Z-Box screen with the narrowest 95% confidence interval (CI) encompassing zero most accurately assessed particle distribution. For TMR and HCS, 4.76- and 12.70-mm screens with the Z-Box resulted in the closest agreement with the PSPS method. For CS, the 4.76- and 15.88-mm screens assessed particle distribution most accurately.

Table 1. Mean bias of particles screened using PSPS and corresponding Z-Box sieves for forages and TMR

Sample	Z-Box Sieve < (mm)	PS Screen < (mm)	Mean bias ± SD	Upper 95% CI	Lower 95% CI
CS	3.18	8	–12.92± 3.0	–11.01	–14.83
	4.76	8	–4.31± 2.26	–2.88	–5.75
	6.35	8	6.28± 1.80	7.42	5.13
	12.7	19	–11.92± 5.09	–8.69	–15.16
	15.88	19	0.66± 1.10	1.36	–0.04
HCS	3.18	8	–21.49± 6.19	–17.56	–25.42
	4.76	8	–6.04± 5.45	–2.58	–9.50
	6.35	8	11.76± 4.69	14.74	8.78
	12.7	19	0.29± 1.85	1.46	–0.88
TMR	3.18	8	–13.03± 3.11	–12.05	–14.01
	4.76	8	0.20± 3.06	1.17	–0.76
	12.7	19	–0.38± 4.53	1.05	–1.81

Key Words: particle distribution, forage, total mixed ration

M430 Zinc and heat treatments reduce ruminal protein degradation of grass leaf protein. K. L. Kammes*, B. D. Bals, B. E. Dale, and M. S. Allen, *Michigan State University*, *East Lansing*.

Leaf protein (LP) produced as a coproduct of cellulosic ethanol production can be utilized by ruminants. Effects of grass maturity, chemical and heat treatment, and conservation method on ruminal protein degradation of LP extracted from orchardgrass (OG) were evaluated. Two maturities of OG were harvested from the same field in 2008 with crude protein (CP) concentrations of 17% (immature) and 13% (mature). Grasses (fresh, stored, or wilted) were chopped and protein rich juice was extracted with a screw press. The juice was chemically treated with concentrated hydrochloric acid (HCl, pH 3.3) with or without zinc (Zn, 2.085 g zinc chloride per liter) and treated with heat (100 or 140°C for 1 h) or without (21°C; control) followed by centrifugation to harvest precipitated LP. Crude protein concentrations of LP approximately doubled that of the original grass to 34.4 and 25.8% for immature and mature, respectively for all chemical and heat treatment combinations. In vitro protein degradation of LP was evaluated using enzymes extracted from rumens of lactating dairy cows. The HCl+Zn, 140°C treatment decreased CP degradation the greatest extent compared with HCl, control for fresh OG LP (4 vs. 20% degraded in 12 h). An interaction ($P < 0.10$) between maturity and Zn was observed with Zn decreasing CP degradation of immature OG more than mature OG after 4 h incubation. The HCl+Zn treatment decreased CP degradation more than HCl alone (3.0 vs. 9.9% after 4 h and 5.5 vs. 13.8% after 12 h; $P < 0.05$). Heat also decreased CP degradation with temperatures of 100 and 140°C resulting in similar degradation, which were lower than control (4.0 vs. 11.3 after 4 h and 7.3 vs. 14.4% after 12 h; $P < 0.05$). There was an effect of conservation method on HCl+Zn, 140°C treated OG LP with similar degradability for stored (7.7%) and wilted (9.8%), which were higher than fresh (1.7%; $P < 0.01$). Leaf protein from fresh OG treated with zinc and heat resulted in decreased ruminal CP degradation.

Key Words: leaf protein, protein degradation, bypass protein

M431 Prediction of residual feed intake in beef heifers by infrared thermography. J. J. Colyn*[1], A. L. Schaefer[1], J. A. Basarab[2], E. K. Okine[3], T. Liu[1], K. L. Robertson[2], and S. L. Scott[4], [1]*Agriculture and Agrifood Canada, Lacombe Research Centre*, *Lacombe, AB, Canada*, [2]*Alberta Agriculture*, *Lacombe, AB, Canada*, [3]*Department AFNS, University of Alberta*, *Edmonton, AB, Canada*, [4]*Agriculture and Agrifood Canada*, *Brandon, MB, Canada*.

The cow herd is estimated to require 65–75% of the total energy required for beef production. Measurements of residual feed intake (RFI) to improve feed efficiency in beef breeding programs have mainly focused on replacement bulls but potential for improvements exist in replacement heifer selection. A limitation to the widespread use of measuring RFI is the cost and complexity of collecting individual daily feed intake. An alternative method to predicting RFI, which has shown utility in mature cows, growing bulls, and steers, is to measure radiated energy losses by infrared thermography (IRT). The purpose of the present study was to investigate the potential of IRT as a predictor of RFI in growing replacement heifers. Sixty-one crossbred beef heifers were fed a balanced conventional barley silage ration. At Day 0, 94, and 113 a sequence of IRT images of the head were collected with a FLIR S60 camera. Average IRT temperature of the cheek region (CHK) was calculated for each date. Actual feed intake (FI), as measured by the Growsafe feeding system was regressed against average daily gain, metabolic mid-point weight and final ultrasound backfat to obtain expected feed intake (EFI). RFI was the difference between FI and EFI, and values ranged from −1.55 to 2.19 kg d-1 as-fed (avg = 0.0; sd = 0.777). Heifers were then classified into low, medium, or high RFI groups based on ± 0.5 of the standard deviation around the RFI mean. Using CHK for each date in a repeated measure analysis, heifers with a low RFI value (n = 17; avg = −0.915 kg d-1; sd = 0.316) or a medium RFI value (n = 27; avg = −0.003 kg d-1; sd = 0.214) displayed a CHK temperature of 19.98°C (se = 0.230) and 20.33°C (se = 0.184) respectively and were significantly different ($P <$ 0.01) from heifers with a high RFI value (n = 17; avg = 0.919 kg d-1; sd = 0.552) which displayed a CHK temperature of 21.31°C (se = 0.230). Data from this study suggest measurements of IRT may have utility as a rapid screening tool to predict growth efficiency in heifers.

Key Words: feed efficiency, cattle, infrared

M432 Predicting ME and metabolizable protein (MP) balances of Santa Gertrudis cows under grazing conditions using a nutrition model. A. D. Aguiar*[1,4], L. O. Tedeschi[1], K. McCuistion[2], D. S. DeLaney[3], and S. Moore[3], [1]*Texas A&M University*, *College Station,* [2]*Texas A&M University-Kingsville*, *Kingsville,* [3]*King Ranch*, *Kingsville, TX,* [4]*University of Florida*, *Gainesville*.

Predictions of Santa Gertrudis cow requirements of ME and MP (g/d) grazing pastures containing Kleberg bluestem (*Dichanthium annulatum*) and Coastal bermudagrass [*Cynodon dactylon* (L.) Pers] were performed using the Large Ruminant Nutrition System (LRNS). Simulations were performed using measured clime, forage, and animal data; and concentrate DMI. Forage DMI was predicted by the LRNS. Three reproductive cycles were evaluated: P1 (05/06 – 04/07), P2 (05/07 – 04/08), and P3 (05/08 – 04/09). The fractional fermentation rate (kd) of monthly forage NDF was determined using in vitro gas production technique. TDN values were estimated as 0.98 × (100 - NDF - CP - EE - ASH) + Digestible CP + 2.25 × (EE - 1) + (NDF - NDIN) × (kd/(kd + kp) + IDNDF) – 7 in which EE is ether extract, NDIN is N in the NDF, IDNDF is indigestible NDF, and kp is fractional passage rate. When kp was assumed to be 4%/h, predicted values had the greatest accuracy (Cb = 0.82), the least mean bias (−2.19%), but the least precision (r^2 = 0.59) compared with a published theoretical equation. The predicted TDN varied from 48.5 to 59 (P1), 46.6 to 61.5 (P2), and 46 to 59.6% (P3). The predicted DMI by the LRNS was 1.75, 1.99, and 1.86% BW for P1, P2, and P3; respectively, contrasting with literature data of 2.6% BW. When the LRNS predicted DMI was used, ME and MP balances were negative for most months of the year. When 2.6% of BW was used, the ME and MP balances were negative only for May and Jun for P1; Apr (ME) and Apr to Jun (MP) for P2; while cows in P3 had predicted positive ME and MP balances for Jul, Aug, and Sep. The results of 2.6% BW to predict DMI were more consistent with the observed BW and BCS changes during these periods (ADG = 0.16 kg/d), suggesting that cows had an overall positive MP and ME balances and likely used the surplus of nutrients for growth and to increase BCS. The LRNS underpredicted forage DMI given the predicted forage TDN. The use of empirical equations to predict DMI of grazing beef cows may not be acceptable in designing supplementation strategies. More integrated and mechanistic nutrition models are needed to predict DMI.

Key Words: cattle, requirements, supply

M433 Estimating rumen microbial crude protein in vitro using purine analysis or real-time PCR. E. Castillo-Lopez*, P. J. Kononoff, and J. L. Miner, *University of Nebraska-Lincoln*, *Lincoln*.

In ruminants, microbial crude protein (MCP) contributes to metabolizable protein. Estimation of MCP has traditionally been based on purine analysis, but it may be confounded by purines not originating from microbial DNA, therefore, a more direct approach is needed. The objectives of this experiment were to compare real-time PCR and purine analysis on estimates of MCP and to evaluate the impact of fermentation time, and lastly to evaluate the impact of dried distillers grains and solubles (DDGS) when replacing hay and corn. For each treatment, 1 g of substrate was incubated in 100 mL of rumen inoculum and replicated 3 times. A 3X2X2 factorial design experiment was used to determine the impact of 3 fermentation substrates at 2 times estimated with 2 methods on MCP. Treatments were as follows, CONTROL (50% grass hay and 50% rolled-corn), LOW DDGS (33% grass hay, 33% rolled-corn and 33% DDGS) and HIGH DDGS (100% DDGS.). At each time point a pellet was isolated and bacterial, protozoal and yeast crude protein was estimated using real-time PCR and purine analysis. To do so, microbial markers (primers and probe) were designed from the 16S rRNA, 18S rRNA and the second chromosome; for bacteria, protozoa and yeast (*Saccharomyces cerevisiae*), respectively. Estimates of MCP were different ($P < 0.05$) and were 221 and 246 (SEM = 6.55) mg/g DM according to the real-time PCR assay and that based on purine analysis. Fermentation substrate affected ($P < 0.05$) yield of MCP which was 263, 243 and 195 (SEM = 7.77) mg/g DM for CONTROL, LOW DDGS, and HIGH DDGS respectively. Fermentation time did not ($P = 0.25$) affect yield of MCP which was 229 and 239 (SEM = 6.34) mg/g of DM at 0 and 48h fermentation respectively. There was no method by diet interaction (P = 0.44). Inclusion, the real-time PCR estimates of MCP differed from those obtained with the purine analysis and it may be a feasible approach for the estimation of MCP. In addition, increasing level of DDGS may affect the in vitro synthesis of MCP.

Key Words: DDGS, microbial crude protein, purine analysis, real-time PCR

M434 An in vitro gas production technique to evaluate the effect of microwave irradiation on fermentation potential of cottonseed hulls using medium of ruminal fungal isolation. A. Faramarzi Garmroodi, M. Danesh Mesgaran*, H. Jahani-Azizabadi, A. R. Vakili, A. Tahmasbi, and A. R. Heravi Moussavi, *Dept. of Animal Science (Excellence Center for Animal Science), Ferdowsi University of Mashhad*, *Mashhad, Iran*.

Gas production parameters of microwave irradiated cottonseed hulls (CH) were assessed using gas production procedure of medium containing ruminal fungal isolation. Cottonseed hulls were hydrated by distilled water as 25 g/kg DM, then, irradiated (microwave, 900 W) for 4, 6 and 8 min (mic4, mic6 and mic8, respectively). Approximately, 0.3 g of each sample was placed in a 100 mL glass syringes (n = 4), then, incubated into 40 mL of buffered protozoa and bacteria free rumen fluid (ratio of buffer to rumen fluid was 2:1) for 2, 4, 6, 8, 12, 24, 48, 72 and 96 h. Rumen fluid was obtained from 3 sheep (body weight, 49.5 ± 2.5 kg) fitted by rumen fistulae, before the morning feeding, and strained through 4 layers of cheesecloth. The animals were fed 1 kg/d DM of alfalfa hay and 0.3 kg/d DM of concentrate (165 g CP/kg DM). Rumen fluid was centrifuged (10 min, 3000 rpm) and a solution of penicillin and streptomycin was added to protozoa free supernatant to remove the bacterial population. Data of gas produced over the incubations were applied to an exponential equation of $P = b(1\text{-}e)^{-ct}$ where (b) is the amount of produced gas from the fermentable fraction, (c) is the fractional constant rate and (t) is time. Data were analyzed using the GLM procedure of SAS 9.1 and the means were compared by the Tukey test ($P < 0.05$). The amount of gas produced from the fermentable fraction (b ± SEM) was 3.7 ± 2.82, 3.9 ± 2.17 and 4.4 ± 2.98 for mic4, mic6 and mic8, respectively. The fractional constant rate parameters (c ± SEM) were 0.01 ± 0.011, 0.01 ± 0.011 and 0.01 ± 0.018 for mic4, mic6 and mic8, respectively. Present data indicate that the physical procedure used has not any benefit on fermentation potential of CH while a medium of isolated ruminal fungal was used.

Key Words: cottonseed hulls, gas production, microwave irradiation

M435 The effect of microwave irradiation on gas production parameters of cottonseed hulls using medium containing ruminal bacterial isolation. A. Faramarzi Garmroodi, M. Danesh Mesgaran*, H. Jahani-Azizabadi, A. R. Vakili, A. Tahmasbi, and A. R. Heravi Moussavi, *Dept. of Animal Science (Excellence Center for Animal Science), Ferdowsi University of Mashhad*, *Mashhad, Iran.*

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Key Words: cottonseed hulls, gas production, microwave irradiation

M436 The influence of extrusion of low-glucosinolate full-fat rapeseed and whole pea on site and extent of protein digestion in dairy cows. C. Bayourthe* and F. Enjalbert, *UMR 1289 INRA/INPT/ENVT TANDEM*, *31326 Castanet-Tolosan, France*.

The objectives of the study were to develop suitable treated blends for protection of low-glucosinolate rapeseed (canola) proteins from rumen degradation and to determine the protein quality after rumen exposure. Full-fat canola seeds (CS) were mixed either with canola meal (CM) or with canola meal plus whole pea seeds (PS). The effect of extrusion at 130 and 150°C on in situ crude protein (CP) degradability of raw and treated blends was measured by the nylon bag technique using 3 fistulated non-lactating Holstein cows. Ruminal degradation rate of CP was estimated as percent nitrogen degradation (DgN) from polyester bags incubated in rumen for 2, 4, 8, 16, 24 and 48 h. Data were fitted to the nonlinear regression equation: $DgN(t) = a + b(1 - e^{-ct})$ where DgN is percentage disappearance of N at time t, a the soluble fraction and b the less rapidly degradable fraction which disappears at the constant fractional rate c per time t. Heating the blends at 130 and 150°C decreased the effective degradability of crude protein (EDCP) when compared with the raw blend: 37.3 and 33.6 respectively vs 57.2% for CM/CS blend; 53.8 and 42.4 respectively vs 62.5% for the CM/CS/PS blend. Total CP disappearing in the digestive tract was estimated by incubating bags in the rumen for 16h, followed by a pepsin bath for 2h and then introduced into the duodenum for subsequently recovery in feces. For the CM/CS blend, amounts of rumen undegraded dietary CP digested in the intestine were increased from 32.7 (raw blend) to 49.3% at 130°C and 53.6% at 150°C. Similarly, for the CM/CS/PS blend, corresponding values were 27.9 for the raw blend to 38.2 and 53.3% respectively for 130 and 150°C heat treatments. The results showed that PS was the most effective carrier of rapeseed during extrusion. The tested blends and the treatments applied appeared to be a viable and consistent method of increasing the ruminally undegradable protein fraction

Key Words: extrusion, canola, ruminal degradation

M437 In situ ruminal degradability of dry matter and crude protein of soybean meal treated with formaldehyde and extrusion. A. A. Naserian* and H. Gholizadeh, *Ferdowsi University of Mashhad*, *Mashhad, Iran*.

The objective of this study was to determine effect of formaldehyde and extrusion on in situ ruminal degradability of DM and CP of soybeans. Treatments include; untreated soybean meal (USM) treated with formaldehyde (TF) and extruded soybean (ES). The treated soybean meal was sprayed with 2.5 (w/v) formaldehyde at the rate of 0.2 l/kg. Extrusion was conducted on ground soybeans (EXP 160 KW). Extrusion temperature and residence time averaged 1550 C and 25 s respectively. Four ruminally fistulated steers (400 ± 20 kg, body weight) were used. Steers were fed 5.2 kg of alfalfa hay, 1.3 kg of corn silage and 2.6 kg of concentrate. Bags (12 × 19 cm, pore size of 48 µm) containing 5 g DM of each sample was incubated in the rumen (4 replicates per each animal) for 0.0, 2, 4, 8, 16, 24, 48, and 72 h. After removal of the bags

from the rumen, they were washed using cold water and dried in a forced air oven (60 0C, 48 h), weighed to determination DM disappearance, and CP of the samples determined. Data was fitted to exponential model to calculate degradation parameters of CP and DM (Orskove et al.,1980). TF had the lowest in situ quickly degradable (a) fraction (27%, $P < 0.05$). No difference in (a) fraction of DM was observed between ES and USM (42 and 38% respectively, $P > 0.05$). In situ (a) fraction of CP was highest for USM (27%, $P < 0.05$) and had no difference between ES and FT (7 and 11% respectively, $P > 0.05$). Slowly degradable (b) fraction of DM did differ between treatments ($P < 0.05$). USM had the highest (b) fraction (63%) and did not differ between TF and ES (34 and 27% respectively, $P > 0.05$). Slowly degradable (b) fractions of CP had no difference between ES and USM (78 and 72% respectively, $P > 0.05$), were higher than TF (34%). Rate of degradation (c) of DM and CP were significant ($P < 0.05$). TF had a lower (c) fraction of DM and CP (3 and 1% respectively) compared with USM (9 and 9%) and ES (12 and 4%) compared with USM. It was concluded that TF decreased (a) and (b) fraction of DM and CP relative to USM. But, ES led to decreased (a) and increased (b) fraction.

Key Words: soybean, extrusion, formaldehyde

M438 Disappearance of total carotenoids in the rumen and intestine of steers measured using a mobile nylon bag technique. R. G. Cruz-Monterrosa*[1], I. Guerrero-Legarreta[1], and E. Ramirez-Bribiesca[2], [1]*Universidad Autonoma Metropolitana*, *D.F., Mexico*, [2]*Colegio de Postgraduados*, *Texococo Mexico*.

There are few studies on the disappearance of total carotenoids in tropical forages. However, it could be a contributing factor in the wide variation in bio-availability of carotenoids of natural forages. The disappearance of dry matter (DM) and total carotenoids were measured in 4 Holstein steers (312 kg) using a mobile nylon bag technique. In situ effects and differences between forage in rumen and intestine, and total tract disappearance of DM, and total carotenoids were analyzed using the GLM procedure of SAS with Tukey multiple range test used for the comparison of means. A higher ($P < 0.05$) proportion of the dry matter and total carotenoids in the *Cynodon* spp. disappeared drastically in the rumen during the first 12 h, and after were stabilized from 24 to 72 h. A similar trend ($P < 0.05$) was evident in the disappearance of the total carotenoids in the *Cynodon* spp. Correlation value within *Cynodon* spp. between the disappearance of DM and total carotenoids in the rumen was 0.997 ($P < 0.001$). 53% of the carotenoids in the *Cynodon* spp. disappeared from the duodenal bags in the lower digestive tract when it was not incubated in the rumen. Bags with longer incubation in the rumen contain less carotenoids and therefore the efficiency of disappearance in the small intestine decreased ($P < 0.05$). In the total disappearance of carotenoids content in digestive tract was half when the grass sample was not incubated into the rumen; subsequently, the disappearance of total carotenoids in the small intestine increased in forage samples with significant differences between ruminal hours post incubation ($P < 0.05$). These results show that apparent availability in the total digestive tract was higher to 0.70 of intake. The concentration of total carotenoids in *Cynodon* spp. was 627 mg/kg DM. It is concluded that degradability of total carotenoids contained in *Cynodon* spp. is high and not all absorbed as carotenoids. Thus, the yellow color of beef fat is caused by accumulation of carotenoids in the fat depots.

Key Words: carotenoids, *Cynodon* spp., cattle

M439 The relationship between intestinal digestibility of crude protein and dry matters and the protein fractions with ruminant feedstuffs. R. Zhou, J. Q. Wang*, F. M. Pan, D. P. Bu, H. Y. Wei, and L. Y. Zhou, *State Key Laboratory*, *Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, P. R. China*.

The study was to find out the relationship between the degradation and the digestibility and the contents of each protein fractions of 11 feeds common used in China. Chemical contents were determined according to the methods provided by CNCPS Version 5.0. The mobile nylon bag technique was used to investigate the apparent small intestinal digestibility of crude protein (CP) and dry matters (DM).Three dairy cows fitted with permanent ruminal cannulas and T-type duodenal cannulas were used to investigate intestinal digestibility of CP and DM by mobile nylon bag technique in soybean meal (SBM), cottonseed meal (CSM), rapeseed meal (RSM), peanut meal (PM), flaxseed meal (FSM), linseed meal (LSM), distillers dried grains (DDGS), expanded soybean (ES), corn grain (CG), brewer's grains (BG), alfalfa hay (AH), chinese wildrye (CW) and whole corn silage (WCS). The content of undegraded DM after 16 h incubation was affected by the NDF and PB3 fractions ($r^2 = 0.9088$). The content of ruminal undegraded protein (RUP) have a high relationship with contents of the NDF and PA fractions ($r^2 = 0.6227$). The absorbed DM in intestine increased while the feeds have more NDF. The protein content absorbed in the intestine can be mainly predicted by the NDF and PC content ($r^2 = 0.7344$). In our result, we can see that the intestinal absorbed DM and CP have a high relationship with the content of each protein fractions.

Key Words: protein fractions, intestinal digestibility, ruminants

M441 Enzymatic activity of microorganisms attached to solid residues of *Festulolium*, fermentation variables and in vitro kinetics of gas production. I. Almaraz-Buendía[1], S. S. González-Muñoz*[1], O. Loera[2], L. A. Miranda-Romero[3], M. A. Cobos-Peralta[1], M. Meneses-Mayo[1], B. Alarcón-Zúñiga[3], and R. Bárcena-Gama[1], [1]*Colegio de Postgraduados*, *Montecillo, Edo. de México, México*, [2]*Universidad Autóoma Metropolitana–Iztapalapa*, *México D.F., México*, [3]*Universidad Autónoma Chapingo*, *Chapingo, Edo. de México, México*.

The objective of the present study was to determine the effect of *Festulolium*, harvested either at 28 (T1) or 35 d, on enzymatic activities from microorganism attached to this fermented substrate [IU/g DM; at 39°C and pH 6.8: after 1 h for carboxymethycellulases (CMCases) and after 30 min for xylanases], in addition to VFA, N-NH3 and in vitro DM disappearance (IVDMD). Samples of enzymatic extract (EE) were obtained at 12, 16, 24 and 48 h of fermentation. Xylanolytic activity was determined at substrate concentration ranges ensuring linear release of reducing sugars (R2 = 0.99 for up to 60 min). Maximal gas volume (Vmax), lag phase (L) and fractional rate (S) were calculated with a logistic model and PROC NLIN (SAS). The experimental design was incomplete randomized blocks with a split-plot arrangement and data was analyzed using PROC MIXED (SAS). Enzymatic activity and N-NH3 were similar among treatments ($P \geq 0.05$). The highest CMCase activity ($P \leq 0.05$) was obtained at 12 (T1:8.19, T2:7.75 IU/g DM) and 16 h (T1:7.75, T2:7.65 IU/g DM) of fermentation, whereas maximal xylanolytic levels ($P \leq 0.05$) were observed after 16 (T1:51.09, T2:46.68 IU/g DM) and 24 h (T1:51.23, T2:46.15 IU/g DM). The highest concentration ($P \leq 0.05$) of acetic (30.05 vs 42.92 mM/L), propionic (9.69 vs 12.3 mM/L) and butyric acids (8.03 vs 12.04 mM/L) were detected ($P \leq 0.05$) in T2 after 48 h of fermentation. Both maximal ($P \leq 0.05$) IVDMD and Vmax were also observed in T2, whereas L and S were highest ($P \leq 0.05$) in T1. According to these results, in vitro CMCases and xylanases from microorganism attached to *Festulolium*, harvested either at 28 or 35 d, remain unchanged; however IVDMD and gas

production kinetics did show an effect as a function of harvesting date of *Festulolium*.

Key Words: *Festulolium*, enzymatic activity, microbial attachment

M442 Use of in vitro starch and neutral detergent fiber degradation rates to predict carbohydrate availability. M. A. Brooks*, N. F. Johnson, R. M. Harvey, and M. S. Kerley, *University of Missouri*, *Columbia*.

The purpose of this in vitro experiment was to compare degradation rates (K_d) of ruminally degradable starch and neutral detergent fiber (NDF) of various feedstuffs, then use these data to predict carbohydrate (CHO) release. The feedstuffs, ground corn (GC), corn bran (CB), corn starch (CS), dried distiller's grains (DDG), soy hulls (SH), and ground alfalfa (AL), were fermented in rumen inoculum. Carbohydrate degradation was determined at 0, 4, 8, 12, 16, 24, 36, and 48 h for each feed. Undigested feed was separated via differential centrifugation (1,000 × g, 15 min) and dried at 55°C. Samples were analyzed for total starch and NDF. The time point at which degradation reached extent (no further starch or NDF was degraded) was set to 100%. Carbohydrate mass at each time point was calculated as proportion of starch or NDF remaining. Data were analyzed using proportion of potential degradation as the dependent variable with flask as the experimental unit to determine homogeneity of slope with the means adjusted to time as a covariate. Pair-wise comparisons for similarity were then done of each feed using a significance level of $P > 0.01$. Slope of the data was indicative of degradation rate over time. All R^2 values were >0.80, and since these data were evaluated as proportions and were corrected for extent of degradation, all intercepts values were similar to 1.0. The starch K_d values for AL, CB, CS, DDG, GC, and SH were 5.01, 6.08, 4.80, 5.51, 2.31, and 4.14% h^{-1}, respectively. Analysis showed GC had a slower K_d ($P < 0.01$) than all other feeds, which were not different from each other ($P > 0.01$). The NDF K_d values for AL, CB, CS, DDG, GC, and SH were 2.18, 2.24, 2.16, 2.18, 2.44, and 2.31% h^{-1}, respectively. Analysis showed no differences in NDF K_d ($P > 0.01$). Digestion of CHO in the rumen occurred at similar rates independent of feedstuff. Similarity of starch and NDF K_d across feeds, when adjusted for passage rate, makes possible prediction of CHO digestibility in the rumen by ruminal microbes and prediction of microbial growth and efficiency potential.

Key Words: starch, NDF, ruminant

M443 Effect of lysozyme-adapted *Lactobacillus acidophilus* on fermentation in an artificial rumen system (Rusitec). M. L. He[1,3], T. A. McAllister*[1], and L. M. Rode[2], [1]*Agriculture and Agri-Food Canada, Research Centre*, *Lethbridge, AB, Canada*, [2]*AB Sage Biosciences Inc.*, *Edmonton, AB, Canada*, [3]*University of Saskatchewan*, *Saskatoon, SK, Canada*.

Direct-fed microbials are increasingly being used as an alternative to subtherapeutic antibiotics in dairy and beef production because of their potential to enhance animal performance without promoting the emergence of antibiotic-resistant bacteria. Lysozyme is an enzyme that hydrolyzes the 1,4-β-linkages between N-acetylmuramic acid and N-acetyl-D-glucosamine residues in the peptidoglycan of gram-positive bacteria. The cell wall of lysozyme-adapted bacteria may exhibit increased rigidity and thereby contribute to their perseverance in highly competitive environments such as the rumen ecosystem. The Rumen Simulation Technique (Rusitec) was used to evaluate the effect of a lysozyme-adapted (L- BT1386) or a non-adapted strain (BT1386) of *Lactobacillus acidophilus*, as well as strain La 14, on ruminal fermentation. Ruminal fluid for the Rusitec was collected from 3 Holstein cows fed a 90% concentrate:10% silage diet. Sixteen fermenters (920 mL capacity; dilution rate 0.029/h) were provided fresh substrate daily (8 g steam-rolled barley grain + 2 g silage; DM basis). Four fermenters per treatment were inoculated with 5×10^{10} cfu/d of the specified strain or with buffer only. Compared with non-inoculants, L-BT1386 increased ($P = 0.04$) gas production (mL/d) and BT1386 increased ($P = 0.02$) VFA and ammonia production. Methane emissions (mL/d) were numerically greater ($P = 0.09$) in inoculated fermenters than in non-inoculants, as were disappearances (at 48 h) of DM, ADF, NDF and N from barley grain and silage ($P = 0.20$ to 0.66). Protozoal numbers were similar among treatments ($P = 0.21$) but decreased ($P < 0.05$) over time (d 9 to 18). Measured fermentation parameters did not differ between L-BT1386 and BT1386. Studies using strain-specific molecular probes are underway to determine if exposure to lysozyme increased the numbers and persistence of BT1386 within the Rusitec.

Key Words: direct fed microbials, rumen fermentation, rumen simulation technique

M444 Development of a PCR assay for the detection of *Zymomonas mobilis* in distillers grains. M. A. Rasmussen* and F. H. Benahmed, *U.S. Food and Drug Administration, Center for Veterinary Medicine, Office of Research*, *Laurel, MD*.

The objective of this project was to develop a PCR assay for the detection of *Zymomonas mobilis* (Zm) in distillers grains (DG). This bacterium can produce ethanol at rates and concentrations exceeding those of yeast. This has made Zm, an attractive alternative or supplement to *Saccharomyces cervisiae* for ethanol production. Naturally occurring Zm can only ferment glucose, fructose and sucrose and as a result there has been an ongoing effort to modify the microbe to broaden its substrate range. However, the use of Zm as a primary fermentative microorganism may alter the nutritional content of DG and the extent of its use for ethanol production is currently unknown. Therefore, we developed an assay for DG that can be used to determine if Zm is being used for ethanol production. PCR is a useful and sensitive technique that can detect the bacterium even if nonviable or nonculturable. Reference strains of Zm were obtained from the ARS culture collection in Peoria, IL and were cultivated in YP media under oxygen limiting conditions. Overnight cultures were serially diluted into buffer supplemented with Tween 20. Zm cells were harvested and tested directly by PCR. Primer sequences specific for Zm targeted a 900 bp rRNA overlapping region of the 16s gene Z16p3 and the 23s gene Z23p5. For tests in the relevant matrix, the assay was tested on DG samples inoculated with serial dilutions of Zm cells. A single PCR band was visualized in all Zm strains investigated and no band was observed in the negative control DG matrix. Additionally, plate culture was used for assay optimization and confirmation. The limit of detection for the PCR assay was determined to be 10 cfu/ml of the DG wash/suspension buffer or 100 cfu/g of DG. Current activities are directed at optimizing the assay for use with DG field samples to determine if Zm is present. In conclusion, this assay can be used to test for Zm and is more rapid and sensitive than traditional culture methods.

Key Words: distillers grains, *Zymomonas*, bioethanol

M445 Intake prediction using *n*-alkanes in beef cattle fed a mixture of switchgrass and alfalfa hay. S. J. Chavez*, C. Baum-Lane, E. Leonard, J. Burns, and G. B. Huntington, *North Carolina State University*, *Raleigh*.

The objectives of the study were to use *n*-alkanes to predict intake in beef cattle fed mixed forage and to predict intake of forage constituents based

on forage alkane concentrations. In May and June 2009, 11 Angus-cross steers and 1 heifer (BW = 283 ± 25 kg) were housed under a roof on expanded metal flooring with access to 6 feeding stations. Cattle were fed 1 kg of a soyhull and corn supplement once daily at one feeding station that was sprayed with dotriacontane (C32) and hexatriacontane (C36). Cattle consumed approximately 300 mg each of C32 and C36. Cattle were offered a switchgrass:alfalfa (3:1 as fed) mixed hay at 0.6% BW at each feed station. Hay was ground in a hammer mill to minimize sorting. Periods consisted of one week adaptation followed by 14 d of feeding supplement with added alkanes. Fecal grab samples were collected between 0800 and 1000 during the last 5 d. Fecal samples were stored frozen and oven-dried to constant weight at 60°C. Hay and fecal samples were saponified, alkanes were extracted with heptane, and samples analyzed by gas chromatography for alkane concentrations. One steer was removed from data analysis due to inconsistent eating and rear leg inflammation and another was removed for highly variable fecal ratios of hentriacontane (C31) and C32. Tetratriacontane (C34) was used as an internal standard for saponification and extraction with recoveries ranging from 80 to 90%. When feed and fecal ratios of C31 and C32 were used in prediction equations, predicted daily DMI (5.96 ± 0.70 kg) was not different ($P < 0.35$) from measured intake (5.51 ± 0.68 kg). Using simultaneous equations and concentrations of nonacosane (C29) and C31 in the hays, the predicted ratio of switchgrass:alfalfa (3.09:1) was similar to the actual ratio. Using C36, predicted digestibility was 58.7 ± 2.2% for the switchgrass and alfalfa hay. Alkanes can be used to predict intake in cattle fed a mixed forage diet and also predict the proportion of each forage consumed.

Key Words: cattle, alkane, intake

M446 A comparison of methods to evaluate in vitro intestinal digestibility. D. A. Ross*, M. M. McCullouch, and M. E. Van Amburgh, *Cornell University*, *Ithaca, NY*.

Various assays are used to evaluate the intestinal digestibility of dry matter (DM) and nitrogen (N) in ruminant feeds (Casamiglia and Stern, 1995; Gargallo et al. 2006). The objective of this study was to evaluate in vitro (IV) intestinal digestibility of DM and N of 7 feeds (fishmeal, corn silage, alfalfa silage, 2 soy products and 2 DDG) following in situ (IS) or ruminal IV procedures. We wanted to determine if ruminal IV or IS exposure or length of exposure altered the IV intestinal digestibility and further, if the pore size of the incubation bag affected variation of the assay. Samples (0.5g) were placed in 3 pore size (15, 25 or 50 µm) bags (5 × 5 cm) and incubated for 12-h or 24-h ruminal digestion either IS or IV (Daisyincubator, Ankom, Macedon, NY) followed by IV intestinal digestion (modified Gargallo et al. 2006). Empty bags were incubated for correction. Data were analyzed as a factorial design using GLM in SAS and Tukey's method to separate means. Incubation time in the rumen or rumen fluid affected digestibility, but there was no difference in IV intestinal digestibility based on ruminal exposure time (Table 1). Digestibility of DM and N_DM were significantly lower in the 25 µm pore bags; however no differences among bag pore sizes were detected for IV intestinal digestion parameters. The effect of bag pore size for ruminal IV or IS digestion was not linear, due to characteristics of the bag material and will be discussed.

Table 1. The mean (± SD) values for digestible DM and N

	RDM	RNDM	TDM[1]	TNDM[1]
n	164	163	159	159
RumDigTime				
IV12	0.43 ± 0.13[a]	0.68 ± 0.15[a]	0.78 ± 0.18	0.98 ± 0.04
IV24	0.43 ± 0.13[†]	0.71 ± 0.15[a]	0.80 ± 0.17	0.98 ± 0.03
IS12	0.43 ± 0.13[a]	0.59 ± 0.16[b]	0.82 ± 0.18	0.98 ± 0.05
IS24	0.53 ± 0.17[b†]	0.70 ± 0.18[a]	0.85 ± 0.15	0.98 ± 0.04
BagPore,µm				
15	0.47 ± 0.13[a]	0.69 ± 0.14[a]	0.82 ± 0.17	0.99 ± 0.02
25	0.39 ± 0.13[b]	0.58 ± 0.17[b]	0.78 ± 0.18	0.97 ± 0.05
50	0.52 ± 0.15[a]	0.74 ± 0.15[a]	0.84 ± 0.16	0.98 ± 0.04

[ab]Means with different letters are significant, $P < 0.05$.

[†]Common superscript show trends, $P < 0.10$.

[1]Cumulative digestion.

Key Words: in vitro, in situ, intestinal digestion

M447 The role of ADIN in determining nutrient availability in new co-products from bio-ethanol processing. W. G. Nuez-Ortín* and P. Yu, *Department of Animal and Poultry Science, College of Agriculture and Bioresources, University of Saskatchewan*, *Saskatoon, SK, Canada*.

The objectives of this study were to investigate the role of acid detergent insoluble nitrogen (ADIN) in determining the nutrient availability in the new co-products of bio-ethanol processing and the relationship between ADIN content and nutrient utilization of the bioethanol co-products in ruminants. The corn DDGS, wheat DDGS and blend DDGS (70% wheat: 30% corn), and wheat and corn samples with 3 to 5 different batches were obtained during 2007–2008. The results showed that compared with the grains, DDGS contained higher ($P < 0.05$) acid detergent insoluble crude protein (ADICP) level from 1.2 to 7.6%CP vs. 0 to 0.1% crude protein (CP) in the grains. However, all ADICP levels were lower than 13% of total CP across DDGS samples, revealing no effects ($P > 0.05$) on protein ruminal digestion with a correlation between ADICP and rumen-degradable protein (RDP): R = −0.08, $P = 0.74$. However, the difference in the ADICP content was reflected in largely numerical differences in the intestinal digestibility of rumen-undegradable protein (RUP) in vitro, which ultimately affected ($P < 0.05$) the intestinal availability of RUP (ARUP) as well as the predicted total post-ruminal protein supply and availability (the correlation between ADICP and metabolizable protein (MP): R = −0.74, $P < 0.05$). This suggests a higher sensitivity to low ADICP levels in the rumen than that in the small intestine in the DDGS samples.

Key Words: nutrient utilization and availability, bio-ethanol co-products, ADIN

M448 A comparison of models used to estimate kinetics of in vitro degradation of alfalfa hay dry matter. C. A. Old*[1] and D. A. Sapienza[2], [1]*California Chapter of the American Registry of Professional Animal Scientists*, *LeGrand, CA,* [2]*Sapienza Analytica, LLC*, *Des Moines, IA*.

To determine more accurately alfalfa hay quality California ARPAS undertook a project to estimate metabolizable energy, rate, site and extent of degradability of selected chemical and proximate entities and use these as part of a set of prediction equations in near infrared (NIR) spectrophotometry. This study had in vivo, in vitro and in silico components based on 150 samples of alfalfa hay collected during the

2008 growing season in California. The diversity of samples can be seen from the range of crude protein and acid detergent fiber content, the former was 13 percentage points and the latter 30 percentage points. Samples for in vitro analysis were ground through a 6-mm screen and incubated from 1 to 120 h. Losses of N were calculated from 16-h amino acid losses and averaged 63%. Disappearance of individual amino acids ranged from a low of 57% (Leu) to a high of 75% (Pro). Variation in losses among samples was less than variation among amino acids. Dry matter losses, at 120 h, averaged 80.2%. Kinetics of in vitro dry matter degradation were estimated using a heterogeneous, stochastic model assuming a gamma distribution of rates (HS): $C_t = D(1+\beta[t-\tau])^{-\alpha}+I$, a single exponential deterministic model (SE): $C_t = C_0e^{-kt}$ and a biexponential deterministic model (BE):$C_t = C_{01}e^{-k1t}+ C_{02}e^{-k2t}$. C_t is the residue at time t, D is the degradable fraction, β and α are shape parameters of a gamma distribution, τ is lag time, I is the undegradable fraction,C_{0n} is compartment n at time 0 and k_n is the rate constant for compartment n. Average residual sum of squares for models HS, SE and BE were 0.012, 4.29 and 0.160, respectively. As a result of this study, kinetics of alfalfa hay degradation will be described in the NIR model using a heterogeneous, stochastic model.

Key Words: alfalfa hay quality, kinetic models, amino acids

M449 Application of near infrared spectroscopy to estimate composition of NuPro. G. A. Harrison*, M. D. Meyer, E. C. Taylor, and K. A. Dawson, *Alltech*, *Nicholasville, KY*.

The properties of near infrared spectroscopy (NIR) make this technology attractive in quality assurance programs. Provided reliable reference methods are utilized to determine component concentrations in calibration samples, NIR can potentially replace routine wet chemistry. The objective of this project was to determine the feasibility of using NIR to estimate the composition of NuPro (an extract of a select yeast strain containing a combination of amino acids, peptides, nucleotides, inositol, and glutamic acid) in the Alltech Quality Assurance Program. From an initial 239 NuPro samples, 100 calibration samples and 20 test samples were randomly selected with equal representation from each of 2 manufacturing sites. Samples were scanned in triplicate using a Bruker MPA FT-NIR Spectrometer (Bruker Optics, Inc., Billerica, MA). For each component, 3 calibration models were developed using cross validation and various spectral preprocessing methods. Multiple criteria were utilized to determine the best fit model including coefficient of determination (R2), root mean square error of cross validation (RMSECV), and residual prediction deviation (RPD). Additionally, NIR-predicted values of test samples were compared with values measured by reference methods. Bias and percentage of samples with predicted values within 5 and 10% of measured were calculated. A 2-tailed paired *t*-test was used as the final criterion. The best fit DM model had an R^2 of 84.6, RMSECV of 0.479, and RDP of 2.55 with 100% of samples were within 5%. The best fit N model had an R^2 of 93.0, RMSECV of 0.072, and RDP of 3.77 with 100% of samples within 5%. For total nucleotides, the best fit model had an R^2 of 86.6, RMSECV of 0.603, and RDP of 2.73 with 60 and 80% of samples within 5 and 10%, respectively. Statistical analyses by paired *t*-test found no difference between measured and predicted values for DM, N, C, H or total nucleotides ($P > 0.10$). For quality assurance purposes, composition of NuPro can be estimated through the use of NIR models.

Key Words: near infrared spectroscopy, quality assurance

M450 Ability of NIR to predict crude fat, fatty acids and unsaturated fatty acids in total mixed ration fed to dairy cattle. S. Weaver*[1], R. Ward[1], and R. A. Patton[2], [1]*Cumberland Valley Analytical Services*, *Maugansville, MD*, [2]*Nittany Dairy Nutrition*, *Mifflinburg, PA*.

It is known that formation of CLA due to consumption of high levels of linoelic and linolenic acids may have a negative effect on milk fat production depending on the rumen environment. Determination of the amounts and types of fatty acids (FA) in total mixed rations (TMR) would allow nutritionists to better control these elements. At present determination of fat and FA percent as well as individual fatty acid amounts is expensive and time consuming. We postulated that NIR has the potential to rapidly and inexpensively predict the amount of fat, percentage of FA, and the FA composition of this fat in TMR. A data set of 89 individual TMR samples were analyzed for crude fat by the AOAC method for feeds (2003.05). Fatty acids were analyzed as methyl esters on a Restek 30 m capillary column (90% biscyanopropyl / 10% phenylcyanopropyl polysiloxane) using a Perkin Elmer Autosystems GC with a flame ionization detector using the method of Sukhija and Palmquist (1988. J. Agric. Food Chem. 36:1202–1206). Comparisons of observed versus NIR predicted values were by the MSPE method described by Bibby and Toutenburg (1977). NIR predicted crude fat values were close to values for chemically defined fat (observed mean = 4.68, predicted mean = 4.74, RMSPE = 0.45 with 96% random error). The prediction of total FA was even more precise (observed mean = 3.63, predicted mean = 3.63, RMSPE = 0.2 with 99% random error). However, predictions of individual unsaturated fatty acids, although reasonable for mean values, displayed considerable regression bias. This suggests that further research may yield better NIR prediction equations for individual fatty acids.

Key Words: fatty acids, TMR, NIR

M451 Evaluation of models to predict passage rate in cattle. S. J. Krizsan*[1], S. Ahvenjärvi[2], and P. Huhtanen[1], [1]*Department of Agricultural Research for Northern Sweden, Swedish University of Agricultural Sciences*, *Umeå, Sweden*, [2]*MTT-Agrifood Research Finland, Animal Production Research*, *Jokioinen, Finland*.

The passage rate (k_p) prediction equations in the National Research Council (2001) and the Cornell Net Carbohydrate and Protein System (CNCPS) were evaluated with compiled data of rumen evacuation studies. Data were comprised of 172 treatment means from 49 studies conducted in Europe and in the USA. A total of 145 diets were fed to dairy cows and 27 to growing cattle. The primary objectives of the trials included in the database were to study dietary effects on digestion and passage kinetics of fiber fractions. The concentration of indigestible NDF (iNDF) was determined by long-term ruminal incubations or in vitro incubations in rumen fluid. National Research Council (NRC) and CNCPS give separate k_p prediction equations for concentrate and forage feed. Therefore, an aggregated k_p was calculated according to: k_p (%) = 100 × Flux of indigestible component into the compartment (kg/h) / Rumen pool of indigestible component (kg). Preferably intake of iNDF of forage and concentrate (n = 165), else intake of NDF from forages and concentrates (n = 7) were used to calculate the aggregated k_p. Rumen pool sizes of iNDF and NDF were defined separately for concentrate and forage feed and total pool size was estimated from the sum. Mixed model regression analysis including a random study effect was used to investigate the relationships between NRC and CNCPS predictions and observed k_p of iNDF. Prediction equations were evaluated by regressing residual values on the predicted values. Relationships between predicted and observed k_p were $y = 0.53(\pm0.187) + 0.41(\pm0.0373)x$ and $y = 0.58(\pm0.162) + 0.46(\pm0.0377)x$ for the NRC and CNCPS models, respectively. Residual analysis of the NRC and CNCPS models resulted

in both significant ($P < 0.001$) mean biases of −2.40 and −1.70% and linear biases of −0.59 and −0.53, respectively. This evaluation suggested that both the NRC and CNCPS models grossly overestimated ruminal particulate matter k_p.

Key Words: cattle, evaluation, passage rate

M452 Net portal absorption of energy nutrients in ruminants: Assessment of prediction models. C Loncke*[1], P Nozière[1], G Kraft[1], I Savary-Auzeloux[1], J Vernet[1], H Lapierre[2], D Sauvant[3], and I Ortigues-Marty[1], [1]*INRA, UR 1213*, *Theix, France*, [2]*Agriculture and Agri-Food Canada*, *Sherbrooke, QC, Canada*, [3]*INRA-AgroParisTech, UMR 791*, *Paris, France*.

In ruminant nutrition, the evolution of feed evaluation systems toward nutrient-based systems is an important challenge. Net portal appearance (NPA) of total VFA, acetate (C2), propionate (C3), butyrate (C4), glucose, β-hydroxybutyrate (BHBA), and lactate can be estimated with response equations based on ration intake and composition characterized according to INRA Feed Tables for Ruminants and derived from meta-analyses on the FLORA database. The present objective was to evaluate the models using the results of a recent study, conducted on 6 growing lambs, catheterized at the portal level. The lambs were fed 3 diets made of 30% hay and 70% of 1 of 3 concentrates, according to a Latin Square design. The control diet (C) was designed to offer a balanced and adequate supply of protein and ME for growing lambs according to INRA allowances. Low nitrogen (LN) and energy (LE) diets presented a 23% and 20% deficit in protein and ME supply respectively compared with the C diet. To evaluate the prediction ability of the models, observed (Y) and predicted NPA (X) was compared using a GLM model including a within-animal effect. The slopes obtained were equal to 0.88 ± 0.13, 0.78 ± 0.21, 1.06 ± 0.22, 0.88 ± 0.22, 0.80 ± 0.25, 1.30 ± 0.50, respectively for total VFA, C2, C3, C4, BHBA and lactate NPA and proved not different from 1. Moreover the intercepts of all models were not different from 0 ($P > 0.2$). The slope (12.4 ± 2.4) of the relation between observed and predicted values of glucose NPA showed a lower adjustment probably due to larger uncertainties on the ruminal starch degradability required for the prediction. In most cases the best prediction was observed for the C diet probably because diet compositions of LN and LE were not fully included in the meta-design range of validity used to establish the models. In conclusion, this work suggested that the energy nutrients NPA could be predicted with a good accuracy.

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Key Words: meta-analyses, energy nutrients, ruminants

Small Ruminant: Sheep Production 1

M453 Milk yield and composition from dairy ewes fed two sources of lipid supplements associated or not with conjugated linoleic acid (CLA). M. Baldin[1], R. Dresch[1], J. Souza[1], E. C. Sandri[1], F. Batistel[1], E. Ticiani[1], A. Panzera[1], L. O. Tedeschi[3], M. A. S. Gama[2], D. Fernandes[1], and D. E. Oliveira*[1], [1]*Santa Catarina State University*, *Chapecó, Brazil*, [2]*National Dairy Catlle Research Center*, *Juiz de Fora, MG, Brazil*, [3]*Texas A&M University*, *College Station*.

It is known that rumen-protected lipid (RPL) supplements or CLA may affect milk fat content in dairy ewes, but their combination has not been fully investigated. The objective of this study was to evaluate the effects of 2 sources of RPL with or without CLA supplement (29% t-10 c-12 and 29% c-9 t-11 isomers) on milk yield and milk composition of dairy ewes. Thirty-six East Friesian ewes (50 to 70 DIM) were used in a 2 × 2 factorial design and received the following treatments: 1) 30 g of calcium salts of long chain fatty acids from soybean oil (LCFAS); 2) 27 g of calcium salts of long chain fatty acids from palm oil (LCFAP); 3) 30 g of LCFAS plus 20 g of CLA; and 4) 27 g of LCFAP plus 20 g of CLA. The lipid supplements were isocaloric. CLA, LCFAS, and LCFAP were added into a corn-based concentrate (1.0 kg/d, as-fed) and individually fed twice daily after morning and afternoon milkings. Ewes were grazing *Panicum maximum* Jacq. cv. Aruana pasture during the experimental period (53 d) of which 5 d were used for adaptation, 40 d for data collection, and 8 d for residual effects. Data were analyzed in a repeated measure design, including RPL, CLA, d, and their interactions as sources of variation. Milk yield was unaffected by CLA (1.17 kg/d; $P = 0.64$) and RPL (1.15 kg/d; $P = 0.95$). There was an interaction between CLA and RPL ($P = 0.02$) for milk fat content. For ewes receiving CLA, milk fat content was similar ($P = 0.49$) between LCFAP and LCFAS (4.31 vs. 4.18%, respectively). However, when CLA was not fed, milk fat content was greater ($P = 0.004$) for ewes receiving LCFAP compared with those receiving LCFAS (6.27 vs. 5.52%, respectively). LCFAP increased ($P = 0.02$) milk protein content compared with LCFAS (4.96 vs. 4.77%, respectively). Even though RPL and CLA did not impact milk yield, the source of RPL may affect milk fat composition when CLA is not provided to lactating dairy ewes.

Key Words: cojugated linoleic acid, lactating dairy ewes, milk composition

M454 New management technique in early lactation can improve profitability in dairy sheep farms. S. P. G. Rassu, C. Carzedda, A. Mazzette, C. Dimauro, A. Mazza, and G. Pulina*, *Dipartimento di Scienze Zootecniche, University of Sassari*, *Sassari, Italy*.

The effect of 2 management techniques on farm profitability of dairy Sarda ewes was tested. During the suckling period, i.e., the first month of lactation, 22 Sarda ewes (2–4 year old) were used. Eleven ewes (SL group) were separated from their lambs, starting from 5 d after birth, from 0800 to 1600 h, fed on pasture and milked one time per day before to be rejoined with their lambs. The other 11 ewes (NSL group) were fed on pasture, never separated from the lambs, and milked at the same time of SL group. Lambs of SL group were also supplemented with a commercial feed (0.40 €/kg) to compensate for less available milk. All lambs were slaughtered at 25 d of age. Milk yield of ewes, and body weight of lambs were recorded during the sucking period. Moreover, milk yield, fat and protein contents of ewes were measured during the month after lamb slaughtering. Data were analyzed by a GLM model, using management (SL and NSL), date of the measurement sampling and their interaction as fixed factors. Milk yield was higher in SL compared with NSL group both during suckling period (g/d 645 ± 38 vs 83 ± 38; $P = 0.000$) and during first month after lambs slaughtering (g/d 1494 ± 31 vs 1334 ± 33; $P = 0.001$). Body weight at slaughter (SL kg 11.4 ± 0.2 vs NSL kg 11.1 ± 0.2; $P = 0.563$) and daily growth of lambs (SL g/d 267 ± 9 vs NSL g/d 263 ± 9; $P = 0.703$) were not different between experimental groups as well as milk fat (SL 5.46% ± 0.09 vs NSL 5.67% ± 0.09; $P = 0.087$) and milk protein content (SL 5.12% ± 0.05 vs NSL 5.06% ± 0.05; $P = 0.323$). Therefore, profitability of SL group was higher than NSL group, in particular during suckling period. Indeed, return of the SL group is equal to 0.393 €/head/d (gain from milk = production 0.645 g/head/d × 0.650 €/kg of milk) minus 0.026 €/lamb/d cost of feeding lambs (pellet feed consumed 65 g/head/d × 0.40 €/kg of pellet) that is equal to about 8.0 €/head in 25 d of suckling. Return of the NSL group is equal to 0.054 €/head/d (no cost for lambs feeding and little gain from milk) that is equal to about 1.0 €/head on the same period.

Key Words: sheep, milk, lamb

M455 Assessment of milk yield and milk composition in ewes fed diets with canola, sunflower or castor oil. M. O. Maia*, I. Susin, A. V. Pires, E. M. Ferreira, R. S. Gentil, C. Q. Mendes, D. B. Galvani, and A. L. M. Selegato, *University of São Paulo/ESALQ*, *Piracicaba, SP, Brazil*.

The inclusion of fat sources in ruminant diets is an alternative to achieve nutritional requirements, especially in early lactation. Additionally, vegetable oils can modify milk fatty acid profile. Forty-four Santa Inês ewes (66.6 ± 4.9 kg BW and 14 ± 3 d in milk) were penned individually and used in a complete randomized block design to determine the effects of adding canola, sunflower or castor oil on DMI, milk production, and milk composition. Ewes were fed a basal diet (14.7 ± 0.1% CP, DM basis) containing 50% concentrate and 50% coastcross hay. The 4 treatments included control (0% oil, CONT), canola oil (3%, CAN), sunflower oil (3%, SUN) or castor oil (3%, CAS). Ewes were fed the diets from the wk 2 to 8 of lactation. Milk production was determined every 7 d during the experiment. Ewes were separated from lambs, oxytocin (10 IU) was infused i.v. to stimulate milk letdown, and ewes were mechanically milked. After 3 h, the procedure was repeated and milk production was recorded and a sample collected for milk composition analysis. Ewes were weighed for 3 consecutive days at the start and end of the experiment. Data were analyzed using SAS PROC Mixed procedure and means compared by Tukey Test. Dry matter intake was greater ($P \leq 0.01$) for ewes fed CONT diet (2.48 kg), whereas, no effect was observed on DMI among diets with oil inclusion (2.06, 2.18, and 2.09 ± 0.03 for CAN, SUN, and CAS, respectively). Milk production, milk protein and milk lactose were not different ($P \geq 0.05$) among diets. However, milk fat (7.9, 8.2, 7.7, and 9.3 ± 0.12% for CONT, CAN, SUN, and CAS, respectively) and total solids (18.6, 18.7, 18.6, and 20.0 ± 0.12% for CONT, CAN, SUN, and CAS, respectively) concentrations were greater ($P \leq 0.001$) for ewes fed the diet containing castor oil. There was no difference on BW change among treatments. In conclusion, the addition of oil regardless of source decreased DMI, but no effect on milk production was observed. Milk fat was increased with the inclusion of castor oil in lactation diets.

Key Words: lipids, oil source, Santa Inês

M456 Effect of different vegetable oils fed to lactating ewes on milk and cheese fatty acid profile. R. Bodas[1], P. Gómez-Cortés[2], A. R.

Mantecón[1], M. Juarez[2], M. A. De la Fuente[2], and T. Manso*[3], [1]*Instituto de Ganaderia de Montaña (CSIC-ULE)*, *León, Spain*, [2]*Instituto del Frío (CSIC)*, *Madrid, Spain*, [3]*E.T.S. Ingenierías Agrarias (Universidad de Valladolid)*, *Palencia, Spain*.

The aim of this study was to evaluate the effects of different vegetables oils fed to lactating ewes on milk and cheese fatty acid (FA) profile. After lambing, 48 Churra ewes were fed 2.1 kg of 40:60 (as-fed basis) lucerne:concentrate total mixed ration (TMR) daily and were milked twice a day. Ewes were assigned to 1 of 4 groups, which received 3% (as-fed basis) of the corresponding oil added daily to the TMR: hydrogenated palm oil (Con), olive oil (Oli), soybean oil (Soy) or linseed oil (Lin). On d 55 of lactation, 3 cheeses per treatment were made from the milk and samples of milk and cheeses were collected for FA analyses. The data were subjected to ANOVA according to a 2 (milk and cheese) by 4 (oils) factorial design using the MIXED procedure of SAS. Regardless the type of oil added to the diet, milk and cheese FA profiles were not different ($P > 0.10$). Cheese and milk samples from Con treatment had the greatest saturated FA (SFA) contents, but the least long chain FA (LCFA, > 18C), vaccenic (VA), and rumenic (RA) acid contents ($P < 0.001$). Milk and cheese from Soy treatment had the least SFA ($P < 0.001$), but the greatest VA, RA and linoleic acid contents and n6/n3 ratio ($P < 0.001$). Lin and Soy ewes produced milk and cheese with the greatest amount of polyunsaturated FA ($P < 0.001$). Olive oil supplementation increased oleic acid and decreased linoleic acid content ($P < 0.001$), whereas Lin gave raise to the greatest linolenic acid content and the least n6/n3 ratio ($P < 0.001$). From the results observed, it can be concluded that supplementing the diet of lactating ewes with oils is a suitable way of modulating naturally the FA profile of their milk and cheese.

Key Words: cheese, fatty acids, sheep

M457 Milk performance of ewes fed fish oil and soybean oil. E. M. Ferreira*, A. V. Pires, I. Susin, C. Q. Mendes, S. Gilaverte, R. S. Gentil, M. O. Maia, D. B. Galvani, and R. C. M. Meneghini, *University of São Paulo/ESALQ*, *Piracicaba, SP, Brazil*.

Dietary fish oil in combination with linoleic or linolenic fatty acid source consistently increases milk vaccenic and conjugated linoleic fatty acid concentrations. However, inclusion of fish oil in the diet can decrease DMI and milk production. Fifty Santa Inês ewes (64.9 ± 5.9 kg BW and 18 ± 2 d in milk) were used in a complete randomized block design and assigned to individual pens to determine the effects of replacing soybean oil with fish oil on lactation performance. The control diet (CONT) contained 29% forage (sugarcane bagasse) and 71% concentrate on a DM basis. In the remaining 4 treatments, fish oil replaced soybean oil (4% on DM basis) at 0, 0.25, 0.50, and 0.75%. Ewes were fed the diets from wk 2 to 8 of lactation. Milk production was measure every 7 d during the trial. Ewes were separated from lambs, oxytocin (10 IU) was infused i.v. to stimulate milk letdown, and ewes were mechanically milked. After 3 h, the procedure was repeated and milk production was recorded and a sample collected for milk composition analysis. Preplanned contrasts were supplemental fat (soybean oil or fish oil) versus no fat and linear, and quadratic contrast of fish oil inclusion. Dry matter intake (2.34, 2.12, 2.13, 2.07, and 2.11 ± 0.02 kg/d for CONT, 0FO, 0.25FO, 0.50FO and 0.75FO, respectively) was greater ($P < 0.01$) for ewes fed the CONT diet vs. fat inclusion, whereas, no effect ($P > 0.05$) was observed on DMI with fish oil inclusion. A linear increase ($P < 0.01$) for milk production (184.1, 190.2, 207.2, and 220.9 ± 4.5 g/3 h for 0FO, 0.25FO, 0.50FO and 0.75FO, respectively) was shown with fish oil inclusion. Milk fat concentration was similar ($P < 0.05$) for all diets. Milk protein (4.8, 4.7, 4.5, and 4.5 ± 0.04% for 0FO, 0.25FO, 0.50FO and 0.75FO, respectively) and total solids (18.0, 17.5, 17.4, and 17.3 ± 0.01% for 0FO, 0.25FO, 0.50FO and 0.75FO, respectively) concentrations decreased ($P < 0.01$) linearly with fish oil addition. Milk lactose (4.6, 4.8, 4.8, 4.8, and 4.8 ± 0.02% for CONT, 0FO, 0.25FO, 0.50FO and 0.75FO, respectively) concentration was greater ($P < 0.05$) for ewes fed the fat-supplemented diets vs. the control. In conclusion, replacing 4% soybean oil with fish oil up to 0.75% of the diet improved milk production without detrimental effect on DMI.

Key Words: milk production, sheep, fish oil

M458 Evaluation of inbreeding depression effect on birth weight of Baluchi sheep breed of Iran. G. Motaghinia*[1], H. Farhangfar[1], M. Bashtani[1], A. Shadparvar[2], H. Saraee[1], H. Janati[3], and J. Modarresi[4], [1]*Birjand University*, *Birjand, Iran*, [2]*Guilan University*, *Rasht, Iran*, [3]*Baluchi Sheep Breeding Station*, *Mashhad, Iran*, [4]*Agricultural Jihad Organisation*, *Birjand, Iran*.

The main objective of this research was to estimate the effect of inbreeding on birth weight of Baluchi sheep breed of Iran. A total of 13,007 birth weight records was utilized. The data were collected from 13,007 lambs (born from 1984 to 2006) in Baluchi sheep breeding station, northeast region of Iran. The lambs were born between December and April. Birth weight average was 4.27 kg. Inbreeding coefficient was calculated for individual lambs using pedigree software. In the data set, minimum and maximum of the inbreeding coefficient were 0 and 0.321, respectively. Dependent variable was birth weight and the data were analyzed by a Mixed Linear Model applied in SAS software. In the model, fixed main effects of herd, year and month of birth, lamb sex, birth type, as well as 2-way interactions between herd and month of birth, sex and birth type, year and sex, year and birth type, month and sex, month and birth type, herd and birth type, and between herd and lamb sex were included. Dam age and coefficient of inbreeding were also included in the model as covariables. The results indicated that dam age (linear and quadratic terms), year and month of birth, sex and birth type of lamb, interactions between year and birth type, sex and birth type and herd and birth type had significant influences on birth weight ($P < 0.05$). Regression coefficient of birth weight on inbreeding was found to be −343 g but it was not statistically significant.

Key Words: Baluchi sheep, birth weight, inbreeding

M459 Cubicle use and maternal bonding in sheep: tests of an alternative lambing management strategy. N. L. Pettifor* and M. L. Thonney, *Cornell University*, *Ithaca, NY*.

Many farm flocks are intensively managed while lambing in barns, where ewes are often kept in high-density areas and moved with their lambs to claiming pens shortly after lambing. Other methods may improve the process of maternal bonding and use less labor. One alternative to traditional lambing management uses "cubicles," open 2.4 × 1.5 m pens in which ewes may choose to isolate themselves at lambing time. As ewes on pasture will naturally seek isolation at lambing, it is expected that more ewes would choose to lamb in the privacy of a cubicle. Additionally, time spent on the birth site may increase the strength of a ewe's bond with her lambs because lambing in a cubicle avoids the disruption of being moved from a lambing area to a claiming pen. To test the cubicle concept, 43 Dorset, Finnsheep, and Dorset × Finnsheep ewes were lambed in a cubicle system. Ewes were regularly added to the lambing area to maintain a stocking density of 1.9 to 2.3 m^2 per ewe and were video-recorded 24 h per day for the duration of the lambing season. An additional 110 ewes were managed traditionally, using claiming pens. After the end of the lambing period, ewes from the traditional system were compared with 2 groups of ewes from the

cubicle system: one set that did use cubicles and another set that did not. Two behavioral tests of maternal bonding, also video-recorded, were used to compare these groups: a 2-choice discrimination task and a modified maternal behavior score (MMBS, 1 to 5) test. Ewes did not preferentially lamb in cubicles: 23.3% of recorded ewes were located in cubicles when they lambed; 29.6% of the total lambing area consisted of cubicle space. MMBS scores were not statistically different between cubicle-using and non-using experimental ewes (4.33 and 4.05 ± 0.47, respectively), but were higher ($P = 0.26$) than the value of 3.15 ± 0.47 for the traditionally managed group. The cubicle approach appeared to result in easier sheep movement and reduced shepherding, and may have improved maternal behavior.

Key Words: behavior, maternal, sheep

M460 Selective genotyping using genome-wide association studies (GWAS) that are associated with fiber diameter in Merino sheep. M. Goher*, W. Rauw, D. Thin, and L. Gomez-Raya, *University of Nevada Reno*, *Reno*.

The objective of this study was to investigate methods and statistical power for mapping quantitative trait loci (QTL) using selective genotyping and Illumina's 50K BeadChip. A large unrelated population is recorded for a phenotypic trait. Animals with extreme phenotypes are used for genotyping with Illumina's arrays and QTL are mapped by linkage disequilibrium (LD). We carried out computer simulations to compute statistical power using this approach after varying QTL allele frequency, proportion selected in the extremes, and population size. For example, power for a population of 1,000 animals after genotyping the top and bottom 5% (QTL effect of 0.5 phenotypic standard deviations, α of 0.01 and allele frequency of 0.1) and assuming maximum LD, was 0.95. The method was tested in a Merino flock with 979 ewes in which fiber diameter (FD) was recorded. Illumina 50K BeadChip was used for simultaneous genotyping of 54,000 SNPs in selected animals. Three different approaches were used to rank and to use selective genotyping of animals: 1) extreme phenotype for FD, 2) extreme estimated breeding value for FD, and 3) extreme phenotypes within the year class with the highest number of animals. Statistical tests were carried out comparing the number of copies for each of the 2 alleles at each SNP in the 2 extreme phenotypes (top and bottom 5%). No genome-wide significant results were obtained when using extreme phenotypes for FD. Analyses using extreme estimated breeding values and extreme phenotypes from the largest year class are currently in progress.

Key Words: GWAS, statistical power, selective genetyping

M461 An alternative wool harvesting system for wool sheep flocks. T. Wuliji*[1], T. Watts[2], A. Qi[1], and T. Filbin[3], [1]*University of Nevada*, *Reno,* [2]*Heiniger Australia Pty*, *Perth, Western Australia, Australia*, [3]*Rafter 7 Ranch*, *Yerington, NV*.

The objective of this investigation is to evaluate the efficacy of a biological wool harvesting system-Bioclip as an alternative to mechanical shearing of the wool sheep flocks in the US, which mostly farmed for meat and wool dual production. Bioclip reagent was developed for a biological wool harvesting in Merino breed or its derived sheep in Australia. Twenty-two 10-mo-old ewes were selected for Bioclip shearing comparison experiment. Ewes were weighed and stratified by BW and breed, and divided into a control (conventional shearing, n = 10) and Bioclip treatment group (n = 12). Treatment group animals were each given 2.5 mL Bioclip injection formula (7.5 mg/ml epidermal growth factor (EGF) subcutaneously on the inguinal bare skin area, and subsequently put fleece retention net on them. Animals were fed alfalfa hay for 4 wk under a semi-sheltered pen until fleece removal at 28 d later. Post treatment wool re-growth was monitored and compared for the control and bio clipped groups. After 5 wk re-growth, wool fiber length (mm) and weight (mg/cm^2) collected from the mid side skin patch area was measured, analyzed and compared for differences. Data were analyzed for one-way ANOVA and mean values compared using *t*-tests. Bioclip injection resulted a simultaneous and complete shedding of fleeces in all treated animals. There was no difference in post treatment BW, weight gain, fiber diameter and wool re-growth rate between control and Bioclip treatment. However, fleece staple length and re-growth fiber length measured significantly ($P < 0.01$) longer for Bioclip harvested wool than conventional shorn sheep. The results suggest that Bioclip can improve wool clip quality, animal welfare, and farm labor intensity. Therefore, Bioclip may be used as an alternative biological wool harvesting system to the traditional mechanical shearing procedure for wool sheep flocks.

Key Words: biological wool harvest, epidermal growth factor, Merino sheep

M462 Comparison of two instruments for measuring fiber characteristics of wool. F. A. Pfeiffer*, C. J. Lupton, and D. F. Waldron, *Texas AgriLife Research*, *San Angelo*.

An experiment was designed to compare an on-farm OFDA2000 instrument with a lab instrument, the OFDA 100 (BSC Electronics, Ardross, W. Australia). The OFDA 100 measures average fiber diameter (AFD) and variability (SDFD and CVFD) of animal fiber snippets (2-mm lengths) and was approved for use in standard methods. Cleaned, conditioned (21°C and 65% RH) snippets are measured between 2 glass slides. Average fiber curvature (AFC), variability (SDFC and CVFC), and comfort factor (CF, % fibers <30 µm) are also estimated. The OFDA2000 measures greasy fiber staples with corrections being made for non-standard atmospheric conditions, grease, and other contaminants on the raw fiber. A retrofitted add-on permits the OFDA2000 to measure cleaned snippets mounted on glass slides. Two sets of greasy wool staples (n_1 = 108, AFD = 22.8 ± 1.5 µm, n_2 = 107, AFD = 25.7 ± 2.1 µm) shorn from rapidly growing yearling Rambouillet rams were first measured on the OFDA 2000. Snippets were then guillotined from the base of each staple, cleaned, conditioned, and spread onto a glass slide. Each slide was measured on the OFDA 100 and then on the OFDA2000. Data were analyzed using the paired *t*-test, and CORR procedures of SAS. Results for the finer set only are presented in Table 1. Average snippet AFD was not different between instruments ($P = 0.11$) though it was for the coaser set (Δ AFD = 0.11 µm, SED = 0.02 µm, $P < 0.01$). All other measured traits were different ($P < 0.01$). Thus, some caution is required when comparing results from the 2 instruments.

Table 1. Means and r values for wool characteristics measured with 2 instruments

Item	1, 100, snippet	2, 2000, staple	3, 2000, snippet	r, 1 vs 2	r, 1 vs 3	r, 2 vs 3
AFD, µm	22.8^a	21.6^b	22.8^a	0.88	0.99	0.87
SDFD, µm	3.9^a	3.6^c	3.8^b	0.87	0.99	0.89
CVFD, %	17.0^a	16.5^b	16.5^b	0.81	0.95	0.83
CF, %	95.8^c	97.7^a	96.1^b	0.86	0.96	0.89
AFC, °/mm	100.1^a	86.2^c	97.8^b	0.77	0.97	0.76
SDFC, °/mm	57.7^a	58.5^a	55.8^b	0.65	0.93	0.63
CVFC, %	57.8^b	68.0^a	57.2^c	0.26	0.82	0.23

^{a,b,c}Within a row, means without common superscripts differ ($P < 0.01$).

Key Words: fiber diameter, objective measurement, wool

M463 Comparison of Rambouillet sheep with Australian Merino F1 crosses. C. J. Lupton*[1], F. A. Pfeiffer[1], W. S. Ramsey[2], M. W. Salisbury[3], D. F. Waldron[1], J. W. Walker[1], and T. D. Willingham[1], [1]*Texas AgriLfe Research*, *San Angelo,* [2]*Texas A&M University*, *College Station,* [3]*Angelo State University*, *San Angelo, TX.*

The objective of this study is to estimate the differences in wool production and value between Rambouillet (R) and R × Australian Merino (M) crosses. Semen from the desired type of M sires (n = 5 in 2007, 3 in 2008) was located and purchased. The M sires had similar mature BW but greater fleece weight and finer wool than R rams. R ewes (n = 407, 3–5 yr of age, BW = 61.5 ± 6.9 kg, average fiber diameter [AFD] = 21.3 ± 2.1 μm) were bred to the M rams via laparoscopic artificial insemination in June 2007 and October 2008. Contemporary R lambs were produced naturally by exposing R ewes (n = 235) to R rams (n = 4 in 2007 and 2008). Lambs born in 2008 and 2009 were weighed at 5 mo of age. Fleece weights (greasy and clean, GFW and CFW) and fiber characteristics were determined on yearling fleeces. Data were analyzed using the MIXED procedure of SAS. The model included fixed effects of genotype and sex and a random effect of sire within genotype. BW at 5 mo of age (27.1 kg) for lambs born in 2008 and 2009 was not different between genotypes. Least squares means of yearling fleece weights and fiber characteristics for lambs born in 2008 are presented in Table 1. Fleece weights and average staple length (ASL) did not differ between genotypes. The M × R yearlings produced higher yielding and finer (more valuable) wool with less crimp (lower average fiber curvature, AFC) than R sheep. Female yearlings produced coarser wool than males.

Table 1. Fleece and fiber characteristics of yearling sheep

	Genotype			Sex		
Dependent variable	M × R (n = 47)	R (n = 44)	P	Female (n = 45)	Male (n = 46)	P
GFW, kg	4.3	4.1	0.543	4.1	4.2	0.509
CY, %	60.8[a]	56.3[b]	0.005	57.9	59.1	0.119
CFW, kg	2.6	2.3	0.119	2.4	2.5	0.239
AFD, μm	17.8[b]	18.7[a]	0.015	18.6[a]	17.9[b]	0.012
ASL, mm	12.0	11.4	0.429	12.0	11.4	0.077
AFC, deg/mm	87.2[b]	95.5[a]	0.019	90.7	92.0	0.519

[a,b]Within a row and within genotype or sex, means with a different superscript letter differ ($P < 0.05$).

Key Words: Merino, Rambouillet, wool

M464 Effects of substituting distillers dried grains for cottonseed meal and milo on wool and carcass characteristics in lamb finishing diets. T. R. Whitney*, A. E. Lee, M. G. Williamson, C. D. Swening, and R. L. Noland, *Texas AgriLife Research Center*, *San Angelo*.

Distillers dried grains (DDG) should continue being an economical feed if the market remains saturated. Cottonseed meal and sorghum grain are common feed sources for lamb finishing diets, especially in Texas, but the sheep industry's interest in using greater concentrations of DDG has increased. Limited research exists evaluating carcass characteristics of lambs fed diets containing greater than 50% DDG. Rambouillet wether lambs (n = 42, initial BW = 28.8 ± 3.3 kg) were individually fed ad libitum diets containing DDG that replaced 0% (0DDG), 25% (25DDG), 50% (50DDG), or 75% (75DDG) of the CSM and milo for 72 d in a completely randomized design. On d 72, 35 randomly-selected wethers were humanely slaughtered and evaluated for carcass characteristics. Quadratic trends ($P < 0.05$) were observed for hot carcass weight (22.0, 23.2, 24.6, and 22.5 kg ± 0.7) and 12th-rib back fat thickness (0.5, 0.5, 0.6, 0.4 cm ± 0.06) as percentage of DDG increased in the diet, and backfat thickness was greater ($P = 0.04$) for lambs fed 0DDG than 75DDG. The LM area was similar ($P > 0.14$; 14.4, 14.8, 15.6, 14.5 cm^2 ± 0.54) among lambs. Quadratic trends ($P < 0.07$) were also observed for body wall thickness (1.4, 1.7, 1.7, 1.4 cm ± 0.8) and leg circumference (30.35, 30.96, 31.61, 30.70 cm ± 0.4). Results suggest that carcass characteristics are affected by increasing percentage of DDG in lamb diets; the quadratic trends were unexpected.

Key Words: carcass characteristics, distillers dried grains, lambs

M465 Nutrient intake in Santa Inês sheep fed different levels of metabolizable energy in the ration. R. M. Fontenele*, E. S. Pereira, P. G. Pimentel, M. S. de Souza Carneiro, A. B. S. Villarroel, and J. G. L. Regadas Filho, *Federal University Ceará*, *Fortaleza, Ceará, Brazil*.

The objective of this study was to evaluate the nutrient intake of Santa Inês sheep fed different levels of metabolizable energy (2.08, 2.28, 2.47 and 2.69 Mcal/kg DM) in diets. Twenty lambs, average weight of 13 kg and age 50 d, were distributed in randomized block design with 5 replications. The roughage used was the Tifton 85 hay. Since the experimental variables were subjected to ANOVA and regression using the Statistical Analysis System and Genetic - SAEG. Was found among the energy levels on the dry matter intake, g/day ($P = 0.002$) (695.02, 914.17, 1030.16 and 1287.06, to 2.08, 2.28, 2,47, and 2.69 Mcal/kg DM, respectively) and g/$kg^{0,75}$ ($P = 0.02$) (80.54, 93.27, 98.70 and 107.02, to 2, 08, 2.28, 2.47 and 2.69 Mcal/kg DM, respectively). For the dry matter intake, in %BW, there was no influence ($P > 0.05$) of energy levels in diets. Intake in g/day of organic matter ($P = 0.002$) (713.50, 946.88, 1071.10 and 1349.90 to 2.08, 2.28, 2.47 and 2.69 Mcal/kg DM, respectively), crude protein ($P = 0.001$) (107.58, 172.19, 205.81 and 253.64 to 2.08, 2.28, 2.47 and 2.69 Mcal/kg DM, respectively), ether extract ($P = 0.0001$) (11.80, 21.49, 34.96 and 40.28 to 2.08, 2.28, 2.47 and 2.69 Mcal/kg DM, respectively), non-fibrous carbohydrates ($P = 0.00001$) (148.69, 243.35, 360.52 and 511.00 to 2.08, 2.28, 2.47 and 2.69 Mcal/kg DM, respectively) and total digestible nutrients ($P = 0.001$) (695.02, 914.17, 1030.16 and 1287.06, to 2.08, 2.28, 2.47 and 2.69 Mcal/kg DM, respectively), performed equal to the intake of dry matter. There was also increased intake of total carbohydrates ($P = 0.01$), despite the decrease of this nutrient as increased energy levels in diets (538.38, 671.18, 803.37 and 873.01 to 2.08, 2.28, 2.47 and 2.69 Mcal/kg DM, respectively). Observed influence of the energy levels on the use of neutral detergent fiber, in %BW ($P = 0.0004$) (44.40, 45.27, 40.27 and 33.77 for 2.08, 2.28, 2.47 and 2.69 Mcal/kg DM, respectively) and g/$kg^{0.75}$ ($P = 0.009$) (44.40, 45.27, 40.27, and 33.77 for 2.08, 2.28, 2.47 and 2.69 Mcal/kg DM, respectively). The daily intake of acid detergent fiber were not affected ($P > 0.05$) by the dietary energy.

Key Words: lambs, performance, ruminants

M466 Body composition and net energy requirements for growth of Santa Inês lambs. J. G. L. Regadas Filho[2], E. S. Pereira[1], P. V. R. Paulino*[2], A. B. S. Villarroel[1], P. G. Pimentel[1], R. M. Fontenele[1], and I. S. G. Maia[1], [1]*Universidade Federal do Ceará*, *Fortaleza, Brazil*, [2]*Universidade Federal de Viçosa*, *MG, Brazil*.

This study was conducted to determine the body composition and energy requirements for maintenance and growth of Santa Inês lambs. Twenty-four non-castrated males, 50 d old and with 13.00 ± 0.56 kg of initial body weight were used. Four animals were slaughtered at the beginning of the trial, as a reference group, to estimate the initial empty body weight (EBW) and body composition. The remaining ani-

mals were assigned in a randomized block design with 5 replicates per block and 4 diets, with increasing metabolizable energy contents (2.08; 2.28; 2.47 and 2.69 Mcal/kg of DM). The animals were slaughtered at 28.00 ± 0.97 kg of BW. The logarithm of heat production (HP) was regressed against metabolizable energy intake (MEI) and the net energy requirements for maintenance (kcal/kg $EBW^{0.75}$/d) were estimated by extrapolation, when MEI was set to be zero. Regression equations of the logarithm of body fat and body energy on the logarithm of EBW were adjusted. The derivatives of these equations allowed the estimation of the fat content of empty body weight gain (EBWG) and the net energy requirement for EBWG, respectively. The net energy requirement for maintenance obtained was 50.72 ± 1.20 kcal/kg $EBW^{0.75}$/d. The energy and fat contents of the EBW of the animals increased from 1.91 and 85.18 to 2.78 Mcal/kg and 221.23 g/kg of EBW, respectively, as the BW increased from 15 to 30 kg. Similarly, the composition of the EBWG consisted of more fat and energy as the animals became heavier. The net energy requirements for EBWG increased from 2.94 to 4.28 Mcal/kg of EBWG for body weights of 15 and 30 kg, respectively. The net energy requirement for maintenance of Santa Inês lambs is lower than values commonly recommended by the main evaluation systems of food and nutritional requirements of sheep.

Key Words: empty body weight, maintenance, tropical sheep

M467 Body composition and net protein requirements for Santa Inês lambs. J. G. L. Regadas Filho[2], E. S. Pereira[1], P. V. R. Paulino*[2], A. B. S. Villarroel[1], P. G. Pimentel[1], R. M. Fontenele[1], M. R. G. F. Costa[1], and M. S. Duarte[2], [1]*Universidade Federal do Ceará*, *Fortaleza, Brazil*, [2]*Universidade Federal de Viçosa*, *MG, Brazil*.

This study was conducted to determine the body composition and protein requirements for maintenance and growth of Santa Inês lambs. Twenty-four non-castrated males, 50 d old and with 13.00 ± 0.56 kg of initial body weight were used. Four animals were slaughtered at the beginning of the trial, as a reference group, to estimate the initial empty body weight (EBW) and body composition. The remaining animals were assigned in a randomized block design with 5 replicates per block and 4 diets, with increasing metabolizable energy contents (2.08; 2.28; 2.47 and 2.69 Mcal/kg of DM) and crude protein (CP) (12.74; 14.36, 15.97 and 17.65% CP of DM). The animals were slaughtered at 28.00 ± 0.97 kg of BW. A regression equation of nitrogen intake (g/kg $BW^{0.75}$/d) on nitrogen retention (g/kg $BW^{0.75}$/d) was adjusted. When N intake was set to be zero, the negative intercept of regression equation was considered as the endogenous N losses, which represents the maintenance requirements. A regression equation of the logarithm of body protein content on the logarithm of EBW was adjusted. The derivative of this equation enabled the estimation of the net protein requirements for gain of empty body weight (EBWG). Endogenous nitrogen loss was estimated to be 277 ± 0.05 mg/kg $BW^{0.75}$/d, which corresponds to the net protein requirement for maintenance of 1.73 ± 0.31 g/kg $BW^{0.75}$/d. Protein content of EBW decreased from 157.83 to 144.33 g/kg of EBW as the animals BW increased from 15 to 30 kg, respectively. The protein deposited in the EBWG decreased from 137.47 to 125.71 g/kg as the animals BW increased from 15 to 30 kg, respectively. Endogenous nitrogen loss and protein requirement for maintenance of Santa Inês lambs are lower than the values commonly cited by the main systems of feed evaluation and nutrient requirements of sheep.

Key Words: empty body gain, requirements, tropical sheep

M468 Effects of dietary copper level on serum cholesterol and nonesterified fatty acids in lambs. S. Hasanlou*, A. Zali, M. Ganjkhanlou, and M. Dehghan, *Tehran University, Tehran, Iran.*

An experiment was conducted to determine the effect of dietary Cu on serum cholesterol and NEFA in lambs. Twenty-four castrated male Lori-Bakhtiary lambs (3 to 4 mo of age; average BW = 26 ± 0.5kg) were used in this experiment. Lambs were housed in individual pens and were assigned randomly to one of 3 treatments. Treatments consisted of 1) control (no additional supplement), 2) lambs received 5 mg Cu/d, and 3) lambs received 10 mg Cu/d. Treatments were gavaged daily (esophagus gun) before AM feeding. Blood samples were collected from the jugular vein by venipuncture. Serum NEFA concentrations were not affected by the supplementations (0.15, 0.15, and 0.21mmol/L). Total cholesterol of serum had tendency to be lower in groups received 5 mg Cu/d relative to the other supplemented groups ($P = 0.06$). Animals received 5 mg Cu/d had significantly ($P = 0.01$) higher serum HDL-cholesterol compared with others. Whereas serum LDL-cholesterol concentrations was similar between supplemented groups (19.43, 19.39, and 17.34 mg/dL respectively). The Cu concentrations of serum were higher in lambs received 10 mg Cu/d compared with the other supplemented lambs ($P < 0.001$). Based on the current results, Cu supplementations had beneficial effect on reduction of serum cholesterol in lambs.

Key Words: copper, cholesterol, lambs

M469 Effects of dietary copper level on growth, performance, and carcass characteristics in lambs. S. Hasanlou*, A. Zali, M. Ganjkhanlou, and M. Dehghan-Banadaki, *Tehran University, Tehran, Iran.*

An experiment was conducted to determine the effect of dietary Cu on growth, performance, and carcass characteristics in lambs. Twenty-four castrated male Lori-Bakhtiary lambs (3 to 4 mo of age; average BW = 26 ± 0.5kg) were used in this experiment. The lambs were housed in individual pens and were assigned randomly to 1 of 3 treatments. Treatments consisted of 1) control (no additional supplement), 2) lambs received 5 mg Cu/d, and 3) lambs received 10 mg Cu/d. Treatments were gavaged daily (esophagus gun) before AM feeding. Daily feed intake and orts were recorded daily. Body weight was measured at the start and the end of experimental period. Least squares means of feed intake was similar for Supplemented and control lambs (1.13, 1.13, and 1.14 kg/d respectively). Lower daily gain observed for lambs received 10 mg Cu/d compared with control and those were fed 5 mg Cu/d ($P < 0.05$). Gain:feed were affected by Cu level, so that lambs received 10 mg Cu/d had the lowest level. Dressing percentage was not affected by supplementations (45.54, 43.54, and 46.95% respectively). Lambs received 10 mg Cu/d had lower back fat versus others ($P < 0.05$). Based on the current results, Cu supplementations had no beneficial effect on the performance characteristics of lambs.

Key Words: copper, lambs, carcass

M470 Effect of zilpaterol and ractopamine feeding program on growth performance and carcass characteristics of finishing lambs. M. A. Lopez-Carlos*[1,2], R. G. Ramirez[2], J. I. Aguilera-Soto[1], C. F. Arechiga[1], F. Mendez-Llorente[1], H. Rodriguez[1], and M. Rincon[1], [1]*Universidad Autonoma de Zacatecas*, *Zacatecas, Mexico*, [2]*Universidad Autonoma de Nuevo Leon*, *Nuevo Leon, Mexico.*

The objective of this trial was to determine the response on growth and carcass traits when ractopamine (RAC) and zilpaterol (ZIL) were administered at 3 feeding programs (constant, increasing and decreasing concentration) in the diet of finishing lambs for the last 27 d before

harvest. Eighty-four lambs (30 ± 1.6 kg) were used in a split-plot design with 7 treatments, 3 blocks (grouped by weight) and 3 periods (9, 18 and 27 d; subplots). Treatments were: Control, RAC and ZIL constant (RC and ZC) (0.20 and 0.70 mg/kg BW respectively, main plot), RAC increasing (RI) (0.35, 0.70 and 1.05 mg/kg BW), ZIL increasing (ZI) (0.10, 0.20 and 0.30 mg/kg BW), RAC decreasing (RD) (1.05, 0.70 and 0.35 mg/kg BW), and ZIL decreasing (ZD) (0.30, 0.20 and 0.10 mg/kg BW). Adjustments for RAC and ZIL concentration were made at beginning of each evaluation period. Basal diet was 18% CP and 3 Mcal/kg of ME. The data analysis was performed using the GLM procedure of SAS. Differences between treatments were established by Duncan's test. Total gain (GT), average daily gain (ADG), dry matter intake (DMI), feed:gain (F:G), hot and cold carcass weights (HCW and CCW), meat and fat color (MC and FC), fat thickness (FT), carcass classification (CC) and longissimus muscle area (LM), were determined. During the first period there was a decrease ($P < 0.01$) for DMI, ADG and feed efficiency (FE) for lambs that consumed ractopamine and zilpaterol respect to Control. However, in subsequent periods, growth variables were higher ($P < 0.05$) for ZIL and RAC regardless of dosing schedule. Hot carcass weight (HCW), CCW, CC and LM were higher for RI, ZI, RC and ZC. MC, FC and FT were improved ($P < 0.05$) with RAC and ZIL administration independently of dosing schedule. In conclusion, increasing concentration of dietary RAC and ZIL to finishing lambs prolongs the growth response on time, while constant and increasing dietary RAC and ZIL improve carcass characteristics.

Key Words: sheep, zilpaterol, ractopamine

M471 Use of zeranol and reimplantation on performance of finishing hair lambs. D. Domínguez, G. Amaya*, G. Villalobos, H. Castillo, J. A. Ortega, and L. Carlos, *Universidad Autónoma de Chihuahua*, *Chihuahua, Chihuahua, México*.

Use of zeranol has improved daily gain and gain efficiency of lambs, leading to a higher profitability in sheep industry. This study evaluated the effect of using different zeranol levels and its reimplantation on dry matter intake, body weight, average daily gain and gain efficiency of finishing hair lambs. Thirty-two weaned intact male lambs (21.2 ± 1.58 kg and 60 d old) crosses of Dorper × Pelibuey and Kathadin × Pelibuey were blocked by initial body weight and randomly assigned to 4 treatments (n = 10, 5 pens and 2 lambs per pen): Z0 (control); Z12 (12 mg of zeranol, Ralgro), Z24 (24 mg of zeranol in a single application), and Z12–12 (12 mg of zeranol given twice). Lambs were implanted 12 d before starting the experiment, and animals of Z12–12 were reimplanted 28 d after starting the study. Lambs were fed ad libitum a 80:20 concentrate:forage diet (% DM) containing 2.7 Mcal ME/kg DM and 18.2% CP. Dry matter intake (DMI) was determined daily, while body weight, average daily gain (ADG) and gain efficiency (GE) were recorded every 14 d during the 56 d trial. Data were analyzed as a complete random design with repeated mesarurements on time, using the PROC MIXED. Implanted animals had similar DMI vs. non implanted (1.42 vs. 1.47 kg). Final body weight of implanted animals was not improved vs. non implanted (40.0 vs. 36.9 kg), and was similar among implanted treatments. The ADG of implanted lambs was 12.4% higher vs. non implanted (0.326 vs. 0.290 kg/d; $P < 0.05$), and it was 6.2% enhanced in lambs of Z24 compared with lambs of Z12 (0.340 vs. 0.320 kg/d; $P < 0.05$), and was similar between Z24 and Z12–12 treatments. Implanted lambs had 17% higher GE (4.4 vs. 5.3; $P < 0.05$), and it was 8.7% superior in Z24 vs. Z12 (4.2 vs. 4.6), and was similar between Z24 and Z12–12 treatments. Implanting finishing lambs with 24 mg of zeranol in a single dosis showed the best animal performance.

Key Words: implants, finishing lambs, zeranol

M472 Fatty acid profile and lipid oxidation of meat from Sarda lambs managed in different feeding systems. S. P. G. Rassu, C. Carzedda, R. Boe, M. G. Manca, and A. Nudda*, *Dipartimento di Scienze Zootecniche, University of Sassari*, *Sassari, Italy*.

Fatty acid composition and the lipid oxidation of raw meat were evaluated in suckling lambs managed in 2 different feeding systems. Twenty-two Sarda male lambs were divided into 2 feeding system groups: 11 lambs (SL group), after 5th day of age, were confined in a fold and every day separated from their dams from 8.00 a.m. to 4.00 p.m. and then rejoined after ewes milking. These lambs were also fed with a suitable pellet feed ad libitum to compensate smaller available milk. Remainine 11 lambs (NSL group) were never separated from their dams and herded to pasture with them and confined in a fold during the night. At d 25 of age, the 5 heavier lambs of each group were slaughtered. Mean BW and ADG for NSL and SL group were, respectively: 4.70 and 6.08 kg at birth ($P = 0.012$), 11.2 and 13.4 kg at slaughter ($P = 0.000$) and 270 and 287 g/d ($P = 0.382$). After 24 h of refrigeration at 4°C, the lumbar region was dissected from each right half-carcass and used for analysis. Fatty acid profile was determined by gas-cromatography while lipid oxidation was measured by the Thio-Barbituric Acid Reactive Substances (TBARS) method. Data were analyzed with a one-way ANOVA using group as the main effect. Lipid oxidation was not significantly influenced by group but was higher in NSL group than SL group (0.42 vs 0.34 mg MDA/kg of meat). The content in fat and protein were not significantly affected by feeding system (Table 1). Fatty acid composition was not significantly influenced by group (Table 1).

Table 1. Composition of raw meat from suckling lambs raised with 2 different feeding system

	Group	
	NLS	SL
Protein	20.32	20.42
Fat	1.98	2.31
Fatty acid (g/100g of FAME)		
PUFA n-3	9.98	8.79
PUFA n-6	2.79	3.27
SFA	42.72	44.47
UFA	57.28	55.53
MUFA	43.66	43.92
n-6/n-3	3.65	2.82
SFA/UFA	0.75	0.80

Key Words: fatty acid, lipid oxidation, lamb

M473 Deciding whether light lambs should be weaned or left with the dam until slaughter age. M. Terré[1], A. Nudda[2], and A. Bach*[3,1], [1]*Institut de Recerca i Tecnologia Agroalimentàries*, *Barcelona, Spain*, [2]*University of Sassari*, *Sassari, Italy*, [3]*Institució Catalana de Recerca i Estudis Avançats*, *Barcelona, Spain*.

The objective was to compare the performance and meat quality of 2 different lamb rearing systems: weaning lambs at 7 wk of age and then either feeding concentrate and forage or rearing lambs with their mother until sacrifice. A total of 22 lambs from 17 ewes were assigned to weaning (W) treatment and 20 lambs from 16 ewes to unweaning (U) treatment. Lambs in U treatment were kept with their mother and fed a concentrate ad libitum. Lambs in W treatment were weaned at 7 wk of age and fed concentrate and straw ad libitum. Lambs were weighed weekly until sacrifice. Carcasses were weighed after slaughter. After sacrifice (48 h), Longissimus dorsi (LD) was sampled from 8 male

lambs per treatment to determine color, texture, fat content and fatty acid (FA) composition. Data were analyzed using a fixed effects model with pen as the experimental unit. Lambs in the U treatment tended ($P = 0.09$) to weigh more than W lambs 4 wk after weaning (19.7 vs 18.3 ± 0.06 kg BW, respectively). Lambs in U treatment were 13 d younger ($P < 0.001$) at slaughter than the W lambs. Dressing percentage was greater ($P < 0.05$) in U than in W lambs (44.9 vs 42.0 ± 1.23%, respectively). Colorimetric parameters of LD indicated that L and a values were similar in both treatments, whereas b values were greater ($P < 0.05$) in W than in U lambs (12.9 vs 12.3 ± 0.16, respectively). There were no differences in texture measurements (WBSF) and total fat in LD. The LD from U lambs had a greater ($P < 0.05$) percentage of 16, 18:3 n-3 FA and a lower ($P < 0.05$) percentage of 17, 17:1 FA than LD from W lambs. However, the ratio n-6/n-3 was lower ($P < 0.01$) in U than in W lambs (6.47 vs 9.19 ± 0.527, respectively). Rearing lambs with the ewe until sacrifice reduces days to slaughter and improves FA composition of LD.

Key Words: light lamb, weaning, meat quality

M474 Lamb finalization allowing free-choice intake of roughage and concentrate. P. Martinez-Hernandez*, C. Sanchez-DelReal, E. Cortes-Diaz, E. Maldonado-Siman, and R. Lazo-Soto, *Animal Science Department, University of Chapingo*, *Texcoco, Mexico, Mexico*.

The objective of this study was to determine performance and feeding behavior of lambs offered roughage and concentrate as either a mixed diet or split feeds free-choice. Three treatments were evaluated: mixed diet, or concentrate offered once (C1) or twice (C2) a day with roughage provided for ad libitum intake. Mixed diet was 78:22 concentrate:roughage, concentrate was: 78.53% milo; 10.26% soybean meal; 10.18% meat meal poultry; and, 1.03% mineralized salt (estimated ME 2.87Mcal/kg). Roughage sourece was ground (1.8 cm screen) corn stover. Experimental design was a completely random with 3 replicates; experimental unit was a pen with 2 lambs. Feeding trial lasted 32 d. Rambouillet lambs with initial weight of 37.7 ± 3.1 kg and less than one year old were used. Feed offered was adjusted daily to provide 15% above the day-before intake. Intake was calculated daily by weighing feed offered and rejected. Mixed diet, corn stover and concentrate of C1 and half of C2 were given at 7:00 h, the other half of C2 at 18:00 h. Mixed diet and C1 showed the highest and lowest ($P < 0.05$) of both daily total and concentrate intakes, respectively. Average daily gain, final weight, feed conversion and total time-spent-eating were not different ($P > 0.05$) among treatments. At the beginning, daily time spent eating concentrate in C1 lambs was up to 53% higher ($P < 0.5$) than in C2 lambs, but toward to the end of the trial there was no difference ($P > 0.05$); C1 lambs decreased 38% in time eating concentrate. Daily rumination time was 38% lower ($P < 0.05$) in C1 lambs than the rest of the lambs. Incidence of lambs off-feed was 3 times higher ($P < 0.05$) in C1 than in the other 2 treatments. It was concluded that controlled offering of concentrate could allow for feeding roughage and concentrate as split feeds.

Key Words: mixed diets, feeding system, lamb performance

SYMPOSIA AND ORAL PRESENTATIONS

Graduate Student Paper Competition: ADSA Southern Section

37 Biohydrogenation intermediates of ^{13}C-labeled docosahexanoic acid in ruminal batch cultures. C. M. Klein* and T. C. Jenkins, *Clemson University*, *Clemson, SC*.

There are no reported pathways of docosahexanoic (DHA) biohydrogenation; however, DHA is metabolized by ruminal microorganisms. In this study a 0.5mg pulse dose of uniformly 13C labeled DHA in ethanol was injected at 0h as a metabolic tracer. This study did not examine every fatty acid metabolite, but rather identified several saturated and trans-18:1 fatty acid metabolites and set a foundation for future work. Ruminal microorganisms collected from a lactating Holstein cow were incubated in 10 mL batch cultures for 0, 6, 24 and 48 h. Treatment groups were 0.5% 13C DHA and 0.5% DHA. Duplicate cultures were methylated and then separated on a 100-m CP-Sil 88 column. Abundances of the quasimolecular (M) and M+n ions were determined by mass spectroscopy in chemical ionization mode. Enrichment was calculated as {M+n/[M+(M+n)]} × 100 in labeled minus unlabeled cultures and tested for their difference from zero by *t*-test ($P < 0.01$). DHA decreased from 0.207mg to 0.041mg between 0 and 48h and had an enrichment of 98.1%. Oleic, linoleic, and linolenic acids decreased 0.431, 0.962 and 0.081mg in the same time period. Stearic acid increased 1.37mg and trans-18:1 monenes increased 0.415 mg. Palmitic, eicosanoic, and docosanoic acids increased 0.196, 0.008 and 0.005 mg respectively. Palmitic, stearic, all trans-18:1, eicosanoic, and docosanoic acids were examined for enrichment. Docosanoic acid was highly enriched at 24h and 48h to 20.2% and 16.3% (SE = 0.466; $P < 0.01$). Neither eicosanoic acid, nor any trans-18:1 monenes were enriched at any time ($P < 0.05$). Low levels of enrichment (<0.1%; $P < 0.01$) were found in palmitic and stearic acids. This study clearly identifies docosanoic acid as an intermediate of DHA biohydrogenation. It also identifies that, in this system, eicosanoic acid and trans-18:1 fatty acids were not intermediates. Stearic acid had minor enrichments, but DHA only made up 3.13% of total fat or 10.3% of metabolized unsaturated fat.

Key Words: docosahexanoic acid, biohydrogenation

38 Cows genetically more susceptible to mastitis have altered neutrophil migration patterns. A. A. Elliott*, S. Minkin, J. Biggerstaff, J. Dunlap, and G. M. Pighetti, *University of Tennessee*.

The largest loss in profit for dairy farmers occurs with mastitis, an inflammation of the mammary gland. Our prior research identified a marker in the CXCR1 gene associated with mastitis and decreased neutrophil migration in vitro. Because neutrophil migration is critical for eliminating most infections, our ongoing research seeks to identify the specific mechanisms causing impaired migration. The first study evaluated actin polymerization, one of the first steps in neutrophil migration, in cows with different CXCR1+777 genotypes. Neutrophils from cows with GG (n = 11) and CC (n = 11) genotypes were isolated and stimulated with zymosan activated sera (ZAS). Cells were fixed and stained for F-actin and subsequently evaluated for F-actin content, distribution, and cell morphology. Neutrophils of the CC cows had significantly lower average F-actin polymerization than the GG cows ($P = 0.05$). Because F-actin polymerization drives neutrophil movement, lower amounts could partly explain reduced migration. In contrast, cell morphology and F-actin distribution was similar between genotypes. Our second study focused on directed migration of neutrophils toward interleukin-8 (IL8). The migration of neutrophils from GG (n = 4) and CC (n = 4) genotypes was captured under a microscope and velocity, acceleration, distance of the path, distance from origin, largest X distance and largest Y distance were analyzed for each individual cell. Cells from GG genotype traveled further and more directly compared with CC genotype cells. Our findings suggest lower F-actin polymerization in combination with a lower ability to directly and efficiently move toward the site of infection could impair neutrophil response to infection in cows with the CC genetic background and may contribute to increased mastitis susceptibility.

Key Words: mastitis, chemotaxis, neutrophil

39 Effects of different levels of cottonseed hulls on rumen development and growth in dairy calves. R. M. Doescher*, C. C. Williams, C. F. Hutchison, B. F. Jenny, and A. H. Dolejsiova, *LSU AgCenter*, *Baton Rouge*.

A study was conducted to determine the effects of varying levels of cottonseed hulls on growth and metabolic indications of rumen development of dairy calves. Sixty-four Holstein calves (Heifers, n = 40; Bulls, n = 24) were randomly assigned to one of 4 dietary treatments which included calf starters containing no cottonseed hulls (control; C), 10% cottonseed hulls (10% CSH), 15% cottonseed hulls (15% CSH), or 20% cottonseed hulls (20% CSH). Calves were fed their respective treatments beginning on d 8 until d 56 of age. Body weights were measured at birth and biweekly thereafter until d 56 of age. Wither and hip heights were measured beginning on d 14 and biweekly thereafter until d 56 of age. Feed intake and fecal scores were recorded twice daily through d 56. On d 14, 28, 42, and 56, rumen fluid was collected for analysis of pH, volatile fatty acids (VFA), and ammonia (NH3), and blood was collected for analysis of plasma urea nitrogen (PUN) and β–hydroxybutyrate (BHBA). There was no treatment effect ($P > 0.1$) on average daily starter intake, fecal scores, body weight, wither height, and hip height. Calves consuming CSH had higher ($P < 0.05$) rumen pH than C. Rumen pH also decreased ($P < 0.01$) as calves aged. There was no treatment effect ($P > 0.1$) on rumen acetate, propionate, butyrate, and total VFA concentrations. There was a trend for a treatment by week interaction ($P < 0.1$) and a treatment effect ($P < 0.1$) on NH3 production, with calves consuming 10% CSH having higher concentrations. There was no significant treatment effect ($P > 0.1$) on BHBA, but a main effect of sex ($P < 0.05$) was observed in which males had higher BHBA concentrations. There was no significant treatment effect ($P > 0.1$) on PUN concentrations, but a main effect of sex ($P < 0.05$) was observed with females having greater concentrations. Overall, incorporating cottonseed hulls into a calf starter showed no significant effect on growth and rumen development in Holstein dairy calves.

Key Words: cottonseed hulls, dairy calves, rumen development

Graduate Student Paper Competition: ADSA-ASAS Northeast Section

40 Effects of herbs and essential oils on in vitro batch culture ruminal fermentation. J. A. Tekippe*[1], A. N. Hristov[1], K. S. Heyler[1], V. D. Zheljazkov[2], J. Ferreira[3], and G. A. Varga[1], [1]*Pennsylvania State University*, *University Park,* [2]*Mississippi State University, NMREC*, *Verona,* [3]*USDA-ARS*, *Beaver, WV*.

Medicinal herbs and essential oils were evaluated in a batch culture in vitro screening experiment as potential anti-methanogenic additives for ruminant diets. A total of 88 essential oils and 14 herbs were tested. Rumen inoculum enriched with particle-associated microorganisms was collected from a lactating dairy cow, 2 h before feeding. Incubation was conducted in serum bottles containing 1 g of a feed mixture (0.7 g alfalfa hay, 0.2 g corn starch, and 0.1 g solvent-extracted soybean meal), 1 mL of essential oils (10, 50, and 100 mg/L, final medium concentration), 19 mL of McDougall's buffer with 5 g/L glucose and 2.5 g/L acid-hydrolyzed casein, and 20 mL of ruminal inoculum. Bottles were then flushed with CO2 and incubated at 39°C for 6 h. Corresponding 50 mL tubes were incubated for 24 h for NDF degradability analysis. Herbs were tested using the same procedure, except a portion of the alfalfa hay was replaced with 12.5, 50, 100, and 200 mg of plant material (air-dry basis), and NDF was tested using the DAISY apparatus. Blanks and monensin (5 mg/L, final medium concentration) were also incubated. At the end of the incubations, total gas and methane production, VFA and ammonia concentration, and NDF degradability were measured. Treatment by application level interactions were not significant for any of the essential oil treatments. Two of the essential oils increased acetate production, 12 increased propionate production, 10 increased butyrate production, 3 reduced methane production (by 20 to 30%), and 2 decreased ammonia production. With the herbs, 1 increased acetate production, 2 increased propionate production, 1 decreased methane production (by 30%), and 1 decreased ammonia production. Eight of the herbs increased NDF degradability at various inclusion levels. Overall, these results indicated that some essential oils and medicinal herbs may have a significant effect on ruminal fermentation in vivo.

Key Words: essential oil, medicinal herb, rumen fermentation

42 Use of environmental protection best management practices by Maryland horse farm operators. N. M. Fiorellino*, K. M. Wilson, and A. O. Burk, *University of Maryland*, *College Park*.

A survey study was conducted to identify use of environmental protection best management practices (BMPs) by horse farm operators in Maryland (MD). A 35-question survey was mailed to 1,000 MD horse farm operators using a multiple wave mailing strategy. Data were collected from February to March 2009. Survey response rate was 43.9%, with responses received from 91.3% of counties. Respondents housed 16.8 ± 1.6 horses on 11.6 ± 1.6 ha of turnout with a mean stocking density of 0.81 ± 0.04 ha horse^{-1}. Primary use of horse farms was recreational (32.8%), boarding (30.7%), and breeding (14.7%). On a scale from 1 (low) to 5 (high), respondents reported they had the least knowledge of farm cost-share programs (2.0 ± 0.06), grass and weed identification (2.8 ± 0.05), and soil conservation plans (3.0 ± 0.05) and the most knowledge of recommended stocking density (3.6 ± 0.06), rotational grazing (3.6 ± 0.05), and manure management (3.5 ± 0.05). Most respondents assessed their pasture vegetative cover at >70% (78.5%); however, respondents operating a farm with a high stocking density (<0.4 ha horse^{-1}) reported lower rates. The majority of respondents used a recommended stocking density of ≥0.61 ha horse^{-1} (53.9%). Only 15.4% of respondents did not maintain a proper vegetative buffer between horses and water sources. However, 71.4% of respondents stored their manure on an impermeable or permeable surface uncovered, 30.7% allowed horses unlimited access to surface water, 39.4% did not utilize sacrifice lots to rest pastures, and more than half (55.4%) of respondents reported soil erosion in their pastures. Soil erosion was noted less by respondents operating a farm for recreation and those with a low stocking density (>0.81 ha horse^{-1}). Only 3 of 10 recommended BMPs were being used correctly by the majority (≥51%) of respondents, with proper manure storage, use of sacrifice lots, and rotational grazing being used by the lowest percentage of respondents. BMPs with low adoption rates should be the focus of future education programs for horse farm operators in MD to minimize environmental impact to the Chesapeake Bay Watershed.

Key Words: best management practices, horse, survey

43 Sources of variation and importance of the quantification of the in vitro NDF digestibility for estimating rates of NDF digestion. E. Raffrenato* and M. E. Van Amburgh, *Cornell University*, *Ithaca, NY*.

Accurate and precise estimations of intrinsic NDF digestibility and digestion kinetic parameters have been shown to be important for the evaluation of forages. Methods for measuring NDFD are more variable than those for NDF and there is no standard method. Within laboratories, the standard deviation (SD) of repeatability for single determinations of NDFD is 1.5 to 2 times that of the NDF assay. The SD of reproducibility among laboratories for single in vitro determination is 3 to 5 times that of NDF and can greatly impact the calculations for rate of digestion. Recently a method has been proposed to standardize the inoculum (Goeser et al., 2009) and although the CV of multiple runs was reduced, the method appeared to result in lower NDFD values. Our objective was to evaluate the sources of and reduce the variability of both NDF and NDFD assays. Several hundred forages were analyzed for aNDFom (Mertens, 2002), ADL (Van Soest et al., 1991) and NDFD using Goering and Van Soest buffer in 125 mL Erlenmeyer flasks under CO_2 using inoculum from multiple lactating cows within 20 min of collection and filtered in crucibles. One of the factors impacting the outcome of NDF, ADL and NDFD was the loss of soluble materials through the Gooch crucible. The use of glass filters (Whatman, 934-AH, 1.5 µm) improved recoveries from 0 and 4% ($P < 0.05$) and 0 and 8% ($P < 0.05$) for NDF and NDFD, respectively, and reduced the CV below 2% for intra-run and below 3% for inter-runs, among all forages. In vitro (240 h) and in situ (360 h) NDF recovery was improved up to 15% with the use of the filter and through the use of bags with porosity of 15 µm, respectively. Further, the use of the filter increased ($P < 0.05$) recovery of ADL from 3 to 36%. In conclusion improved recovery and inoculum handling allowed better estimations of NDF, NDFD, ADL and indigestible NDF and result in a more precise and accurate estimations of the rate of digestion (Van Amburgh et al., 2004). This data will serve to provide recommendations for the standardization of the NDFD procedure.

Key Words: NDF, NDFD, ADL

44 Effect of capsicum oil on feeding behavior and milk production in lactating dairy cattle. L. R. Tager* and K. M. Krause, *West Virginia University*, *Morgantown.*

A preliminary study was conducted to study the effect of capsicum oil on feeding behavior and milk production in lactating dairy cows. Twenty lactating dairy cows (16 Holstein and 4 Ayrshire) were used in a crossover design using the Growsafe monitoring system (Growsafe

Systems Ltd., Airdrie, AB, Canada). After balancing for milk yield and DIM, 10 cows were randomly assigned to each of 2 pens (5 Growsafe bins/pen). Cows were fed a TMR with a 54:46 forage:concentrate ratio (DM basis) ad-libitum twice daily. Experimental treatments included: 2 g/cow/d capsicum oil (CAP; XT 6933; Pancosma S.A., France) or no oil (CON). Data was collected until 20 d of sound data were accumulated for each experimental period. There was no difference in DMI (23.05 kg/d vs. 23.17 kg/d; $P = 0.91$), number of meals/d (12 vs. 12; $P = 0.34$), total h spent eating/d (3.22 h vs. 3.16 h; $P = 0.89$), mean meal length (17.24 min vs. 17.23; $P = 0.96$), length of first meal after feeding (43.3 min vs. 46.2 min; $P = 0.21$), or feeding rate (7.49 kg/h vs. 7.78 kg/h; $P = 0.80$) between CAP and CON. Milk yield did not differ between CAP and CON (27.6 kg/d vs. 28.1 kg/d; $P = 0.72$). Based on this preliminary study, feeding CAP at 2 g/cow/d does not change feeding behavior or milk production. To add more experimental units and confirm the results of the preliminary study, this project is currently being replicated.

Key Words: capsicum, feeding behavior

45 Digestive fate of free ferulic acid in lactating dairy cows. M. A. Soberon*, D. J. R. Cherney, and D. A. Ross, *Cornell University*, *Ithaca, NY*.

Ferulic acid (FA), a phenolic compound with antioxidant and anti-cancer activities, naturally occurs in plants as one of the building blocks of lignin. Many veins of research have been devoted to releasing FA from the lignin complex to improve digestibility of plants fed to livestock. Thus, it is of interest to study the fate of a given dosage of FA in the dairy cow to determine the likelihood of its transfer from ingested feed to milk when available in free form. Six mid to late lactation Holstein cows at the Cornell Research Farm were given 14 d adaptation to diet and stall. Ad libitum access to a total mixed ration based on haylage and corn silage (31.1% NDF, 5.52 mg/g FA) was provided during the study. A cross over design was used so that each cow alternated weekly between Treatment (Trt) and Control. On d 1, jugular cannulas and urine catheters were placed in all cows. On d 2, Trt cows received a single dosage of 150 g pure FA powder via their fistula (n = 4) or a balling gun for nonfistulated cows (n = 2). Plasma, urine, feces, feed, orts, milk and rumen fluid were sampled intensively for the next 36 h. On d 8, the cows crossed over and the experiment was repeated. All samples were analyzed for FA concentration. FA administration did not have an effect on DMI ($P = 0.593$), milk yield ($P = 0.501$), milk fat yield ($P = 0.457$), milk protein yield ($P = 0.959$), SCC ($P = 0.495$), NDF content of orts ($P = 0.462$) or NDF content of feces ($P = 0.393$). The level of FA in the feces did not change as a result of Trt ($P = 0.399$). As expected, [FA] increased dramatically upon FA dosage and decreased over time until returning to basal levels in rumen fluid (detectable until 4.25 h post-dosage), plasma (detectable until 5.5 h post-dosage), and urine (detectable until 23 h post-dosage). Baseline values for FA in urine and rumen fluid were variable among cows and had an effect on [FA] in Trt cows. FA was detected in the milking following FA dosage (6.5 h post-dosage) at significantly higher concentrations in Trt cows. From this study, it is observed that orally ingested FA can be transported into the milk and that the physiological transfer of FA occurs from rumen to urine within 1 h and milk within 6.5 h.

Key Words: ferulic acid, cow

46 The effect of form of trace mineral supplementation on lactation, neutrophil function, and vaccination response in Holstein cows. L. M. Nemec*[1], J. D. Richards[2], C. Atwell[2], D. E. Diaz[2], and T. F. Gressley[1], [1]*University of Delaware*, *Newark*, [2]*Novus International Inc.*, *St. Charles, MO*.

The aim of this study was to compare inorganic versus chelated forms of supplemental Cu, Mn, and Zn on production, neutrophil activity, antibody titer, and plasma and milk mineral concentrations. Holstein cows (n = 25) averaging 63 d in milk were assigned to a 12-week completely randomized design study in 2 groups. Diets were supplemented at 100% of NRC requirements either by inorganic trace minerals (ITM) in sulfate and oxide forms, or by chelated trace minerals (Mintrex; Zn, Cu and Mn as Mintrex Zn [$Zn(HMTBa)_2$]; Mintrex Cu [$Cu(HMTBa)_2$]; Mintrex Mn [$Mn(HMTBa)_2$]; Novus International Inc., St. Charles, MO). Intake and milk production were recorded daily. Milk composition was measured weekly, and milk Cu, Mn, and Zn was determined at wk 0 and 8. Blood Cu and Zn concentrations and neutrophil activity were measured at wk 0, 4, 8, and 12. Neutrophil activity was measured by in vitro assays of phagocytosis, reactive oxygen species (ROS) production, and chemotaxis. A rabies vaccination was administered at wk 8, and vaccine titer response at wk 12 was measured by both Rapid Fluorescent Focus Inhibition Test (RFFIT) and ELISA. Wet chemistry analysis of the total mixed rations indicated dietary Cu was 17 and 24 ppm, Mn was 40 and 62 ppm, and Zn was 84 and 138 ppm for the ITM and Mintrex diets, respectively. There was no effect of treatment on milk production (42 kg/d), milk composition, plasma minerals, neutrophil ROS production, or neutrophil chemotaxis. Dry matter intake tended to be lower for Mintrex than ITM cows (24.1 vs. 25.3 kg/d, $P = 0.06$). Milk Cu concentration was greater for Mintrex than ITM cows (76 vs 57 ï g/L, $P < 0.01$). Neutrophil phagocytosis tended to increase for the Mintrex treatment ($P = 0.09$). Rabies antibody titer was approximately 2.5 fold higher for Mintrex than ITM cows, regardless of assay ($P = 0.08$ for RFFIT; $P = 0.009$ for ELISA). In summary, the Mintrex treatment increased bioavailability as indicated by increased milk Cu and enhanced both innate and adaptive immune responses as indicated by increased neutrophil phagocytosis and vaccine titer response, respectively.

Key Words: trace minerals, neutrophils, parity

47 The effects of length of storage on the composition and nutritive value of corn silage. M. C. Der Bedrosian*[1], L. Kung Jr.[1], and K. E. Nestor Jr.[2], [1]*University of Delaware*, *Newark,* [2]*Mycogen Seeds*, *Indianapolis, IN*.

The objective of this study was to evaluate the effect of length of storage on the composition and nutritive value of corn silage. The primary treatments were a brown midrib (BMR) and a non-BMR silage hybrid (nBMR) harvested at a normal DM (32%) and a high DM (41%). Forages were vacuumed and heat-sealed in quintuplet storage bags and ensiled for various periods of time between 0 to 360 d before analyses. Nutrient analysis, fermentation end products and in vitro NDF (NDF-D; 30 h) and starch digestion (starch-D; 7 h) techniques were used to evaluate the samples. Over both maturities and time of ensiling, compared with nBMR, BMR silage was lower ($P < 0.01$) in lignin, CP and ADF but higher in starch content. The NDF content of silages was not affected by treatment. Of the fermentation end products, the concentration of acetic acid increased substantially with length of storage for all treatments specifically increasing as much as 140% between d 45 to d 365 for normal DM BMR silage. The NDF-D was greater overall all times for BMR (68% DMB) than nBMR (52%) but there was an interaction ($P < 0.01$) between hybrid and maturity. Increasing maturity did not affect NDF-D of nBMR but it decreased for BMR by approximately 5

percentage units. Fiber digestion did not change substantially between 45 and 365 d regardless of hybrid or DM content. Starch digestibility was highest ($P < 0.01$) in normal DM nBMR samples at d 0 (about 80%) and lower (65 to 68%) for other treatments. This was most likely due to the fact that normal DM nBMR had a low starch content (21%) compared with other treatments (31 ± 3%). Starch-D increased ($P < 0.01$) about 6 to 8 percentage units for nBMR silages but increased ($P < 0.01$) approximately 15 percentage units for BMR silages over the ensiling period. Relative to the 2 corn silage hybrids used in this study, the results show that time of ensiling does not affect NDF-D but it results in marked increases in starch digestion. The NDF-D of BMR but not the nBMR hybrid was affected by harvesting at a higher DM. Allowing corn silage to ensile for prolonged periods of time can improve its nutritive value.

Key Words: Silage, BMR

48 Effect of forage particle length on rumen fermentation and chewing activity of late lactating and dry dairy cows. F. X. Suarez-Mena*, G. I. Zanton, and A. J. Heinrichs, *The Pennsylvania State University*, *University Park*.

The objective of this study was to determine forage particle size effects on chewing activity, rumen pH, and rumen fill in dairy cattle fed rations with similar physically effective NDF but different mean particle length. Two experiments were conducted to determine chewing behavior, rumen pH, and rumen fill. Treatments consisted of 3 diets differing only in forage length (geometric mean length, mm): hay (5.40, 8.96 and 77.90, for short (S), medium (M) and long (L) diets, respectively) for Experiment 1 (E1), and straw (10.16 S, 24.68 M and 80.37 L) for Experiment 2 (E2). Hay or straw comprised the sole source of forage (50% for E1 and 75% for E2). Both experiments used 3 rumen cannulated, non-pregnant Holstein dairy cows, late lactating in E1 and dry in E2, with 3 × 3 Latin square designs. Chewing behavior was visually monitored for 48 h at 2-min intervals. In E1, DMI (18.3 ± 2.1 kg/d), pH (6.4 ± 0.1), time spent eating (280 ± 22.5 min/d), time spent ruminating (487 ± 17 min/d), and total time spent chewing (767 ± 34 min/d) were not different, while min/kg of DMI and min/kg of NDF intake tended to increase linearly ($P < 0.1$) as forage length increased. Rumen digesta volume (L; 113.3 S, 117.8 M, and 114.4 L ± 17.1) had a quadratic response ($P < 0.05$) and rumen digesta weight tended to respond quadratically ($P < 0.1$); however, differences were numerically small. In E2, DMI (8.3 ± 1.3 kg/d), pH (6.7 ± 0.1), time spent eating (236 ± 23.5 min/d), time spent ruminating (468 ± 45.2 min/d), total time spent chewing (704 ± 67.7min/d) and min/kg NDF intake were not different, while min/kg of DMI had a trend for a quadratic effect ($P < 0.1$). Rumen digesta volume (111 ± 18.8 L) and weight (103 ± 17.4 kg) were not different. Changes in rumen characteristics and chewing in cows in late lactation and dry cows were not detected or were small when the particle size of the forage was changed.

Key Words: particle size, chewing, rumen pH

Alpharma Beef Cattle Nutrition Symposium: "Parameterizing" Health and Performance Expectations of Feedlot Cattle

49 Practical relationships between morbidity and growth performance. V. R. Bremer[1], G. E. Erickson*[1], T. J. Klopfenstein[1], D. R. Smith[1], K. J. Hanford[1], R. E. Peterson[2], L. O. Burciaga-Robles[2], D. B. Faulkner[3], and C. R. Krehbiel[4], [1]*University of Nebraska*, *Lincoln*, [2]*Feedlot Health Management Services*, *Okotoks, Alberta, Canada*, [3]*University of Illinois*, *Urbana*, [4]*Oklahoma State University*, *Stillwater*.

Six trials suggested that bovine respiratory disease (BRD) depresses ADG and carcass finish. These studies did not account for DMI or G:F. Therefore, 5 new data sets were evaluated. Data (n = 978 lots; 276,116 cattle) from 2 Alberta, Canada feedlots with 0 to 70% BRD (CAN) were used to evaluate impact of BRD on performance. A subset (n = 33,074 cattle) had carcass data. A trial (OSU) was conducted with 193 heifers fed (6 heifers/pen) based on 0, 1, 2, 3, or 3+ BRD treatments during receiving, with incidence of 58%. Individual performance of 900 growing and 987 finishing cattle (UNL; 16 and 19% BRD treatment, respectively) were classified by time of BRD treatment at receiving, < 31 d on trial, > 30 d on trial, or no treatment. A third data set of 1,940 individual finishing cattle with 10% BRD treatment (UofI) were analyzed by time of BRD treatment. The CAN pen level closeout data indicate quadratic decreases ($P = 0.03$) in DMI and ADG and a trend for linear ($P = 0.08$) improvement in G:F as % of pen treated for BRD increased. The CAN carcass data indicates quadratic decreases ($P < 0.01$) in HCW, marbling score, and LM area, and a linear decrease ($P < 0.01$) in fat thickness as number of BRD treatments increased. In the OSU trial, feeding heifers based on BRD incidence at receiving indicates ADG linearly increased ($P = 0.01$), DMI was unchanged, and G:F increased as number of BRD treatments increased. Heifers treated 3 or more times required more d to reach a common end point. Growing cattle (UNL) treated > 30 d on trial had decreased ADG and G:F ($P < 0.01$) relative to cattle treated earlier or not at all. Finishing cattle (UNL) treated > 30 d on trial had similar DMI, ADG, and G:F ($P > 0.16$) as cattle treated earlier or not at all. The UofI cattle treated for BRD > 30 d on trial had decreased ($P < 0.01$) DMI and ADG and similar ($P = 0.51$) G:F as other BRD classes and required more d to reach a common end point. Cattle requiring treatment before 30 d on feed have similar performance to healthy cohorts; however, cattle requiring treatment after 30 d on feed may require increased d to reach a similar endpoint as healthy cohorts due to lower DMI and ADG, but G:F is unaffected.

Key Words: bovine respiratory disease, feed efficiency, growth

50 Predictability of feedlot cattle growth performance. M. L. Galyean*, N. DiLorenzo, J. P. McMeniman, and P. J. Defoor, *Texas Tech University*, *Lubbock*.

Predicting performance is vital to management and marketing decisions in commercial feedlots. Agreement between performance predicted from net energy equations or empirical regression relationships and actual performance is generally high, suggesting that factors affecting feedlot performance are fairly well documented. The challenge for feedlot managers is to predict performance with limited information at the start of the feeding period. Sex and initial BW are typically known with greatest certainty when cattle start on feed. Information on background and breeding is potentially important but less reliable. Relationships between initial BW, sex, and performance were evaluated using 3,363 pen records collected over 4 yr from 3 commercial feedlots in the Texas Panhandle. Mixed-model regression was used to account for random effects of feedlot × season × year and fixed effects of initial BW (range = 227 to 451 kg), sex (steer or heifer), and initial BW × sex ($P < 0.10$ for all variables evaluated). As expected, initial BW was positively related to DMI. With intercept and slope adjustments for sex, the R^2 was 0.72 for regression of DMI (adjusted for random effects) on initial BW. Similarly, with adjustments for random effects, regression on initial BW with sex adjustments accounted for 46, 82, and 81% of the variation in ADG, final shrunk BW, and HCW, respectively. Initial BW was negatively related to G:F ($R^2 = 0.22$). Analysis of a university data set (200 pens of steers; initial BW = 300 to 450 kg) indicated that adding ADG from d 0 to 70 of the feeding period increased R^2 for predicting HCW. Similarly, including early DMI data increased R^2 and decreased prediction error for DMI, indicating that updating predictions with interim performance data should prove beneficial. Adding data on previous health issues might improve predictions but is difficult to apply to pen settings. Environmental effects (e.g., severe heat or cold stress) can greatly affect performance and thereby decrease predictability. Overall, results suggest that initial BW has considerable value in predicting growth performance by feedlot cattle.

Key Words: feedlot cattle, initial body weight, predicted performance

51 Applying detection controls in assessing variance in feedlot cattle performance. R. A. Zinn*, *University of California*, *Davis*

ADG and DMI of feedlot cattle are predictable functions of gender, quality score (QS; values range from 1 to 3, increasing inversely with frame size), shrunk initial weight (SIW, kg), average shrunk live weight (SLW, kg), and dietary NEm and NEg (Mcal/kg):

MFWsteer, kg = 509.6 + 0.4697 SIW - 46.54 QS,
MFWheifer, kg = 551.5 - 0.2482 SIW + 0.00119 SIW^2 - 39.84 QS,
ADGsteer, kg = 1.628 + 0.00287 SIW −0.00000107 SIW^2 − 0.461 QS,
ADGheifer, kg = 1.265 + 0.00432 SIW - 0.00000425 SIW^2 − 0.410 QS,
DMIsteer, kg = $(0.0606*((SLW*478/MFW)^{0.75})*ADG^{0.905})/NEg) + (0.077LW^{0.75}/NEm)$,
DMIheifer, kg = $(0.0618*((SLW*478/MFW)^{0.75})*ADG^{0.905})/NEg)+(0.077LW^{0.75}/NEm)$.

Variance in observed vs expected feedlot cattle performance occurs for many reasons, including: inaccurate measures of dietary DM percentage; estimation of dietary NE; unbalanced rations; improper feed mixing; inadequate grain processing; negative associative effects of dietary ingredients (i.e., too much fat); poor weighing conditions; 3) errors in recording live weight and DMI; transferences of cattle from one lot to another; failure to implant, or improper implanting technique; pen location and/ or orientation; inadequate pen, shade, manger, or drinker allocation; poor pen conditions; environmental extremes; poor health; etc. In this presentation, numerous examples using actual feedlot closeout data will be provided to illustrate how performance expectations (standards of performance) are used in fine-tuning feedlot management decisions.

Key Words: feedlot, cattle, performance

Animal Behavior and Well-Being: Animal Welfare Assurance: Science and Application

52 Resource-based versus animal-based criteria in on-farm evaluation of welfare. A. Butterworth*, *University of Bristol, Clinical Veterinary Science*, *Langford, N Somerset, UK*.

Existing farm assurance schemes tend to assess welfare by examination of the provision of housing or resources (Resource Based Measures, RBM), rather than looking at the animals themselves (Animal Based Measures, ABM). Research scientists have for some time suggested that ABMs could provide valid indicators of animal welfare, since welfare is a characteristic of the individual animal, not just of the system in which animals are farmed. The sorts of questions which are being asked are Are the animals properly fed and supplied with water? Are the animals properly housed? Are the animals healthy? Can the animals express a range of behaviors and emotional states? To implement effective use of animal-based assessment methods on farm, it is necessary to adopt the following steps. Step 1, Measure (ABMs and RBMs) → Step 2, Analyze risk factors → Step 3, Inform (producer, purchaser) → Step 4, Support management decisions to create improvements in welfare. Once measures have been carried out on a farm, it may be possible to create a range of 'scores'. The individual measures can be combined to give aggregate scores which can be presented to the producer and the consumer. This requires the attribution of weighted values to the measures, to assess the impact of each measure with respect to animal welfare. In the Welfare Quality project, an Integrated European Research initiative carried out under Framework 6, ABM based assessment systems have been created for Pigs, Cattle and Poultry. There remain many questions regarding practical application of ABMs', - who will carry the cost, can the measures be made in a repeatable and reliable way within the timescale of an routine assessment, how would they work in relation to changing seasons, can a single farm-based score provide useful information, and can ABMs fit into existing assessment frameworks?

Key Words: farm assessment, animal based measures, outcome based measures

53 Developing animal welfare standards: Translating experimental studies to the farm. J. Rushen*[1], E. Vasseur[2], and A. M. de Passillé[1], [1]*Agriculture and Agri-Food Canada*, *Agassiz, BC, Canada*, [2]*University of British Columbia*, *Vancouver, BC, Canada*.

Considerable research has successfully developed measures of animal welfare and tested the effect of housing and management variables on welfare within controlled laboratory settings. However, there are challenges in extending this research onto farms. We illustrate some of these challenges and offer some solutions by referring to recent developments in welfare standards for dairy cattle. On-farm assessment of animal welfare requires using measures that can be taken by personnel with limited scientific training, in conditions that vary greatly among farms, usually in a short period of time, and often with little technical support. There is a risk that measures are chosen on the basis of feasibility rather than validity. Although the global assessment of animal welfare requires us to examine all aspects of animal welfare, these difficulties in taking measures have resulted in an over-emphasis on health based measures. Automated measures of behavior hold promise as a way of addressing some of this imbalance. Stakeholders prefer that animal welfare standards be science-based, but ensuring that such standards acknowledge the scientific uncertainty is also challenging. Balanced input from all scientific disciplines dealing with animal welfare is needed and the process of obtaining scientific input must be transparent and unbiased. Compliance with animal welfare standards requires buy-in from all stakeholders. The process used in developing the recent Canadian standards for the welfare of dairy cattle illustrates some methods for achieving this.

Key Words: animal welfare, dairy cattle

54 Integration of science, regulation and training in animal welfare auditing programs. J. C. Swanson*, *Michigan State University*, *East Lansing*.

Corporate social responsibility policies are employed by food retailers to publically convey an internal commitment to address an important consumer issue like farm animal welfare. Private sector social responsibility policies, coupled with increasing public scrutiny and calls for regulatory oversight of farm animal care practices, have led the US livestock and poultry industries to create voluntary guidelines and on-farm animal welfare assurance and audit programs. Third party audits, an audit in which the auditor has no conflict of interest with the farm he or she is auditing, are becoming a condition of doing business with the food retail sector. In addition, recent state legislative actions have created requirements for government oversight of standards of farm animal care that have been socially negotiated. Together, these social responsibility and legislative mandates create a need for highly trained farm animal welfare auditors. The objective of this paper is to examine the challenge of successfully integrating science and diverse regulatory mandates into an effective animal welfare auditing program.

Key Words: science, animal welfare, audits

Animal Health-Johne's Disease (JDIP): Basic Biology/Immunology/ Vaccine Development

55 A novel approach to evaluate the cost-benefit of use of Johne's disease vaccine while considering effects on the bovine tuberculosis eradication program. F. J. Zagmutt*[1], L. A. Espejo[2], H Groenendaal[1], J. R. Lima[2], E. Patton[3], I. A. Gardner[4], and S. Wells[2], [1]*Vose Consulting*, *Boulder, CO*, [2]*College of Veterinary Medicine, U. of Minnesota*, *St. Paul,* [3]*Division of Animal Health, Wisconsin DATCP*, *Madison, WI*, [4]*School of Veterinary Medicine, U. of California Davis*, *Davis*.

Johne's disease (JD) vaccination has the potential to reduce losses for individual herds. However, the effectiveness of widespread adoption of JD vaccination on JD control, and the effects of cross-reactivity (CR) between *M. avium* ssp. *paratuberculosis* (MAP) and *M. bovis* on the control and eradication of each disease is unknown. The objective of this study was to assess the cost-benefit of Johne's Disease (JD) vaccination on MAP infected dairy herds, and its effect on the bovine tuberculosis (bTB) eradication program in the USA. The results of 12,957 parallel fecal culture (HEY media) and serum ELISA (IDEXX) from 8 dairy herds enrolled in the MN JD Demonstration Herd Program over 9 years, and 970 fecal culture from 3 JD-vaccinated dairy herds enrolled in the WI JD Demonstration Herd Program for 4 years were used to build a model for the within-herd spread of JD and estimate its parameters. The uncertainty in the parameters was linked to the progression of the disease in each animal based on tests results. Herd and test parameters estimated with a latent-class Bayesian analysis were used to calculate the confidence in the disease status of each animal in time, and then the status of animals in each iteration was grouped to calculate spread parameters dynamically. The parameters were used to simulate disease spread in vaccinated and non-vaccinated herds. The model predictions using different scenarios of vaccine efficacy and disease spread were used in an economic break-even analysis. As bTB animal prevalence in the US may change in time, the threshold of bTB prevalence that would make JD vaccination not economic was calculated for each scenario. Even in scenarios with very high bTB prevalence (1% and higher) and a 10% relative drop in Sp of CFT in vaccinated herds, vaccination provided financial benefits (NPV > 0). However, while vaccination reduced herd-level JD losses at the producer level, the majority of the costs of CR due to JD vaccination are borne by the government. This economic threshold was highly sensitive to the reduction of JD losses resulting from vaccination.

Key Words: Johne's, bovine tuberculosis, modeling

56 Stochastic simulations of a multi-group compartmental model for Johne's disease on US dairy herds with test-based culling intervention. Z. Lu*, Y. H. Schukken, R. L. Smith, and Y. T. Gröhn, *Cornell University, Ithaca, NY.*

The objective of this study was to evaluate the effectiveness of test-based culling intervention and its impact on fadeout of Johne's disease in dairy herds using a stochastic modeling approach. Infection elimination may be an important goal of control programs; only in stochastic infection models can true infection elimination be observed, as fadeout. To investigate the stochastic dynamics of Mycobacterium avium ssp. paratuberculosis (MAP) infection in US dairy herds with test-based culling intervention, we developed a continuous time Markov chain model with both horizontal and vertical transmission. The stochastic model predicted fadeout and within-herd prevalence to have a large variance. Although test-based culling generally decreased prevalence over time, it took longer than would be desired by producers to eliminate an endemic MAP infection from a herd. Uncertainty analysis showed that, either using annual fecal culture tests and culling only high shedding animals or culling of both low and high shedders while delaying culling of low shedders for 12 mo, MAP infection persisted in many herds beyond 20 years. Using a semi-annual whole-herd fecal culture test and culling of both low and high shedders, with a 6-mo delay in culling of low shedders, MAP infection in many herds would be extinct within 20 years. Sensitivity analysis of the cumulative density function of fadeout suggested that combining test-based culling and reduction of transmission rates, through decreased contact between susceptible calves and shedding animals, may be more effective than either control strategy alone in eliminating endemic MAP infection. We also examined the effects of other factors, such as herd size, heifer replacement, and adult cow infection on the probability of fadeout.

Key Words: Johne's disease, test-and-cull, stochastic modeling

57 Unrestricted transmission of highly pathogenic Indian Bison type of *Mycobacterium avium* ssp. *paratuberculosis* in India. S. V. Singh*, B. Singh, A. Tiwari, A. Kumar, P. K. Singh, and A. V. Singh, *Central Institute for Research on Goats*, *Makhdoom, Farah, Mathura (UP), India, 281 122*.

The aim of present study was to determine the status of MAP infection and its genotype in free ranging wild species, primate, soil, river water, milk and humans to understand the disease transmission for future evaluation of regional and national JD control programs and improvement in diagnostics and vaccine designing. A total of 74 fecal samples from wildlife species [Monkeys (Primate)-25, Hog Deer-20, Wild bison-7, Chinkara deer-16, Blue bull-6], 39 stool samples from humans (with/ without inflammatory bowel disease; IBD), 51 soil samples (from grazing land), 8 water samples from different Yamuna river bank, were collected from North India and screened for the presence of MAP and further its genotyping by IS1311 PCR-REA. In 74 fecal samples from wild animals 50% and 46.9% were positive by microscopy and PCR [40.0, 20.0, 42.8, 100.0 and 66.6% (by microscopy) and 4.0, 15.0, 57.1, 75.0, and 66.7% (by PCR) Monkeys, Hog deer, Wild Bison, Chinkara deer and Blue bull, respectively). Of the 51 soil samples, 52.9 and 29.4% were positive for MAP by microscopy and PCR, respectively. In 8 samples from Yamuna river 12.5 and 37.5% sample were positive by microscopy and PCR. Out of 39 stool samples from humans 28.21 and 20.51% samples were positive in microscopy and PCR. There was significant high occurrence of MAP in samples collected from persons suffering from IBD. All the PCR positive samples in present study were showed restriction profile of 'MAP Bison type' by IS 1311 PCR-REA. High presence of MAP of same genotype i.e. Bison type in different free ranging wild animal species, primate, human, soil and river water indicated host unrestricted and high rate of transmission among different animals species, serious risk to human health and active biohazard for environment.

Key Words: *Mycobacterium avium* ssp. *paratuberculosis*, wild ruminants, environmental samples

58 *Mycobacterium avium* subspecies *paratuberculosis* produces endospores. E. A. Lamont*[1], J. P. Bannantine[4], A. Armién[1], D. S. Ariyakumar[3], and S. Sreevatsan[1,2], [1]*Veterinary Population Medicine,*

University of Minnesota, *Saint Paul*, [2]*Deptartment of Biomedical Sciences, University of Minnesota*, *Saint Paul*, [3]*Veterinary Diagnostic Lab, University of Minnesota*, *Saint Paul*, [4]*National Animal Disease Center, USDA-Agricultural Research Service*, *Ames, IA*.

Achievement of latency represents pathogenic mycobacteria's ultimate stratagem for survival, yet it remains one of the least understood and ill-defined aspects of its lifecycle. Two debated viewpoints concerning latency are that 1) bacilli are in a non-replicating state of chronic persistence (dormancy) and 2) replicating bacilli periodically escape from the granuloma and enter adjacent vessels to infect new sites. We hypothesize and show that MAP is capable of spore production in one year old MB7H9 cultures and AK-sporulation media. Experiments were conducted in triplicate. All MAP endospore samples, including germinated spores, were positive for IS900. All cultures were determined to be free of contamination by absence of growth on BHI plates. In addition to spore visualization, we have identified several mycobacterial candidate genes corresponding to those in the sporulation pathway of several *Bacillus* and *Streptomyces* species. Research investigating Bacillus spp. pathogenicity indicates that the stringent response regulated by carD is essential to robust spore production. Quantitative real-time PCR (Qt-RT-PCR) analysis of dormant MAP cultures show a 15-fold upregulation of carD compared with log-phase controls. MAP cells primed by carD may utilize sporulation as an alternate survival tactic to combat a hostile host environment to achieve latency. The hypothesized critical roles of carD and sporulation in latent infection is expected to aid in novel mitigation strategies to combat MAP infection, which may have far reaching benefits to other mycobacterial infections, including M. tuberculosis.

59 Transcriptional analysis of MAP genes contributing to invasion and persistence in ileal mucosa of cattle. S. Khare*[1], K. Drake[2], and L. G. Adams[1], [1]*Department of Veterinary Pathobiology, Texas A&M University*, *College Station*, [2]*Seralogix Inc.*, *Austin, TX*.

Mycobacterium avium ssp. *paratuberculosis* (MAP) initiate the disease process by invading and passing through the intestinal epithelium. This triggering mechanism is generally very rapid and may lead to a persistent infection. MAP undergoes a complex extracellular and intracellular environment. However, little is known about the bacterium-host interactions that occur at these stages. We hypothesize that MAP meets the challenges of hostile changing environments of ileum as soon as it comes into the contact of the host. We have used the MAP isolated from ligated ileal loop model to test our hypothesis. The objective of the current study was to determine the temporal changes in the MAP gene expression during the early invasion in the ileum. Tissue-associated MAP RNA from MAP infected bovine ligated ileal loop were enriched using "Prokaryote Enrichment kit" that selectively removes the Eukaryotic RNA. This enriched prokaryotic RNA is amplified using MAP-genome derived primers during in vitro transcription. Genomic DNA from in vitro grown MAP was labeled with Cy5 and used as the reference RNA. Enriched and amplified tissue-associated MAP was labeled with Cy3. The Cy5 labeled g-DNA and Cy3 labeled tissue-associated cDNA were co-hybridized on the MAP microarray (obtained from JDIP core facility). After hybridization arrays were washed and dried by centrifugation and were immediately scanned. We will describe in detail the groups of interrelated genes that as a whole represent the activation (perturbation) of pathways or GO biological processes over the time-course of these experiments (1h, 2h, 4h, 8h, 12h). This approach ranks groups of genes/proteins across all time points instead of individual genes in a single time point, to determine differences between experimental conditions. Using this approach, we have identified several mechanistic genes that play key regulatory role during invasion and persistence of MAP in the ileum.

Key Words: Johne's disease

60 The transcriptome of *Mycobacterium avium* subspecies *paratuberculosis* during infection. C.-W. Wei and A. M. Talaat*, *University of Wisconsin-Madison*, *Madison*.

Mycobacterium avium ssp. *paratuberculosis* (M. ap) causes an enteric infection in cattle, with a great impact on the dairy industry in the United States and worldwide. Before contracting a new host, M. ap are known to survive the harsh intracellular microenvironments, especially those inside activated macrophages. To improve our understanding of the pathogenesis of M. ap and help in a better control strategy against Johne's disease, we profiled the transcriptional responses of M. ap mutant or wild type following exposure to variable stress conditions including macrophage microenvironments. Mycobacterial cultures were exposed to heat shock, nitric oxide or H2O2 treatments. Other aliquots were used for infecting J774 cell lines at the 10 MOI (Bacteria: Macrophage). Following each stress, mycobacterial RNA samples were extracted using a Trizol-based protocol. Using DNA microarray analysis, Bayesian statistics revealed the presence of 123 genes that were significantly regulated when in vitro samples were compared with samples collected from M. ap isolated from 2 h post infection of macrophages. This group of genes includes sigH (a global gene regulator) and aceA that were shown before to play a role during infection. Further analysis identified additional 67 genes that were regulated when IFN-γ treated cells were compared with naïve cells before infection including genes involved in iron metabolism (e.g., fdxA). Currently, analysis is underway to generate specific gene mutants to examine their role in M. ap virulence using the mouse model of paratuberculosis. Overall, our analysis indicated a significant change in mycobacterial gene expression once they encounter the macrophage microenvironment. Additionally, the activity status of macrophages seems to play a role in directing the mycobacterial transcriptome to a specific stress-responsive profile.

Key Words: M. ap, genomics, pathogenesis

61 The response of auxotrophic MAP leuD mutant under environment stresses. J.-W. Chen*, J. Scaria, S. Chandra, and Y. F. Chang, *Cornell University*, *Ithaca, NY*.

Mycobacterium avium ssp. *paratuberculosis* (MAP) causes Johne's disease in ruminants. In M. tuberculosis, deletion of leuD gene results in severely attenuated phenotype. To explore the possibility of using leuD mutant strain of MAP as a vaccine candidate for Johne's disease, and to understand the mechanism of attenuation of MAP leuD deletion, a phage-mediated allelic exchange method was used to construct a leuD mutant strain in MAP K10 strain. The leuD deletion was confirmed by both PCR and DNA sequencing. In the absence of leucine supplementation, the growth of leuD mutant is completely inhibited in 7H9 medium. With supplementation of leucine the growth of mutant is restored but grows at a slower rate than that of wild type. To analyze the mechanism of leuD attenuation, mutant and wild type were subjected different environmental stress and following Agilent protocols. Three ug of RNA from mutant and wild types were competitively hybridized against a whole genome Agilent expression array of MAP. Array results were analyzed using Genespring GX 7.3. Arrays were log-transformed and subjected to lowess normalization and fold change analysis of mutant vs. wildtype was performed. Expression levels changes 1.5 fold or more were considered significant. The results of array studies demonstrate that leuD plays an important role in the MAP metabolism and that

there are more than 500 genes that belong to different pathways that are modulated in different stress conditions. These genes are distributed across Cluster of Orthologous Gene (COG) categories. The major COG categories include energy production and conversion, lipid transport and metabolism, inorganic transport, secondary metabolite production and cell membrane biogenesis. These results indicate that deletion of leuD in MAP results in global changes in lipid transport, cell secretion apparatus and changes in cell membrane biochemistry. Mice studies showed that inoculation of 107 cells of leuD mutant can provide partial protection of mice when challenged after 16 weeks with wild type.

Key Words: Johne's disease, LeuD mutant, microarray

62 A gene specific to *Mycobacterium avium* ssp. *paratuberculosis*, but only at the transcription-translation level. J. P. Bannantine*[1], R. E. Briggs[1], E. A. Lamont[2], J. R. Stabel[1], and S. Sreevatsan[2], [1]*National Animal Disease Center*, *Ames, Iowa,* [2]*University of Minnesota*, *St. Paul*.

There is no known antibody that detects *M. avium* ssp. *paratuberculosis* and does not cross react with other *M. avium* subspecies. In the present study, a monoclonal antibody was identified from mice immunized with a cell membrane fraction of *M. avium* ssp. *paratuberculosis* strain K-10. This antibody detected a protein in *M. avium* ssp. *paratuberculosis* whole cell extracts, but did not bind to any of the 20 non-paratuberculosis subspecies strains tested in immunoblot assays. The antibody was further tested with 15 strains of *M. avium* ssp. *paratuberculosis* and showed variable expression levels of the target binding protein in select strains. This target binding protein was identified by screening a *M. avium* ssp. paratuberculosis-lambda phage genomic expression library with the monoclonal antibody. The identity of the protein was encoded by a gene that was not annotated in the *M. avium* ssp. *paratuberculosis* K-10 genome sequence and showed no similarity to other proteins in sequence databases. Furthermore, this gene has extensive overlap with an annotated gene on the opposite strand. The epitope detected by the mAb was precisely mapped to 7 amino acids and served as an anchor point in studies that identified the start and stop locations for this unique gene. Similarity searches reveal that the DNA sequence is present in other MAC complex species. However, expression analysis shows that only *M. avium* ssp. *paratuberculosis* makes a transcript and expresses the protein in macrophages as well as when cultured in Middlebrooks 7H9. The protein is not a strong antigen, but it is detected in the context of Johne's disease. These findings have new implications for comparative genomics and gene regulation differences among mycobacteria.

Key Words: protein, antibody, Johne's disease

63 Binding affinity of *Mycobacterium avium* ssp. *paratuberculosis* 85 complex to 40 kDa domain of fibronectin. C. J. Kuo*[1], J. Bannantine[2], V. Kapur[3], and Y. F. Chang[1], [1]*Cornell University*, *Ithaca, NY*, [2]*NADC*, *Ames, Iowa*, [3]*Pennsylvania State University*, *University Park*.

Antigen 85 complex proteins (Ag85), consisting of members 85A, 85B and 85C, have been shown to be the important secreted antigens and are retained in the cell wall of Mycobacterium avium ssp. paratuberculosis (MAP). Ag85 binds specifically to a host extracellular matrix protein, fibronectin (Fn), which consists of N-terminal domain (NTD), gelatin-binding domain (GBD), cell-binding domain (CBD), and 40kDa domain. Fibronectin-binding proteins are important virulence factors of MAP and Ag85 may contribute to the adherence, invasion, and dissemination of organisms in host tissue. However, the critical residues of Fn involved in Ag85 binding are still unknown. Our objective of this study is to identify the Fn binding domain(s) to antigen 85 complexes. In this study, we constructed and overexpressed antigen 85A of MAP in *E. coli*. Four domains of Fn were tested for Ag85-Fn interaction by using native gel electrophoresis and ELISA. Except the 40 kDa domain (including 12, 13, 14, and v region), no significant binding was observed for other Fn domains. Subsequently, the synthesized peptides based on the binding sequence of Fn were subjected to a competition binding assay. Our data shows that these peptides can partially abolish the interaction between MAP and host cells. This is the first report to identify the Fn binding domain in Ag85.

Key Words: fibronectin, Johne's disease, adhesin

64 *MAP* induces calcium-dependent phagosome acidification to enlist IL-1β processing and macrophage recruitment. E. A. Lamont*[1], S. M. O'Grady[3], T. Eckstein[4], and S. Sreevatsan[1,2], [1]*Veterinary Population Medicine, University of Minnesota*, *Saint Paul*, [2]*Department of Veterinary Biomedical Sciences, University of Minnesota*, *Saint Paul*, [3]*Department of Animal Sciences, University of Minnesota*, *Saint Paul*, [4]*Department of Microbiology, Immunology and Pathology, Colorado State University*, *Fort Collins*.

Processing of *MAP* by the host epithelium involves a dynamic innate immune response initiated by *MAP*-epithelial cell cross-talk, which may also be further augmented by interactions between host pathways and/or cell types (epithelial-macrophage). We show that *MAP* induces phagosome acidification within MacT cells as early as 10 min., resulting in upregulation of IL-1β at transcript and protein levels. Previous studies report that IL-1β is a potent macrophage chemoattractant. We hypothesized that *MAP* harnesses host responses to recruit macrophages to the site of infection to ensure its survival and dissemination. These initial host-pathogen interactions may dictate a form of cooperative self-destruction in which the host is deceived into reacting to the benefit of *MAP*; thereby, setting the tone for the ensuing infection. We investigated macrophage recruitment in response to *MAP* using a MacT-bovine macrophage coculture system. All time points were conducted in triplicate. Within 10 min of *MAP* infection, macrophages were recruited to the apical side of Mac-T cells ($P < 0.05$, ANOVA). Inhibiting phagosome acidification with bafilomycin treatment abrogated this response ($P < 0.05$, ANOVA). Since IL-1β cleavage and subsequent release to the epithelial milieu is dependent upon calcium influx, we next sought to define the role of calcium oscillations in phagosome acidification and macrophage recruitment. Pre-treatment of Mac-T cells with BAPTA-AM, an established intracellular calcium chelator, abolishes phagosome acidification and IL-1β processing to its active form. Thus, *MAP* guidance of phagosome-acidification enlists IL-1β processing in a calcium dependent manner to efficiently transverse the epithelium and into its niche—the macrophage.

65 Macrophages infected with *Mycobacterium avium* subspecies *paratuberculosis* are highly resistant to apoptosis, while uninfected culture mates are highly apoptotic. E. Kabara* and P. M. Coussens, *Michigan State University*, *East Lansing*.

Mycobacterial infections have long been implicated in altering the apoptosis status of infected macrophages. Previous research has linked more virulent mycobacteria to an increase in macrophage apoptosis. However, this research often does not take into account that most macrophage culture infections with mycobacteria are mix of infected and uninfected cells, with the infected macrophages comprising less then 50% of the total cell population. More recent studies specifically looking at the differences between infected and uninfected macrophages in a culture

show that most of the infected macrophages are highly resistant to cell death while the uninfected macrophages are more likely to undergo apoptosis. While most of this evidence has arisen from research with Mycobacterium tuberculosis, a large scale microarray project recently performed by our group implicated infection with Mycobacterium avium subspecies paratuberculosis (MAP), the causative agent of Johne's disease in cattle and possibly Crohn's disease in humans, as changing the apoptotic potential of cultures. We hypothesize that MAP-infection prevents apoptosis in infected macrophages while upregulating apoptosis in uninfected macrophages in the same culture to prevent proper immune function while increasing bacterial survival. To study the true apoptotic status of MAP-infected and MAP-uninfected macrophages in the same culture, fluorescent dye was used to label the bacteria before infection and cells were examined individually using flow cytometry. After using the Annexin V/ 7-AAD apoptosis stains, we clearly show that MAP-infected macrophages are much less likely to undergo apoptosis, while uninfected macrophages in the same culture are highly apoptotic. We further demonstrated that MAP-infected macrophages are much more likely to undergo necrosis when stimulated with hydrogen peroxide, TNFa, and FASL. Conversely, uninfected macrophages in a MAP-infected culture are much more likely to undergo apoptosis than control macrophages unexposed to MAP after stimulation with these same agents.

Key Words: *Mycobacterium*, paratuberculosis, apoptosis

66 Genetic correlations of gross feed efficiency with yield, body weight, body condition score, and energy balance in dairy cattle. C. D. Dechow*[1], J. Vallimont[1], M. D. Dekleva[1], J. M. Daubert[1], and J. W. Blüm[2,1], [1]*Pennsylvania State University*, *University Park*, [2]*Unversity of Bern*, *Switzerland*.

The objective of this study was to estimate genetic correlations of gross feed efficiency with 305 d fat corrected milk yield (FCM), 305 d protein yield, body weight (BW), body condition score (BCS), BCS change (BCSCH) from 5 to 30 d in milk (DIM), and cumulative energy balance (CEB) from 5 to 30 DIM. Intake, BW and BCS were recorded once per month for 6 consecutive months on 11 Pennsylvania tie-stall dairy farms. Feed samples were taken at each visit to determine net energy of lactation intake (NEI) and crude protein intake (CPI). Random regression models were used to analyze 35,390, 3999, 2195 and 4998 test day records of yield, intake, BW and BCS, respectively. Daily phenotypic FCM, protein yield, BW, BCS, NELI and CPI were derived from the random regression model solutions. Daily records were used to obtain 305 d totals (FCM, protein yield, NELI, and CPI), 305 d averages (BW and BCS), and BCSCH. Daily energy balance was derived from daily FCM, BW and BCS observations and summed from 5 to 30 DIM to obtain CEB. Net energy efficiency (NEE) was defined as FCM/NEI, whereas protein efficiency (PE) was defined as protein yield/CPI. The traits were analyzed with multiple-trait animal models that included fixed effects of lactation and herd-year-season of calving; random effects included animal, permanent environment, and error. NEE was genetically (0.92) and phenotypically (0.81) correlated with higher FCM. Likewise, genetic and phenotypic correlation estimates between PE and protein yield were strong at 0.96 and 0.80, respectively. BCS and BW were negatively correlated with NEE and PE (genetic correlation range = −0.42 to −0.54). Genetic correlation estimates of CEB with NEE and PE (−0.51 and −0.52, respectively) and of BCSCH with NEE and PE (0.64 and 0.73, respectively) were unfavorable. Genetic variation exists for feed efficiency, but measures of efficiency not unfavorably correlated with energy balance should be considered.

Key Words: feed efficiency, energy balance, genetic correlation

67 Genetic characterization of feed intake and utilization in performance tested beef bulls. D. H. Crews Jr.*[1], C. T. Pendley[1], G. E. Carstens[2], and E. D. M. Mendes[2], [1]*Colorado State University*, *Fort Collins,* [2]*Texas A&M University*, *College Station*.

Feed intake, growth, and pedigree data from the Midland Bull Test database were used to estimate parameters required for genetic evaluation of feed utilization traits. Length of the feeding period was 70 d, and test ADG was estimated as the slope of the regression of BW on test d. Records on DMI, ADG, and estimated mid-test BW raised to the power of 0.75 (MBW) from bulls (n = 2,346) and heifers (n = 221) representing 11 breeds (1,819 Angus) were included in a multiple trait animal model to estimate variance components using average information REML. The model for all traits included the fixed effects of contemporary group (n = 99) and a linear covariate for age at the start of test, and random animal genetic effects (n = 10,327). Heritability estimates for DMI, ADG, and MBW were 0.45 ± 0.09, 0.35 ± 0.07, and 0.54 ± 0.09, respectively, and genetic correlation estimates (SE <0.13) among the traits were positive, ranging from 0.38 to 0.60. Phenotypic residual feed intake (RFI) was defined as the difference between DMI and expected DMI from regression on ADG and MBW. A 4 trait model including phenotypic RFI failed to converge because of the linear dependence with DMI, ADG, and MBW. Breeding values for genetic RFI were then estimated as the difference between EBV for DMI and expected DMI derived using genetic regression. Genetic RFI has the property of independence from EBV for ADG and MBW whereas traditional EBV for phenotypic RFI could have genetic correlations with ADG and MBW. Genetic RFI EBV ranged from −0.54 to 0.56 kg/d (SD = 0.08). Phenotypic or genetic RFI contain no more information than DMI, ADG, and MBW phenotypes or EBV, respectively. Therefore, genetic evaluation of RFI is equivalent to evaluation of a function of the component traits.

Key Words: beef cattle, feed intake, genetic evaluation

68 Analysis of published genetic parameter estimates for feed utilization traits in beef cattle. C. T. Pendley*, R. M. Enns, and D. H. Crews Jr., *Colorado State University*, *Fort Collins.*

Increasing profitability of beef production through the reduction of inputs has been documented by an increasing number of published genetic parameter estimates for feed intake and utilization traits. The inclusion of input traits in genetic improvement programs requires knowledge of parameters for those traits, but an understanding of these parameters, especially for feed intake, is limited due to the cost of recording individual feed intake on cattle and reports are scarce. Fourteen sets of estimates involving more than 34,000 cattle and published between 1995 and 2010 were included in a meta-analysis of genetic parameters for feed intake and related traits. Papers were required to include individual feed intake, and computed SE for heritability and genetic correlation estimates. A generalized least squares approach was used to compute weighted mean heritability and genetic correlation estimates, as well as their weighted SE, where weights were a function of inverse SE. Weighted heritability estimates for feed conversion ratio (FCR), residual feed intake (RFI), ADG, metabolic body weight (MBW) and DMI were 0.28 ± 0.08, 0.38 ± 0.08, 0.32 ± 0.08, 0.39 ± 0.08, and 0.41 ± 0.07, respectively. Weighted genetic correlations of FCR with RFI, ADG, MBW, and DMI were 0.60 ± 0.11, −0.31 ± 0.14, 0.03 ± 0.15, and 0.35 ± 0.12, respectively. Weighted genetic correlations of RFI with ADG, MBW were near zero, but were 0.38 ± 0.09 with DMI. The phenotypic correlation of RFI with ADG and MBW are forced to zero by definition. The weighted genetic correlation of ADG with MBW was 0.45 ± 0.13. These weighted heritability and genetic correlation estimates may be more useful in the design of genetic improvement programs than relying on estimates from individual studies with low numbers of feed intake observations.

Key Words: feed intake, genetic parameters, meta-analysis

69 Heritability and genetic correlations of residual feed intake between Angus and Simmental bulls and resulting steer relatives. W. C. Rutherford*, L. A. Kriese-Anderson, and G. S. Hecht, *Auburn University*, *Auburn, AL*.

Objectives of this research are to observe breed differences for feed intake (FI) and trait differences of low, medium and high residual feed intake (RFI) bulls and steers, estimate h^2 in central tested bulls and steers and compare RFI in bulls and steers. Individual FI was measured on 1433 Angus, Simmental and composite Simmental-Angus bulls at the Auburn University Beef Evaluation Center (AUBEC) from 1977 to 2007. Bulls were consigned by producers and housed at the AUBEC a minimum of 70 d. Bulls were measured for weight and height biweekly or monthly depending on year. SC and ultrasound measurements for carcass traits

were taken at yearling age (330 to 400 d). FI and carcass trait data from 760 Angus and Simmental-composite steers were acquired courtesy of the American Simmental Association Carcass Merit Project. RFI was determined by regressing metabolic mid-weight and ADG on intake by year of test for bulls and by contemporary group (cg) for steers. High percentage Angus bulls consumed more DM per day, had higher FCR and RFI than purebred Angus, 50% Angus: 50% Simmental (50:50), high percentage Simmental and Simmental bulls. Angus steers consumed more DM per day had higher FCR and RFI than high percentage Angus and 50:50 steers. Heritability was estimated for RFI using a bivariate model and MTDFREML in bulls (0.42 ± 0.05) and in steers (0.20 ± 0.05). Fixed effects for bulls included year and breed percentage. Fixed effects for steers included cg and breed percentage. Covariates of final age, final wt or final frame score were used. Genetic correlations between steer and bull RFI ranged from −0.18 to 0.33 depending on covariate. Bulls and steers classified as low RFI consumed less DM per day and had more favorable FCR than medium and high RFI animals. Results indicate RFI is a moderately heritable trait and improvements for FI and FCR should be achievable when selection is made using RFI. However, selection of bulls based on their RFI in an attempt to sire more efficient steers may not be practical as the genetic relationships between steer RFI and bull RFI were variable and moderate.

Key Words: residual feed intake, heritability, genetic correlations

70 A region on BTA6 is associated with feed intake and gain in beef cattle. A. K. Sexten*[1,2], L. A. Kuehn[1], T. P. L. Smith[1], H. C. Freetly[1], W. M. Snelling[1], and A. K. Lindholm-Perry[1], [1]*USDA, ARS, U.S. Meat Animal Research Center*, *Clay Center, NE,* [2]*Oklahoma State University*, *Stillwater*.

Genetic selection for animals that require less feed while still achieving acceptable levels of production could result in substantial cost savings for cattle producers. The purpose of this study was to identify DNA markers with predictive merit for differences among cattle in feed intake and BW gain. Crossbred steers (n = 1,195) were fed a high-corn diet for 140 d and ADFI, residual feed intake (RFI), and ADG were measured. Steers were genotyped with the Illumina Bovine SNP50 BeadChip. An association analysis of these SNP on each trait was performed using MTDFREML, from which 14 SNP clustered in a 1.7Mb region at BTA6: 37.4 to 39.1 were identified as having significant association ($P \leq 0.009$) with one or more of the 3 traits. All statistical models included fixed effects of year and location; covariates of age, heterosis, and breed percentage; and a random polygenic effect. To develop markers with the maximum ability to discriminate favorable alleles and potentially identify the functional variation, 44 additional SNP, not present on the BeadChip, were identified in and around potential candidate genes in this chromosomal region. These new SNP were genotyped on the same animals and the statistical analysis program Mendel was used to test for association with feed intake and gain. Four markers located in a 90Kb region on BTA6 were significant for both ADFI and ADG. After correction for multiple testing, all markers remained significant for ADG ($P \leq 0.02$) and 2 markers were significant for ADFI ($P \leq 0.01$). These markers are located in a bovine gene that is homologous to a human gene that has been associated with skeletal frame size, thus providing a potential link between the observed bovine variation and growth-related traits of ADFI and ADG. Genetic markers predictive for feed intake and growth in this population of cattle may be useful for the identification and selection of animals that are more efficient, although potential impact of marker-assisted selection on all production traits will need to be assessed.

Key Words: beef cattle, genomics, feed efficiency

71 A neural network approach for association between a low-density whole genome SNP marker panel and residual feed intake and dry matter intake. H. Wang*[1], X. Liu[1], B. Woodward[2], S. Bauck[2], and R. Rekaya[1], [1]*University of Georgia*, *Athens,* [2]*Merial Limited*, *Duluth, GA*.

The predictive ability of a low-density SNP panel derived from the Illumina Bovine SNP50 and developed for marbling, backfat thickness, hot carcass weight, ribeye area, yearling weight, and heifer pregnancy rate was evaluated for residual feed intake (RFI) and dry matter intake (DMI). Data consisted of the genotypes of 1,032 Angus animals and their corresponding EPDs computed from actual individual weight and intake data. Missing genotypes were replaced with the most likely genotype. Linear regression (LR) and neural network (NN) approaches were implemented and compared. For LR, a cross validation procedure was adopted where the data was randomly divided into 5 groups with equal size. In each one of the 5 replicates, 80% of the data was used for training and the remaining 20% for validation. For the NN approach, randomly 2/3 and 1/3 of the data were used for training and validation, respectively. The process was replicated 5 times. A NN is an artificial system of massively interconnected neurons. The network architectures and the learning algorithm define the manner in which the neurons are related and structured. In this study, a feed-forward NN with one hidden layer was used. The parameters of the NN such as the number of neurons in the hidden layer, and learning rate were set heuristically. For RFI, the correlation between the observed and predicted breeding values for the validation data was 0.22 and 0.28 for the LR and NN, respectively. The correlation was 0.23 and 0.36 for DMI using LR and NN, respectively. These results indicate that, although the low-density SNP panel was developed for other traits, it still has some ability to predict RFI and DMI. The lower correlations observed for RFI could be due in part to the uncertainty on the trait of RFI compared with DMI that tends to be more accurately measured. The superiority of the NN approach could be due to its ability to intrinsically accommodate the non-linear relationship between variables.

Key Words: SNP, whole genome, feed efficiency

72 Effects of divergent selection for serum insulin-like growth factor-I concentration on mature weight and growth curves in Angus cattle. Q. Qin* and M. E. Davis, *The Ohio State University*, *Columbus*.

The purpose of this study was to investigate the effect of divergent selection for serum insulin-like growth factor-I (IGF-I) concentration on mature weight estimated using growth curve functions in Angus cattle. Multiple serum IGF-I measurements (d 28, d 42, d 56 of the 140-d postweaning period) from a total of 2,514 animals and weight records from birth to at least 3 yr of age from a total of 172 animals were collected from an ongoing divergent selection experiment involving IGF-I that was initiated in 1989. Four growth curve functions (Brody, Logistic, Gompertz, Von Bertalanffy) were used to estimate the parameters for mature weight (A) and maturing rate (k) using the NLIN procedure in SAS (SAS Inst. Inc., Cary, NC). The heritability estimates for serum IGF-I at different ages and growth curve parameters from each function were estimated using a multiple-trait, derivative-free, REML program. Genetic, environmental, and phenotypic correlations between IGF-I and growth curve parameters were also obtained. The direct heritability (h_d^2) estimates for serum IGF-I at d 28, 42, and 56 were 0.42, 0.42, and 0.33, respectively. The h_d^2 estimates for A from the 4 growth functions ranged from 0.72 to 1.00, whereas h_d^2 estimates for k ranged from 0.01 to 0.21. The genetic correlations between A and k within each growth curve function ranged from −0.57 to −0.49. The genetic correlations

between IGF-I (d 28, 42, and 56) and A within each growth curve function ranged from −0.46 to −0.01. Although serum IGF-I was negatively correlated with mature weight genetically, the phenotypic correlation between these 2 traits was moderate (0.47 to 0.59) due to a highly positive environmental correlation (1.00). The shapes of growth curves from the 4 functions were almost identical, as were the growth curves for the high and low IGF-I selection lines.

Key Words: Angus cattle, growth curve, insulin-like growth factor

73 Bayesian estimation of a genetic covariance matrix with different degrees of belief via a Generalized Inverted Wishart distribution. R. J. C. Cantet*, *Facultad de Agronomía, Universidad de Buenos Aires - CONICET*, *Buenos Aires, CABA, Argentina*.

When taking a Bayesian approach for estimating a genetic covariance matrix, animal breeders use an Inverted Wishart (IW) prior density. The advantage of this formulation is that the posterior distribution is in conjugate form, so that the sampling is from an updated IW. Also, the degrees of belief are the same for all genetic parameters, i.e., any (co)variance component is assumed to have the same amount of prior information. However, there are situations where this assumption does not hold. Take for example a model with grand-maternal effects. There is more prior information and information on the data for the additive direct variance than for the additive maternal variance and this, in turn, has more information than the additive grand-maternal variance. The objective of this research was to develop an algorithm for estimating a genetic covariance matrix with different degrees of belief for the (co) variance components. The method employs the Bartlett decomposition of a matrix to produce a conditional covariance matrix from the generalized inverted Wishart distribution (GIW). As a result, the algorithm consists of successive samplings from inverted chi-squared (or IW) densities for the additive variances, and from normals (or multivariate normals) for the additive covariances. It should be mentioned that the genetic parameters have to be ordered within the covariance matrix so that their degrees of belief decrease when going from the first row (or column) to the last. The algorithm was employed on a beef cattle data set, and the model fitted included additive direct, maternal and grand-maternal effects. The classic algorithm using the IW to sample from the conditional posterior of the additive covariance matrix was also fitted to the data. Convergence was faster for the GIW methods than for the IW, as samples of the (co)variance components were less dependent. In conclusion, the GIW algorithm allowed the use of different degrees of belief for the dispersion parameters and converged faster to the stationary distribution.

Key Words: generalized inverted Wishart, Bayesian estimation, additive covariance matrix

74 A simulation approach for analyzing genomic data using a package of specific FORTRAN 90 functions. P. Faux*[1,2] and N. Gengler[1,3], [1]*University of Liège - Gembloux Agro-Bio Tech*, *Gembloux, Belgium*, [2]*National Research Fund*, *Luxembourg, Luxembourg*, [3]*National Fund for Scientific Research*, *Brussels, Belgium*.

A panel of FORTRAN 90 functions was developed to simulate the distribution of bi-allelic (e.g., SNP) genetic markers along a defined genome and the distribution of their alleles in a given population. The simulation program used 3 parameters, those related to the species studied (number of autosomes, average length of autosomes, average number of crossovers by chromosome), the number of markers and those related to the studied population (pedigree). The simulation proceeds in 3 steps: a) random choice of marker positions and allelic frequencies for the minor allele of each marker (range: 0.05 to 0.475), b) simulation of genotypes of the ancestors in the pedigree based on randomly chosen allelic frequencies and c) planned mating of the ancestors according to the pedigree and according to the average crossover rate as a genetic recombination parameter. The simulation returns a fully-genotyped population. This method is flexible because it can be applied to a wide range of cases (not restricted to a single species) and the FORTRAN functions can be extended and used to simulate phenotypes. It is also realistic, because it performs mating plans and selection of animals based on real pedigrees. Development of this simulation panel was the first step in research around advanced methods to compute and invert genomic relationship matrices.

Key Words: genomic prediction, SNP simulation

ASAS-EAAP Global Issues Symposium: Contemporary and Emerging Issues and International Animal Agriculture Joint Symposium: Global Livestock Production to 2050: Challenges and Opportunities

75 Perspectives for livestock production in developing countries – changes in production systems needed to meet projected demand. R. D. Sainz*[1], G. B. Martha, Jr.[2,3], and L. G. Barioni[4], [1]*University of California*, *Davis*, [2]*Embrapa Cerrados/Embrapa Strategic Studies and Training*, *Brasília-DF, Brazil*, [3]*Fellow, National Research Council*, *Brazil*, [4]*Embrapa Agricultural Informatics*, *Campinas-SP, Brazil*.

According to the medium growth projections of the United Nations, the human population should reach 9.15 billion by 2050, an increase of 33% over the 6.91 billion today. This increase will take place largely in developing countries. Additionally, developing countries are projected to experience a steady increase in per capita income, so that demand for food should increase by close to 70%, and for animal products by perhaps 100%. This scenario raises concerns about use of scarce resources, mainly land and water, as well as other environmental, social and economic impacts. Moreover, these changes will be concentrated in developing regions, and the technological advances in tropical agriculture required to achieve a sustainable path toward food security over the next decades must take all of these factors into account. In particular, opportunities for expanding agricultural frontiers are limited. Clearly, a 100% increase in meat and milk production on the same or only slightly greater crop and pasture land areas will require substantial improvements in productivity. This paper qualitatively and quantitatively describes several technologies and production systems that show promise toward meeting the expected demand. These include genetically improved crops, pastures and animals, integrated crop-livestock-forestry systems, increased animal feeding (particularly with crop and industrial by-products), improved pasture management, and alternative production systems (such as improved aquaculture systems). Development and implementation of these technologies and systems will require major investments by the private and public sectors. A revitalization of agricultural R&D investments to sustain productivity growth over the long run and a comprehensive program of technology transfer are needed if economic, social and environmental objectives are to be met.

76 A European perspective on the challenges for livestock farming to achieve a sustainable contribution to food security and a reduced impact on the environment. P. Herpin*[1], R. Duijghuisen[2], J. Oldham[3], P. Vriesekoop[2], and J. Williams[1], [1]*INRA*, *France*, [2]*Wageningen UR*, *the Netherlands*, [3]*Scottish Agricultural College*, *Scotland*.

World population forecasts are 9.2 billion by 2050. The daily intake of animal products will continue to rise as economies develop. Over 56% of people in the European Union live in rural areas where the livestock sector underpins community cohesion and employment. Its farm gate production value was 152 billion € in 2008, but its contribution to the European economy is greater as it supplies other sectors that generate considerable added value. Sustaining and even expanding the animal-farming sector to meet the demands for food, to reduce the rural exodus, is a priority. The European challenge is complex because we must not only increase efficiency and effectiveness to face very strong global competition but also accommodate major demands for a positive environmental impact, improved animal health and welfare and adapt to possible future changes in the Common Agricultural Policy. Climate change may also alter production capacity differentially across Europe, accelerate the emergence of new animal diseases and menace animal and human health. Both adaptation and mitigation strategies will recognize these challenges and opportunities. Past research reinforced the sector's competitiveness. But we need a 'vision for tomorrow' to face these new grand challenges that will re-design more sustainable, integrated, resource efficient and environmentally acceptable production systems. This will take new knowledge from research, with efficient innovation, implementation, and shifts in stakeholder behavior e.g., exploiting new genomic tools for novel multi-trait selection of robust and healthy animals. Renewed attention to the exploitation of feed resources, to improving reproductive efficiency, to more integrated approaches to disease control and animal welfare, and to generating animal products beneficial to human health is also needed. This research agenda needs to address local issues in a global context, embracing all disciplines and stakeholders. Research teams must question past practices, use open thinking to encompass these new dimensions, dialog with other disciplines and network in a constructive manner with society at large.

77 Sustainability of livestock production globally. H. Steinfeld*, *UN Food and Agriculture Organization*, *Rome, Italy*.

The livestock sector is contributing to the globally increasing pressure on ecosystems and natural resources: land, water and biodiversity. At the same time, the sector is increasingly facing natural resource constraints and growing competition for resources. Awareness is also increasing of the interactions between livestock and climate change, with the livestock sector both contributing to it and suffering from its impacts. Conversely, it is also being recognized that the sector can play a key role in mitigating climate change through improved technologies. Governments and institutions need to develop and enact appropriate policies that focus on and account for livestock-environment interactions. Continued growth in livestock production will otherwise exert enormous pressures on the health of ecosystem, biodiversity, land and forest resources, and water quality, and will contribute substantially to global warming. A key policy focus should be on correcting market distortions and policy failures that encourage environmental degradation, such as subsidies that directly or indirectly promote overgrazing, land degradation, deforestation, over-use of water, or greenhouse gas emissions. Market-based policies should cause producers to internalize the costs of environmental damages caused by livestock production. Environmental damage associated with open-access common-property resources can be addressed by clarifying property rights and promoting mechanisms for cooperation. The promotion of technologies that improve land and feed efficiency can mitigate the negative effects of livestock production on biodiversity, ecosystems, and global warming. Technologies that increase livestock efficiency include improved genetics, improved grazing land management, improved herd health management, and silvopastoralism. Payments for environmental services can be an effective means to promote better environmental outcomes. The livestock sector has an enormous potential to contribute to climate change mitigation. Realizing the potential will require new and extensive initiatives at national and international levels, including the promotion of research and development on new mitigation technologies; and effective and enhanced means for financing.

Extension Education 1

78 Multi-state Beef Reproduction Task Force provides science based recommendations for the application of reproductive technologies. S. K. Johnson*[1], R. N. Funston[2], J. B. Hall[3], D. J. Kesler[4], J. W. Lauderdale[5], G. C. Lamb[6], D. J. Patterson[7], G. A. Perry[8], and D. R. Strohbehn[9], [1]*Kansas State University*, [2]*University of Nebraska*, [3]*University of Idaho*, [4]*University of Illinois*, [5]*Michigan State University*, [6]*University of Florida*, [7]*University of Missouri*, [8]*South Dakota State University*, [9]*Iowa State University*.

Beef extension personnel met in 2000 to determine how best to communicate to beef producers the latest information related to reproductive technologies. Research on estrous cycle control in cattle had expanded to more precise methods that included treatment with progestins, manipulation of follicular waves, and control of the lifespan of the corpus luteum. The rapid development of new protocols to synchronize estrus and ovulation and their associated acronyms created confusion. The Beef Reproductive Task Force was formed to coordinate efforts to identify effective breeding management protocols and to provide leadership for education. Based on research data and field experience, a short list of recommend protocols for synchronization of estrus and ovulation was developed in cooperation with representatives from semen providers, veterinarians and the animal health industry. These protocols are presented uniformly in sire catalogs from all major semen providers. Protocol updates occur annually to incorporate appropriate research findings. In cooperation with the Iowa Beef Center, the Estrus Synch Planner software program now reflects the same recommendations. Since 2002 the Beef Reproduction Task Force has hosted 9 educational workshops in key cow-calf states representing 66% of US beef cows; targeted were producers, AI technicians, veterinarians, allied industry and academia. A national media sponsor has provided online coverage of the last 2 meetings. At the most recent conference, 77% of attendees indicated that information received at the conference would probably or definitely increase the profitability of their operation. When asked what changes they would make in how they applied reproductive technologies, 55% provided a response with 15% responding more use of fixed-timed AI, 13% more use of AI and/or synchronization, and 40% would change something about how they applied the technology such as specific protocols or management changes.

Key Words: estrous synchronization, fixed-timed AI, beef cattle

79 Fundamentals of beef reproduction and management: Focus on estrus synchronization. A new web-based curriculum. D. J. Patterson*[1], R. D. Geisert[1], D. C. Busch[2], N. R. Leitman[3], S. E. Poock[1], J. L. Parcell[1], and M. F. Smith[1], [1]*University of Missouri*, *Columbia,* [2]*KABA Select Sires, Inc.*, *Louisville, KY,* [3]*Boehringer Ingelheim Vetmedica Inc.*, *St. Joseph, MO*.

Reproduction is the major factor impacting profitability in a cow-calf operation. The largest cause of reproductive loss in beef herds is that cows fail to become pregnant during the breeding season. Heifers and cows fail to become pregnant because they do not show estrus or fail to conceive after showing estrus. Estrus synchronization protocols have been developed that increase the proportion of females that conceive early in the breeding season and facilitate the use of AI. Estrus synchronization and AI create the opportunity to add value to a beef cattle enterprise through use of high accuracy sires and enhanced reproductive management. A new web-based curriculum is available for beef producers, animal science instructors, veterinarians, allied industry and students entitled Fundamentals of Beef Reproduction and Management: Focus on Estrus Synchronization. The curriculum includes 3 courses with the following topics. Course 1 provides an overview of physiological principles that underlie estrus synchronization, and a review of commercially available estrus synchronization products. Course 2 reviews estrus synchronization protocols recommended for beef heifers and cows. Course 3 reviews management considerations for implementing an estrus synchronization program and a description of the impact of estrus synchronization on reproductive management. Each module includes assessment questions to evaluate the student's comprehension of the information. The focus of this Extension education program draws on the fundamental basis upon which extension and the Land Grant System were founded: The use and application of what we know to create knowledge. This curriculum will enable participants to effectively implement reproductive strategies into practice. The curriculum is available through the University of Missouri Division of Animal Sciences Web site at http://animalsciences.missouri.edu/, and the NCBA Cattle Learning Center.

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Key Words: curriculum, estrus synchronization, AI

80 Transferring reproductive technologies to the field: Fixed-time AI and high accuracy sires. D. J. Patterson*, D. A. Mallory, J. L. Parcell, S. E. Poock, and M. F. Smith, *University of Missouri*.

USDA-NRI integrated projects require a combination of research, education and extension and are expected to generate new knowledge, coincident with the application of existing knowledge. Project themes are required to be outcome oriented, stakeholder driven and problem focused. Our goal has been to foster the adoption of reproductive technologies focused on expanded use of fixed-time artificial insemination, and coincident with progress in the development of new and more effective methods to synchronize estrus and ovulation in beef cattle. Missouri's Show-Me-Select Replacement Heifer Program provides the infrastructure for effective implementation of new reproductive technologies and economic feedback regarding their use. By-products of adoption of reproductive technologies in beef cattle include enhanced genetic merit of heifers and steers, and improvements in whole herd reproductive management. Beef producers interested in implementing or expanding an AI program are encouraged to identify high accuracy sires for use in their AI programs. The Missouri Show-Me-Select Replacement Heifer Program recently created a Tier 2 classification that distinguishes heifers from high accuracy sires. Economic data collected from the program will be used to value heifers based on genetic merit, and economic indexes for heifers will be determined from steer mates based on feedlot performance and carcass merit. Organized on farm demonstrations facilitated the transfer of technology related to fixed-time AI to 73 herds in Missouri involving 7028 cows. In addition, the Division of Animal Science's Miller Internship in Reproductive Management has provided internship opportunities for 140 students that involved breeding programs in 12 states and over 175,000 cows and heifers. These efforts have lead to the successful integration of research, education and extension programming and are collectively impacting reproductive management in Missouri's beef herds.

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Key Words: technology transfer, beef, AI

81 Evaluation of attitudes, knowledge gained and anticipated behaviors of extension clientele completing food defense training conducted regionally in Missouri. R. L. Weaber*, C. L. Lorenzen, M. K. Hendrickson, A. D. Clarke, M. C. Shannon, R. M. Torres, and K. L. Savage-Clarke, *University of Missouri*, *Columbia*.

Food defense is the prevention of intentional contamination at any point during the food production/processing chain. To increase awareness of food defense government directives and industry initiatives among food producers and processers, a work book curriculum was developed and a series of half-day workshops were conducted in 5 regions of Missouri. In addition to providing basic information about the importance of food defense as a mechanism to help ensure the safety and security of the US food supply, the workshop included training on risk assessment, countermeasure development, construction and implementation of a food defense and a response plan. Workshop participants (n = 81) were surveyed to evaluate the quality of the curriculum, pre- and post-training attitudes, knowledge gain and anticipated behaviors. Participants included livestock producers (15%), crop producers (4%), food processors (22%), producers targeting production to local food systems (35%), and others (25%) that included animal nutritionists, and inspectors/regulatory personnel. Two-thirds of respondents (n = 59) indicated their operation employed only family members or less than 6 individuals. Seven percent of operations had > 100 employees. Prior to the workshops, 22% of respondents (n = 63) were not familiar with the term ′food defense′ while 42% had either written or were familiar with the basics of a food defense plan. 83% of respondents (n = 74) indicated the information was valuable to their operation. A 6-point Likert scale was used to evaluate knowledge gain. More than 90% of participants indicated with scores of 4 or higher (4 = somewhat agree, 5 = agree, 6 = strongly agree) that they could assess risks, describe basic steps, develop a food defense and response plan. Perimeter security was most often cited (19%) as a vulnerability followed by limiting access to internal areas/processes (14%). Following the workshop and development of their own food defense plan, 42% of the participants had an increased awareness of food defense and 50% planned to either implement or maintain their plan.

Key Words: food defense, curriculum, extension

82 Documenting a 60-year trend in improved efficiency for the United States swine industry. M. S. Carlson*, J. A. Lory, R. E. Massey, B. Young, J. Zulovich, S. Edwards, R. Plain, and T. J. Safranski, *University of Missouri*, *Columbia*.

Swine production practices have evolved significantly over the past 60 years. In the mid 1940s, all phases of swine production typically occurred outside on dirt lots and pasture; by 2006, 94% of US commercial production had been moved into buildings. The objective of this project was to use statistical data from state and federal agricultural agencies and a literature review to assess the impact of these changes on the cost of production, herd health, feed efficiency and environmental efficiency for grow-finish pigs. Since 1945, the quantity of pork produced in the United States more than doubled from less than 10 to more than 23 billion pounds annually. Cost of production ($/cwt) has decreased with decreased feed costs more than compensating for increased housing and energy costs. Pig mortality decreased and some parasites such as lungworm (*Metastrongylus* spp.) and kidneyworm (*Stephanurus dentatus*), that once infected 55–95% of pigs, are now rarely seen. Daily gain (kg/d) and feed efficiency (gain to feed) improved from 0.7 to 0.89 and 3.8 to 2.6, respectively, over the past 60 years. Improved animal efficiency combined with increased crop production per hectare increased the pork produced per hectare by more than 200% over the period. Through better diet formulation, feed preparation, genetic selection and management, phosphorus excreted by pigs fed to recommended levels decreased over 50% per kg of pork produced. In summary, current production methods have increased production while reducing the land required for pork production.

Key Words: production efficiency, swine industry, herd health

84 A survey of the economic, environmental, public policy and production issues facing animal agriculture in Louisiana. T. A. Lavergne*, S. M. DeRouen, and G. M. Hay, *LSU AgCenter*.

Beef, dairy, and poultry producers/growers, personnel in allied industries, state agencies, and LSU AgCenter, as well as other leaders in these industries were surveyed on various issues affecting animal agriculture in Louisiana to determine their opinions on these issues. Respondents were asked to rate 10 items within 4 categories of issues: economic, environmental, public policy, and production issues. The items were rated from 5 (extremely important) to 1 (not important). Of the 230 respondents, 85 worked in the beef industry, 71 worked in the dairy industry, and 74 worked in the poultry industry. For economic issues, the overall average ratings ranged from 4.2 to 4.3 for all groups surveyed. “Rising input costs” received the highest rating for economic issues. For environmental issues, average ratings ranged from 3.3 to 4.0 for all groups surveyed. “Public perception of the environmental effects of animal agriculture” received the highest rating for environmental issues. For public policy issues, the overall average ratings ranged from 3.0 to 4.0 for all groups surveyed. “Consumer confidence in food and animal product safety” received the highest rating for public policy issues. For production issues, the overall average ratings ranged from 3.7 to 4.0 for all groups surveyed. “Improving production efficiency” received the highest rating for production issues. Respondents rated most items as moderately, substantially, or extremely important. Economic issues received the most substantially important and higher ratings. The responses indicate that economic, environmental, public policy, and production issues are important to these respondents involved in Louisiana’s animal industries.

Key Words: animal agriculture, environmental issues, economic issues

85 The value of poultry litter to crop producers in South Georgia. C. S. Dunkley* and D. L. Cunningham, *University Of Georgia*.

A survey was conducted to assess the value of poultry litter to crop producers in South Georgia. Respondents were asked 23 questions pertaining to poultry litter use and their farming operations. The questions included; the amount of litter they applied each year, the cost of poultry litter, the cost of inorganic fertilizer, the amount of land they applied litter and inorganic fertilizer to and the length of time they have been using poultry litter. Of the 165 respondents 75.49% of them grew row crops, specifically peanuts, pecans, cotton and corn. The remaining respondents grew forage crops and vegetable crops. When asked whether or not they used poultry litter, a total 50.3% of the respondents stated that they used poultry litter while 49.7% of them did not use it. Of the total respondents who used poultry litter 75.64% of them used poultry litter and inorganic fertilizers as nutrient sources while 24.26% of them used only litter as their nutrient source. When asked about the amount of soil amendment they added each year, about a half of the respondents applied up to 500 lbs of inorganic fertilizer per acre while about 93% of the respondents who used litter applied 2 tons per acre. The amount of money the growers paid per ton for litter ranged from $10 to $55 compared with $500 to $1200 per ton for inorganic fertilizer. Approximately

11% of litter users traveled over 100 miles to obtain the litter compared with 0.78% of inorganic fertilizer users who had to travel a similar distance. More inorganic fertilizer users (14.63%) applied more than once per year when compared with litter users (5.08%). The responses from this survey indicates that crop producers in South Georgia have found poultry litter to be of substantial value for their operations and will travel far distances to acquire the product.

Key Words: poultry, litter use, litter value

86 Testing foam depopulation equipment in the field. D. P. Hougentogler*, E. R. Benson, R. L. Alphin, and C. A. Kinney, *University of Delaware*, *Newark*.

Foam depopulation is currently one of the available options for mass emergency depopulation of floor reared poultry. Conditions including water, foam concentrate, and equipment can change the quality of the foam. Foam quality impacts depopulation efficacy. A method for evaluating foam quality in the field was developed and tested. Foam expansion rate, flowability, and drawdown time are key characteristics to making good foam. These can be evaluated using 2 simple tests. To test foam expansion in the field, a known amount of water and container of known size to generate foam into is required. Expansion rate will vary depending on the foam generation equipment used, but should follow USDA and AVMA standards for foam depopulation. Draw down time and flowability can be tested using flow over time. The field test developed to evaluate foam using a funnel and graduated cylinder measures the amount of foam flow over a given time period. This method uses a 1 L funnel with a 6.3 mm (1/4 inch) outlet, a stopper, and a 2 to 3 L graduated cylinder. Once the funnel is filled, unplug the stopper and measure the time it takes for 99% of the foam to pass through the discharge hole. A range of good flowability would allow 0.3 L to 0.9 L of foam to flow within 60 and 120 s. Foam flowability was used to develop a simple go-no go graphic that can be used in the field to evaluate foam quality. The impact of water quality was also tested using this procedure. While testing salt, hard, and brackish water, with this method it showed that they did not inhibit the production of good quality foam.

Key Words: foam, mass emergency depopulation, poultry

87 Assessing the potential economic value of an automated temperature monitoring system using stochastic simulation. J. M. Bewley*[1,2] and M. M. Schutz[2], [1]*University of Kentucky*, *Lexington,* [2]*Purdue University*, *West Lafayette, IN*.

Numerous automated temperature monitoring systems (ATMS) are marketed to dairy producers. However, the economic benefits of ATMS have not been studied. The primary objective of this research was to identify factors that influence the profitability of investment in an ATMS. An expert opinion survey was conducted to provide estimates of potential improvements arising from adoption of this technology. Experts ranked benefits of ATMS as follows: ability to monitor heat stress, mastitis detection, estrus detection, metritis detection, pneumonia and respiratory disease detection, improved animal well-being and pregnancy detection. A stochastic simulation model of a dairy farm was utilized to perform a Net Present Value (NPV) analysis. This model was developed to evaluate investments in Precision Dairy Farming technologies and was constructed to embody the biological and economic complexities of a dairy farm system within a partial budgeting framework. The @Risk add-in (Palisade Corp., Ithaca, NY) for Microsoft Excel was utilized to account for the stochastic nature of key variables by Monte Carlo simulation. The model comprised a series of modules, which synergistically provide the required inputs for profitability analysis. Benefits of ATMS were estimated by assessing the impact of its use on estrus, mastitis, metritis, and respiratory disease detection rates. In addition, the expert opinion survey results were used to calculate the associated reductions in the negative effects of disease for mastitis, metritis, and respiratory disease. Using model assumptions, the mean NPV of investing in this ATMS was $404,333 ± 208, 474 ranging from -$217,892 to $737,335. The NPV was greater than 0 in 930 of 1000 iterations. Stochastic price variables having the most influence on NPV were milk price, corn price, slaughter cow price, soybean price, and replacement cow price. More importantly, the percentage of estrus events identified using the technology had a considerable impact on investment profitability. Investment in an ATMS may be profitable, but results will be herd-specific.

Key Words: temperature monitoring, investment analysis, precision dairy farming

83 Missouri Goat Camp: Collaborative effort to enhance successful goat production projects by Missouri youth. E. L. Walker*[1], B. Fay[2], H. Swartz[3], and C. Clifford-Rathert[3], [1]*Missouri State University*, *Springfield,* [2]*Univesity of Missouri*, *Greenfield,* [3]*Lincoln University*, *Jefferson City, MO.*

Goat production continues to be the fastest growing segment of Missouri livestock production, and is becoming popular for Missouri 4-H and FFA members. Meat goat participants in Missouri 4-H has increased from 457 in 2007 to 748 in 2008. Current numbers show a total of 1171 members involved in 4-H goat projects. Budget cuts are being proposed for post-secondary education which would severely limit educational programs for youth and adults. As a way to off-set costs and enhance development of goat production, goat camps (GC) have been designed and established jointly by Missouri State University (MSU), University of Missouri Extension/4-H (UME), and Lincoln University (LU). Currently camps are held in Jefferson City at the LU Carver Farm and Springfield at the Darr Agricultural Center. Topics covered include ethics, showmanship skills, selection of goats, quality control, marketing, diseases, parasite management, and reproduction. Promoting more youth-oriented programs like these will ensure quality producers will abound in future years. All topics and instruction culminates with 4-H and FFA youth receiving certification for goat quality assurance, at the same time the adults are also being educated as an added benefit. Participants of the most recent joint camp, the 2010 GC-Springfield, were surveyed resulting in 119 respondents. The camp lasted approximately 6 h with breaks and lunch provided by the organizers. The structure consisted of 7 instructional, 25 min round robin sessions. Survey respondents included 71 youth and 48 adults. Speakers were rated at an overall mean of 1.05 ± 0.18 (1 = educator seemed prepared, 2 = somewhat prepared, 3 = not prepared) and a 2.78 ± 0.61 regarding length of activities (1 = too short, 2 = too long, 3 = just right) and all respondents reported they would recommend the clinic to others. In 2009, 189 participants attended 2 camps hosted by LU consisting of both youth and adults. As more people become interested in goat production and budgets decline, it will become necessary for more joint extension and service activities to occur between major educational entities.

Key Words: goat, youth, Missouri

Food Safety Symposium: Potential Impact of Reduced Antibiotic Use and the Roles of Prebiotics, Probiotics, and Other Alternatives in Antibiotic-Free Broiler Production

89 Probiotics and direct-fed microbials: Practical applications and real-world needs. J. T. Barton*, *The Poultry Federation Lab*.

It seems likely that antibiotic treatments of food animals will end, despite the strong support of antibiotic use by agricultural advocates as well as scientific evidence that the use of antibiotics in food animals is not the major cause of pathogen resistance in the human population. If the post-antibiotic farm comes to pass, farmers will still depend on veterinarians and scientists to deliver effective therapies that relieve animal suffering and protect against financial losses. Probiotics, direct-fed microbials, and perhaps other types of beneficial bacteria appear to be the most likely successors to the functional role of antibiotics in meat and poultry farming. The perception of farmers regarding beneficial bacterial applications in food animal husbandry has evolved from skepticism to curiosity to guarded acknowledgment of positive attributes. These views have changed due, in part, to publications in scientific journals and well as hands-on experience applying beneficial bacterial products. It is certain that the natural diminution of ineffective, yogurt-sourced *Lactobacillus* sp. and the development of species-targeted probiotics and direct-fed microbials have caused a major shift in the use of beneficial bacteria in food animal farming. Future advancement in beneficial bacteria application will depend upon increased knowledge of their mechanism(s) of action as well a continued discovery of novel microbial species for development.

Key Words: probiotic, direct-fed microbial, beneficial bacteria

90 Probiotics: Current limitations and future potential in commercial poultry. B. M. Hargis*[1], G. Tellez[1], R. E. Wolfenden[1], S. Shivaramaiah[1], A. D. Wolfenden[1], S. E. Higgins[2], and T. E. Porter[2], [1]*University of Arkansas*, *Fayetteville*, [2]*University of Maryland*, *College Park*.

During the last 2 decades, we and many colleagues have worked toward development of commercially applicable probiotics (DFM) that could consistently replace or ameliorate removal of antibiotic growth promoters from poultry rations. There have been many educational failures along with some striking successes during this odyssey. In several published manuscripts, we have shown that a highly selected group of compatible lactic acid bacteria could reduce enteric *Salmonella* in laboratory and commercial field studies, improve performance in large broiler and turkey field trials, effectively treat idiopathic diarrhea in commercial turkeys, and prevent necrotic enteritis in challenge studies. The effects of treating *Salmonella*-infected broilers is observed very quickly, between 12 and 24 h, leaving the conventional explanation for mechanism of action, that of competitive exclusion, in doubt. Very recently we have observed very rapid changes in host gene expression through microarray analysis that could explain the rapidity of these observations suggesting that elicitation of a host innate immune response may be partially responsible for the beneficial action of this probiotic. Because lactic acid bacteria are not stable or thermotolerant, we have also worked toward selection of effective spore-forming *Bacillus*-based probiotics using intense in vitro selection criteria, and ultimately, in vivo testing. During this more recent experience, we have concluded that in vitro biological activity of *Bacillus* is not highly predictive of isolates with potential to improve performance or to reduce necrotic enteritis or *Salmonella* infections in vivo. Interestingly, a select subset of *Bacillus* isolates appear to be capable of complete spore-to-spore life cycle completion within the chicken gut, which may be important for selection. Our studies indicate that for effective administration of useful spore-formers in feed, very high concentrations of spores are required (~1×10^6 cfu/g finished feed). Therefore, selection of highly efficient thermotolerant spore-formers is necessary for cost-effective development of feed-additive probiotics (DFM).

Key Words: *Bacillus*, DFM, probiotic

1087 Alternatives to antibiotic treatment for necrotic enteritis. C. L. Hofacre*[1], M. Lee[1], and G. Mathis[2], [1]*The University of Georgia*, *Athens*, [2]*Southern Poultry Research*, *Athens, GA*.

Necrotic enteritis (NE) is the reason poultry producers use growth promoting antibiotics. Our research has shown that it is the subclinical form of NE that affects the birds' small intestines to result in the reduced growth rate and poorer feed efficiency that is seen when antibiotics are not used. The disease-causing agent is the obligate anaerobic bacteria *Clostridium perfringens* and more specifically a strain that produces an exotoxin. These are ubiquitous bacteria; therefore, just presence of *C. perfringens* in the birds' intestines is not enough to cause disease either clinical or subclinical in most cases. There must also be a change in the bacterial normal flora of especially the small intestine to allow the *C. perfringens* to grow and elaborate the toxin. In the past, we have used antibiotics to keep the flora in balance and the *C. perfringens* in check. One of the major causes for shifts in the normal intestinal flora is coccidian infection of the duodenum, jejunum and ileum. When the birds' intestine responds by producing mucus, this provides the mucolytic bacteria, *C. perfringens*, a ready nutrient source which results in rapid growth and elaboration of the toxin(s). This results in further intestinal damage and production of additional mucus and a cycle begins that would be prevented by antibiotics. The presence of the ubiquitous bacteria *C. perfringens* in the birds' intestines does not necessarily mean N.E. will occur. As long as the normal flora of the small intestine stays in balance, the *C. perfringens* level will stay low; however if the intestinal epithelium becomes damaged or the birds experience an extreme level of stress, *C. perfringens* can grow rapidly and produce its toxin resulting in most often slower growth, lower body weights and poorer utilization of feed. In the extreme form of N.E., we see necrosis of the intestinal epithelium and death. Managing the normal intestinal flora of the bird can be a highly effective method of preventing both clinical and subclinical necrotic enteritis.

Key Words: necrotic enteritis, antibiotics

88 Historical perspective: Prebiotics, probiotics, and other alternatives to antibiotics. M. E. Hume*, *USDA, ARS, Food and Feed Safety Research Unit*, *College Station, TX*.

European Union food animal producers have moved away from the use of selected antibiotic growth promoters. Some poultry producers in the United States have opted to reduce or remove antibiotic growth promoters from their production schedules. Additionally, there is increasing public sentiment in the US toward the complete removal in this country of antibiotic growth promoters from poultry and other food animal production. The symposium will examine a history of prebiotic,

probiotic, and other antibiotic alternatives; current needs and expectations of antibiotic replacements; current limitations of probiotic and future potential; current experiences with antibiotic-free poultry production; and bacteriocins as potential replacements for antibiotic growth promoters. The concept of a prebiotic was launched in 1995 by Glenn Gibson and Marcel Roberfroid. An updated definition of a prebiotic was proposed in 2007 by Marcel Roberfroid as "a selectively fermented ingredient that allows specific changes, both in the composition and/or activity in the gastrointestinal microflora, that confers benefits upon the host well-being and health." The notion of a probiotic began at the end of the nineteenth and early twentieth century with the observations of Eli Metchnikoff, who put forth the idea that aging was affected by certain putrefying toxins created by microbes in the large intestine. He went on to state that villagers in eastern Europe who consumed milk fermented by lactic-acid bacteria characteristically lived long lives. A probiotic as redefined in 1989 by Roy Fuller is "A live microbial feed supplement which beneficially affects the host animal by improving its intestinal microbial balance." Fuller stressed the need for the probiotic organism to be viable. Both concepts recognize the importance of developing, supporting, supplementing, and maintaining a healthy digestive microflora. The 2 concepts have been the focus of considerable research and cover a range of materials and formulations in the livestock and human arenas.

Key Words: prebiotic, probiotic, antibiotic growth promoter

92 Effects of microclimate and pasture characteristics on temporal/spatial distribution of beef cows in Midwestern pastures. D. A. Bear*, J. R. Russell, and D. G. Morrical, *Iowa State University*, *Ames, IA*.

Pastures located on southern Iowa cow/calf farms, from 8 to 125 ha in size, were used to evaluate the effects of microclimate, shade, botanical composition, and other pasture characteristics influencing the temporal/spatial distribution of cattle within and outside streamside zones of pastures. Cows were Angus and Angus-cross on 4 of the farms, and Mexican Corriente on the remaining farm. During spring, summer, and fall of 2007–2009, 2 to 3 cows on each farm were fitted with Global Positioning Systems (GPS) collars and used to record location within a pasture at 10 min intervals for periods of 5 to 14 d. One hundred 39 data sets were obtained throughout the 2007–2009 grazing seasons. Data loggers recorded microclimate variables at 10 min intervals. Water sources and fence lines were referenced on a geospatial map and used to establish zones within the pastures; in the stream or pond (water source), closer or further than 30.5 m (Uplands) from the water source. Farm and seasonal effects on cow distribution in pastures were analyzed using the GLM procedure of SAS using years as replicates. LOGISTIC procedure of SAS tested microclimate variables effects on the probability of cattle being in or within 30.5 m of the water. Mean proportions of observations when cattle were in the water source differed ($P < 0.0001$) between seasons. Mean proportion of cattle observations within the streamside zone (defined as being in the water source or within 30.5 m of the water source) differed ($P < 0.0001$) between farms. The proportion of time cattle were within the streamside zone increased with decreasing pasture size ($r^2 = 0.40, 0.55, 0.59$) and increasing the proportion of streamside zone within a pasture ($r^2 = 0.40, 0.64, 0.39$) for the spring, summer, and fall seasons, respectively. Proc LOGISTIC determined the probability of cattle located in the streamside zone increased with increasing ambient temperatures. Implementation of grazing management practices for the protection of pasture streams will likely be most effective on small and/or narrow pastures in which cattle have less opportunity to locate in upland locations.

Key Words: GPS, distribution, water quality

93 Preference for diverse pastures by sheep in response to intraruminal administrations of tannins, saponins, and alkaloids. J. J. Villalba*[1], F. D. Provenza[1], A. K. Clemensen[1], R. Larsen[2], and J. Juhnke[1], [1]*Utah State University*, *Logan,* [2]*University of California*, *Templeton*.

Plant secondary compounds (PSC) are increasingly recognized as important in animal health, welfare and nutrition. We explored how sheep modify their foraging behavior in pastures with different PSC when challenged with a single PSC. Six pairs of lambs received intraruminal administration of a PSC (Treatment) in 3 successive periods (1- Condensed tannins, 2-Saponins, or 3-Ergotamine) of 5 d each. Six other pairs of lambs received just the vehicle (Control). The design was a split-plot with pairs of lambs nested within group (Treatment, Control). Day and period were the repeated measures. Pairs of lambs were allowed to graze a choice of 1) *Lotus corniculatus* (birdsfoot trefoil - BFT), 2) *Medicago sativa* (alfalfa - AA), 3) *Festuca arundinacea* (endophyte-infected tall fescue - TF) with high concentration of tannins, saponins, and alkaloids, respectively, and 4) *Dactylis glomerata* (orchardgrass - OG). Lambs were observed at 1 min. intervals and their behavior recorded (scans). Control lambs manifested a strong preference for AA (75–85% of all scans; $P < 0.0001$) throughout all testing periods. In contrast, lambs treated with tannins had more scans than Controls on BFT ($P = 0.002$) and TF ($P = 0.004$). Lambs that received saponins had more scans than Controls on TF ($P = 0.01$), and animals treated with ergotamine had more scans than Controls on BFT ($P = 0.03$). Lambs showed the lowest proportion of scans on AA after treatment with saponin ($P \leq 0.09$) and on TF after infusions of ergotamine ($P \leq 0.009$). Lambs infused with PSC thus utilized forage species more evenly than did Controls, and they avoided plants (AA, TF) containing PSC (saponin, ergotamine) that matched those delivered into their rumens. Treatment lambs also diluted the effects of the PSC by increasing preference for OG, and selectively increased preference for certain PSC-containing forages such as TF and BFT. Animals offered a diversity of plants with multiple PSC may minimize the negative impacts of PSC in their bodies through changes in their foraging behavior.

Key Words: forage diversity, foraging, plant secondary compounds

94 Grazing behavior of cattle and sheep grazing alone or together on grass swards differing in plant species diversity. H. M. Cuchillo* and J. Isselstein, *Georg-August University of Goettingen, Institute of Grassland Science*, *Goettingen. Germany.*

Grassland composition and animal species may modify the grazing efficiency and ingestive behavior of pasture. However, precise knowledge on potential interactions between sward diversity and mixed grazing is not available. Thus, a trial was conducted to evaluate the main (grazing, walking, and ruminating) and secondary (bites per minute, steps per minute, and bites per step) animal behavior patterns of cattle and sheep grazing alone or together on grass swards differing in botanical composition. The study was conducted in Lower Saxony/Germany from May to September 2009. Three blocks (A, B and C) individually arranged into 6 treatments were employed; i.e., low diversity/cattle, low diversity/sheep; low-diversity/cattle-sheep; high diversity/cattle, high diversity/sheep and high diversity/cattle-sheep. Botanical composition of either mixed grass-legume-forb (14 species per $9m^2$) or grass dominated swards (7 species) was manipulated by the use of herbicides. The stocking density was 3000 kg of animal weight per plot. Animals were moved to the next block when the compressed sward height decreased from 12 to 6.5 cm. The main behavior patterns of 3 core animals within each paddock were recorded 7 times by conducting scan sampling every 10 min from 0600 to 2200 h. Secondary patterns were obtained from 15 measurements per core animal and observation day. Results were analyzed with a Completely Random Variance Analysis in a 2 × 2 factorial arrangement using the Proc Mixed of SAS. Results show that cattle on high diversity swards spent more time grazing, have the lowest time for ruminating and the lowest mean of bites per minute ($P < 0.05$). Co-grazing increased the rumination time of cattle regardless of sward composition ($P < 0.05$). Interestingly, there were no significant differences on main and secondary behavior patterns of sheep, neither due to the type of grazing nor the sward composition ($P > 0.05$). Complementary studies of vegetation consumption preferences joined with ruminal physiology assessments should be done to evaluate the benefits and limitations pasturing on rich or poor diversity swards.

Key Words: grassland, mix-grazing, botanical composition

95 Evaluation of dairy heifer performance and pasture composition when co-grazing heifers and goats. T. S. Dennis*, L. J. Unruh-Snyder, M. K. Neary, J. E. Tower, and T. D. Nennich, *Purdue University*, *West Lafayette, IN*.

Alternative feeding strategies that reduce costs and maintain animal performance improve the sustainability of livestock operations. The objective of this study was to evaluate the effects of co-grazing heifers and goats supplemented with co-product feeds on heifer performance, pasture composition, and DM yield. Forty-eight Holstein heifers (BW = 147.4 kg, BCS = 2.9) were randomly assigned to one of 12 paddocks and allocated to a 2 × 2 factorial design with 2 co-product supplements (dried distillers grains (DDGS) or soybean hulls (SBH)) and 2 grazing strategies (heifers with goats (HG) or heifers without goats (HO)). Heifers were intensively grazed on tall fescue/white clover pastures and supplemented at 0.9% of BW. Body weights were measured biweekly. Wither heights (WH), hip heights (HH), and BCS (1 to 5 scale) were measured and blood samples were collected for plasma urea nitrogen (PUN) analysis monthly. Pasture intakes were estimated 2 times/wk. Pasture composition, DM yield, and nutrient analysis were determined monthly. Heifer data were analyzed by paddock as repeated records using PROC MIXED of SAS. Heifers fed DDGS tended to gain more weight ($P = 0.1$) and had greater changes in HH and WH ($P = 0.02$ and $P = 0.03$, respectively). The percent of weeds in the pasture tended to decrease ($P = 0.06$) for HG. Pasture DM yields for HO and HG did not differ between treatments ($P > 0.1$). Heifer growth and feed efficiency improved when heifers were supplemented with DDGS. Co-grazing heifers with goats did not affect heifer performance ($P > 0.1$).

Table 1. Effects of supplementation type (SUPP) and grazing strategy (GS) over all time periods on intake, growth, feed efficiency, and plasma urea nitrogen in dairy heifers

	DDGS	DDGS	SBH	SBH		P-value		
Item/pd	HO	HG	HO	HG	SEM	SUPP	GS	SUPP x GS
DMI, kg/d	6.1	5.9	5.9	5.8	0.17	0.31	0.43	0.80
ADG, kg/d	0.52	0.55	0.48	0.51	0.02	0.10	0.19	0.82
G:F	0.67	0.61	0.34	0.36	0.09	0.01	0.80	0.63
PUN, mg/dL	11.7	12.8	10.4	11.5	0.31	<0.01	<0.01	0.96
WH change, cm	2.62	2.08	1.82	1.87	0.19	0.03	0.24	0.16
HH change, cm	2.14	1.92	1.61	1.80	0.11	0.02	0.89	0.11

Key Words: dairy heifer, co-grazing, goats

96 Effects of aluminum from water-treatment-residual applications to pastures on mineral status of cattle and forage mineral concentrations. R. K. Madison, L. R. McDowell** G. A. O′Connor, N. S. Wilkinson, P. A. Davis, A. T. Adesogan, T. L. Felix, and M. Brennan, *University of Florida*, *Gainesville*.

Extensive efforts have been focused on finding ways to reduce soluble P in manure-impacted soils. Aluminum binds to P and application of Al could be one potential solution to the problem. Two experiments (145 and 148d) using Holstein steers were conducted to determine the pasture application of water treatment residuals (Al-WTR) on mineral status (primarily P) and performance of grazing cattle. Experiments (1995 and 1996) began June 1st with cattle initially weighing 306 and 169 kg, respectively, on d 0. The experiments were a completely randomized design with treatments replicated 3 times. Four treatments were with and without Al-WTR and with and without P-free mineral supplement. Total pasture application of Al-WTR over 2 years was 75.8 t dry weight/ha. Steers were allotted (3/pasture) to one of 12 0.81 ha bahiagrass (*Paspalum notatum*) pastures. Body weights, blood samples and liver biopsies were taken at d 0, d 84 and 148. Plasma was analyzed for Al, Ca, Cu, Mg, P and Zn; liver for Al, Cu and P and bone for Al, Ca, P and Mg. A second objective was to evaluate the effects of the applied Al-WTR on mineral concentrations of the bahiagrass pastures. Forage samples were taken on d 0 and every 28 d thereafter for 5 mo. The Al-WTR had little or no effect ($P > 0.5$) on weight gains and mineral tissue concentrations. Forage mineral concentrations were generally unaffected by treatment but were affected ($P < 0.05$) by collection dates. Forage P contractions ranged from 0.12 to 0.22%. Most forage samples were deficient in Na (<0.06%), Cu (<10ppm), Se (<0.1ppm) and Co (0 < 0.1ppm) and at various collections deficient in Ca (<0.35%), P (<0.18%), Fe (<50ppm) and Zn (<30ppm). In conclusion, Al-WTR applications had little effect on animal status of P or any other mineral analyzed. Likewise, Al-WTR had little effect on forage mineral concentrations. Applications of Al-WTR are effective in reducing P contamination without affecting forage or cattle mineral status.

Key Words: cattle, forages, water treatment residuals

97 Effect of maturity and nitrogen fertilization on bahiagrass production and nutritive value. N. M. Kenney*, J. E. Sawyer, R. O. Dittmar III, and T. A. Wickersham, *Texas A&M University*, *College Station*.

Bahiagrass (*Paspalum notatum*), a forage resource in the southern United States, often has lower forage quality than cool-season grasses and legumes, but may require fewer nutrient inputs than other available forage options. Our objectives were to determine the effects of N fertilization and maturity on nutritive value, in situ OM digestibility, and yield of bahiagrass. Treatments were arranged as a 4 × 4 factorial with 4 levels of N fertilization (0, 45, 90, and 135 kg N per ha) and 4 maturities (3, 5, 7, and 9 wk after N fertilization). An established stand of bahiagrass was divided into 3 blocks with all treatments contained in each block. In situ determinations were made with 3 steers fed Bermudagrass hay and samples were incubated for 0, 2, 6, 12, 24, 48, and 72 h. Increasing provision of N tended ($P = 0.06$) to quadratically increase in DM yield (3354, 4386, 4876, and 5182 kg DM per ha for 0, 45, 90, and 135 kg N, respectively). Similarly, advancing maturity increased DM yield quadratically ($P < 0.01$; 3206, 4580, 4894, and 5119 kg DM per ha for 3, 5, 7, and 9 wk, respectively). A maturity by N interaction ($P = 0.02$) was observed for CP concentration. Increasing N resulted in more rapid declines in CP with advancing maturity. At 3 wk CP was 8.0% for 0 N and 11.6% for 135 N. In contrast, at 9 wk the CP was 5.0% for 0 N and 6.6% for 135 N. In situ OM digestibilities were determined on samples from wk 5, 7, and 9. A maturity by N interaction ($P = 0.03$) was observed for the rapidly degraded (A) fraction of OM. At 5 wk maturity the A fraction decreased with increasing N fertilization, whereas at 9 wk maturity the A fraction increased with increasing N fertilization. The B fraction was linearly reduced ($P < 0.01$) and the C fraction was linearly increased ($P < 0.01$) with advancing maturity. At a fixed passage rate of 3% per h, the calculated extend of OM degradation was 58.6, 54.9, and 53.4% for maturities 5, 7, and 9, respectively (linear, $P < 0.01$). Overall, additional fertility increased bahiagrass CP content, despite more rapid declines with advancing maturity, and maturity was the primary driver of bahiagrass degradability.

Key Words: bahiagrass, in situ, maturity

98 Effect of mineral supplementation on the performance by stocker cattle grazing winter-wheat pasture. S. A. Gunter*[1] and G. F. Combs[2], [1]*USDA-ARS, Southern Plains Range Research Station*,

Woodward, OK, [2]*USDA-ARS, Grand Forks Human Nutrition Research Center*, *Grand Forks, ND*.

To evaluate the efficacy of mineral supplementing stocker cattle grazing wheat pasture, 2 experiments were conducted. In Exp 1, 72 steer and heifer calves (BW = 228 ± 11.4 kg) were randomly assigned to 12, 4.9-ha pastures on November 12 at 1.2 animals/ha (4 pastures), and February 5 at 2.5 animals/ha (8 pastures) for 84-d. In Exp 2, 38 steers (BW = 248 ± 4.8 kg) were randomly assigned to 12, 2.5-ha wheat pastures on February 24 for 84 d at 1.3 steers/ha. In Exp 2, pastures were planted with conventional tillage or a no-till drill. In Exp 1 and 2, half the pastures received a free-choice mineral mixture (Wheat Pasture Pro; Land O Lakes Purina Feed, LLC; St. Paul, MN; Ca, 16% and P, 4%) provided in ground-type mineral feeders (Exp 1: completely random design; Exp 2: 2 × 2 factorial); feeders were weighed weekly to determine intake. All pastures were drilled the first of September 2008 (67 kg of seed/ha) and were fertilized with 50 kg of urea-N/ha. Standing herbage DM was determined in pastures when cattle were weighed every 28-d by clipping wheat to the ground along 122 cm of drill row at 10 transects. Data were analyzed by AOV with treatment as the fixed effect and pasture as the random effect. In Exp 1, cattle offered the minerals had a 45% faster ADG ($P < 0.01$; 0.75 kg) than cattle not offered minerals (0.52 kg); hence, the supplemented cattle weighed 8% more ($P < 0.01$; 308 kg) after grazing than non-supplemented cattle (289 kg). In Exp 2, supplementation did not interact ($P \geq 0.44$) with tillage. Also, steers offered the mineral had a 30% faster ADG ($P = 0.03$; 1.12 kg) than steers not offered minerals (0.86 kg) and the supplemented cattle weighed 6% more ($P = 0.03$; 341 kg) after grazing than non-supplemented cattle (320 kg). In both experiments, daily standing herbage DM averaged 1,536 kg/animal and never differed ($P \geq 0.13$) between treatments. Mineral intakes averaged 73 (Exp 1) and 168 (Exp 2) g/d, resulting in cost of supplement to kilogram of added BW gain conversions of $0.26 and $0.57 assuming a mineral cost of $0.88/kg. Overall, there was an improvement in ADG and the supplement to added BW gain conversion seemed profitable.

Key Words: cattle, grazing, wheat pasture

99 Effect of corn hybrid on the amount of residue available for grazing relative to grain yield. J. A. Musgrave*, L. A. Stalker, T. J. Klopfenstein, M. C. Stockton, and K. H. Jenkins, *University of Nebraska*, *Lincoln*.

Utilization of corn crop residue by cattle to extend grazing can have positive economic impacts. Cattle primarily consume the leaf and husk portions of the corn residue. Amount of residue available to grazing cattle may be influenced by corn hybrid. Ten corn hybrids were evaluated to determine differences in corn grain yield and crop residue dry matter. Ten hybrids that best represented a wide range of production traits were selected from a total of 40 hybrids grown in a test plot located near Paxton, Nebraska. The following hybrids were evaluated: Pioneer P0541XR, P1173HR, P1395XR, Dekalb 59–35, 61–04, NK N68B–GT, N74C–3000GT, Croplan Genetic 5757 VT3, Golden Harvest 8211 3000GT, and Midwest Genetics 76482R. Each sample consisted of the complete above ground portion of the corn plant and was collected randomly. Each sample was sorted into the following parts: stems, leaves (including leaf sheath), husks, cobs, and corn grain. Plant parts were dried in a forced air oven at 60°C to determine dry matter yield. Data were analyzed as a completely randomized design. There was no difference in corn grain yield among hybrids (13,240 kg/ha ± 788, DMB; $P = 0.23$). Differences were present between hybrids in amount of stems ($P < 0.001$), leaves ($P = 0.05$), husks ($P = 0.01$), and cobs ($P < 0.001$). Considering these differences, it is not surprising that total residue production (sum of stems, leaves, husks and cobs) was different ($P = 0.02$) among hybrids. However, differences also existed in the ratio of corn grain to total residue production ($P < 0.001$) and corn grain to leaf and husk ($P < 0.001$), indicating potential differences in plant efficiency. Corn hybrids differ in the amount of residue produced independent of the amount of grain. Since corn hybrids differ in the amount of residue they produce, possible differences in amount of residue available for cattle to graze, also differs. Using these differences, economic estimates of the ranking identify potential value differences.

Key Words: corn stalks, corn residue, grazing

100 Replacing synthetic N with clovers or alfalfa in bermudagrass pastures for growing calves. P. Beck*[1], D. Hubbell[1], T. Hess[1], K. Haas[2], and J. Jennings[1], [1]*University of Arkansas*, *Fayetteville,* [2]*Haas Hay & Cattle Co.*, *Gurley, AL*.

The objective of this research was to determine the impact of alfalfa or clover additions to common bermudagrass (*Cynodon dactylon* [L.] Pers.) pastures on performance of growing calves and pasture carrying capacity compared with commercial N fertilizer. In October 2008, 0.81 ha bermudagrass pastures were interseeded with 1) a mixture of 13 kg/ha red clover (*Trifolium pretense*, cv. Morningstar, Cal/West Seeds, Woodland, CA) and 3.3 kg/ha ladino white clover (*Trifolium repens*, cv. Regal Graze, Cal/West Seeds, n = 4) or 2) 28 kg/ha alfalfa (*Medicago sativa*, cv. PGI 459, Producers Choice, Woodland, CA, n = 4). The following summer 12 bermudagrass pastures received 0, 56, or 112 kg N/ha as ammonium nitrate. Beef steers (BW = 278 ± 13.6 kg) grazed pastures from 29 May to 9 September in a put and take experiment. Data were analyzed as a completely randomized design with 4 pastures/treatment using the mixed procedure of SAS. A single df contrast was used to determine the linear N fertilization rate effect, and predicted differences separated the effects of alfalfa and clover. Stand counts of alfalfa pastures decreased from 34 ± 10.6% in May to 15 ± 12.7% in October, but remained relatively unchanged in clover pastures 43 ± 12.8% in May and 38 ± 5.2% in October. Daily gains and BW tended ($P = 0.08$) to increase linearly with increasing N rate. Gains and BW of steers from alfalfa pastures did not differ ($P \geq 0.91$) from 56 kg N rate. Gains and BW of clover steers was greater ($P \leq 0.02$) than alfalfa and 56 kg N rate, but did not differ ($P = 0.11$) from 112 kg N rate. Grazing-d/ha and gain/ha increased linearly ($P = 0.01$) with increasing N rate. Grazing-d/ha of alfalfa and clover did not differ ($P \geq 0.31$) from 56 or 112 kg N/ha rates. Pastures containing clover produced more ($P = 0.02$) gain/ha than 56 kg N rate and tended ($P = 0.10$) to produce more BW gain/ha than 112 kg N rate. Gain/ha for alfalfa did not differ ($P = 0.95$) from 56 kg N rate. Clovers produce equivalent BW gains and animal grazing days to 112 kg/ha N, but stands of alfalfa were not dense enough throughout the grazing season to maintain animal performance above that of 56 kg/ha N.

Key Words: alfalfa, clover, bermudagrass

101 Effects of winter swath grazing barley and millet on background and feedlot performance and rumen metabolism of beef calves. R. Kumar*[1], H. A. Lardner[1,2], and J. J. McKinnon[1], [1]*University of Saskatchewan*, *Saskatoon, Canada*, [2]*Western Beef Development Centre*, *Humboldt, Saskatchewan, Canada*.

A 2-year winter grazing and feedlot finishing trial (Exp1) and subsequent metabolic study (Exp2) were conducted to evaluate the effects of swath grazing forage barley *(Hordeum vulgare* cv. Ranger) and foxtail millet *(Setaria italica* cv. Golden German) compared with grass-legume hay fed in drylot on beef calf performance and rumen degradation kinetics.

In Exp1, 120 spring born Angus calves (60 steers, 60 heifers) were fall weaned, stratified by weight, allocated into 20-head groups then assigned randomly to 1 of 3 replicated (n = 2) backgrounding (BG) systems.. Data were analyzed using Proc Mixed with year as a block. Systems were (i) field swath graze barley (BR); (ii) field swath graze millet (ML); and (iii) bunk fed ground hay drylot (DL). Field calves were limit grazed in 8 ha paddocks for 3 d grazing period using electric fencing for 96 d each year, with all groups receiving additional pelleted supplement at 0.62% BW. Calves were weighed at start, every 21 d and end of background period. Following BG period, calves were placed in feedlot, separated by sex and BG treatment and fed a similar finishing ration and harvested once a targeted endpoint of 12 mm backfat was reached. Forage samples collected every 21 d were analyzed for DM, CP and digestible energy (DE). Forage dry matter analyses was greatest ($P = 0.03$) for barley swath (DE = 2.6 Mcal/kg) and lowest ($P = 0.03$) for grass-legume hay (DE = 2.2 Mcal/kg). Calf background ADG was greatest ($P = 0.002$) for BR compared with ML or DL, while feedlot ADG was not different ($P = 0.32$) for all calves. In situ degradability (Exp2) of barley DM and CP was greater ($P = 0.0001$) compared with millet or hay, while millet had greater ($P = 0.0001$) NDF degradability. These findings indicate that swath grazing barley or foxtail millet with beef calves resulted in similar or improved performance compared with a traditional dry-lot pen system.

Key Words: barley, millet, swath grazing

Graduate Student Symposium: Transitions: Preparing for Your Future

102 Surviving the transition from thesis to published manuscript: An editor′s perspective of the review process. J. L. Sartin*, *Auburn University*.

This talk will be oriented to the graduate student with a focus on how the editorial process works behind the scenes. This will range from how reviewers are selected to how decisions are made about whether to publish or reject a manuscript. Common problems cited by reviewers will be listed as well as a discussion of how to respond to the reviewers comments. The end of the session will be a discussion of the options for what to do in the event a paper is not published.

Key Words: journal, review, author

103 Taking the reins: Transitioning from PhD student to associate professor. K. A. Vonnahme*, *Department of Animal Sciences*, *Fargo, ND*.

Congratulations! You are ready to begin your own research program! How can you guarantee your success in getting tenure? The journey toward tenure begins before you accept any job offer. Make sure you start in the right place. Do your homework: Do the values of the institution match your values? What are your future colleagues like? How will your research interests fit in with those that will surround you? After you decide on a place, PLAN. Tenure is just 6 short years away, and you need to have a written game plan that you share with your lab and your significant other. Here are 6 tidbits that aided my way to obtaining tenure. 1) Surround yourself with good people. Ask the right questions as you interview graduate students, post-docs, and technicians. Taking more time before the hire makes the time after you get the job more pleasant. 2) Motivate those around you. Motivation is different for everyone, but people will work hard if you show that you care and appreciate their efforts. Remember that their successes are your successes, too. 3) Find a mentor. A formal mentor may be given to you at hiring, but seek out others whose programs are already successful. They will share their successes and headaches. Listen. 4) Begin your promotion and tenure document the day you begin. This is a tedious task that is a necessary evil—embrace it early. 5) Manage your time. Keep one calendar for both your professional and personal appointments. This leads to greater efficiency. Make use of small pieces of time. 6) Having it all. Make sure you choose your partner wisely. You will take your job home with you quite often, and having the support and understanding of someone at home makes life so much easier. Remember that your PhD program has trained you in many areas that will guarantee success in a tenure track position: excellence in your field of study, how to interact with various types of people, the ability to gather and analyze data, the ability to organize your studies and your time, the confidence to act on intuition, integrity, and resilience. Continue to hone these skills as you transition to an associate professor.

Key Words: career, promotion and tenure, success

104 Animal scientists of the future – Embrace change, challenges and opportunities. M. E. Benson*, *Washington State University*, *Pullman.*

Academia and the animal sciences are in a dynamic era and those who embrace change and see and create new opportunities are those who will be successful. Academic success will continue to require all of the technical skills and competencies that have always existed in a chosen discipline or mission. Changes in funding sources, clientele demographics and the increasing role society will play in influencing research and education priorities and activities will require nimble people capable of responding to and anticipating challenges. Five attributes that can help a new faculty or staff member to be successful include: an ability to thrive in a changing environment, enjoying and valuing interdisciplinary opportunities and relationships, the willingness and ability to be entrepreneurial, the willingness and ability to communicate science and its implications, and the ability to be an innovator. With change also comes the need for individuals to work collectively to accomplish new tasks, teach new courses, respond to emerging issues and extend knowledge to the public. The reality is that new skills and techniques will be required to address tomorrow′s increasingly complex questions. Those who are willing to acquire new skills that can contribute new expertise and who are willing and able to lead interdisciplinary research teams will be those best positioned to achieve external funding success. A skilled innovator will find ways to turn challenges into opportunities and capitalize on those opportunities. Looking for and finding ways to do the *impossible* are characteristics tomorrow′s elite animal scientists will possess. We must capitalize on change and those who can will find exciting and rewarding times ahead.

Key Words: success, innovation, academia

Growth and Development: Regulatory Mechanisms in Growth and Development

105 The effect of feeding frequency on circulating thyroid hormones in turkey chicken. A. Towhidi*, A. Yahyabeig, and E. Dirandeh, *University of Tehran*, *Karaj, Tehran, Iran*.

A strategy that improves growth efficiency is to reduce basal metabolic rate, providing additional energy for growth. Thyroid hormones enhance metabolism and lipolysis. Previous studies have shown that increase of feeding frequency could change blood hormonal profile affecting metabolism and growth in some animals. The objective of this study was to investigate the effect of increased feeding frequency on thyroid hormones status in turkey. Twenty turkey chickens were randomly assigned to 2 groups. In control group, turkey chickens were fed ad libitum, whereas birds in treatment group fed every 4 h and blood samples were collected at 4 intervals. Data were analyzed with Proc Mixed of SAS. Overall mean plasma concentration of triiodothyronine in treated group was higher than control (4.05 ± 0.34 vs. 2.59 ± 0.30 ng/mL, $P = 0.0001$). Mean plasma concentration of thyroxin in treated group was higher than control (47.50 ± 1.6 vs. 24.08 ± 1.7 µg/dL, $P = 0.0001$). It was concluded that increasing feeding frequency failed to decrease thyroid hormones level. As a result, this kind of feeding management may not be efficient to improve growth performance in turkey chicken.

Key Words: turkey, thyroid hormones, feeding frequency

106 The role of syndecan-4 cytoplasmic domain in turkey skeletal muscle growth and development. Y. Song*[1], D. C. McFarland[2], and S. G. Velleman[1], [1]*Ohio Agricultural Research and Development Center, The Ohio State University*, *Wooster,* [2]*Department of Animal and Range Sciences, South Dakota State University*, *Brookings*.

Skeletal muscle formation is a complex process involving the interactions between cells and their extracellular matrix. Syndecan-4 is a cell membrane heparan sulfate proteoglycan that passes signals from the extracellular matrix into the cell. Syndecan-4 core protein is composed of an extracellular domain, a transmembrane domain, and a cytoplasmic domain. The cytoplasmic domain is important in regulating signal transduction into the cell and the formation of focal adhesion complexes which is critical for cell survival. In the current study, the role of the syndecan-4 cytoplasmic domain in muscle cell proliferation, differentiation, fibroblast growth factor 2 (FGF2) responsiveness, and apoptosis was explored. Turkey wild type syndecan-4 (S4) and syndecan-4 without the cytoplasmic domain (S4C) were cloned into the pCMS-EGFP vector and then subcloned into the pcDNA3.1/V5-His TOPO TA expression vector. Wild type syndecan-4, S4C, and the pCMS-EGFP empty vector were transfected into turkey skeletal muscle satellite cells. After transfection, cell proliferation, differentiation, and FGF2 responsiveness were measured. Wild type syndecan-4 and S4C subcloned into the pcDNA3.1/V5-His TOPO TA expression vector were used to test cell apoptosis by a CaspACE assay using CaspACE FITC-VAD-FMK in situ marker which fluorescently labels apoptotic cells. The pcDNA3.1/V5-His TOPO TA expression vector was used because it does not express green fluorescence protein as the pCMS-EGFP vector which will interfere with the CaspACE assay. Results showed that the overexpression of S4C decreased cell proliferation ($P < 0.05$) but did not change cell differentiation, or responsiveness to FGF2 during proliferation and differentiation compared with the cells transfected with S4. The cells transfected with S4C had more apoptotic cells compared with those transfected with S4. These results suggest that syndecan-4 plays a critical role during cell proliferation, and the syndecan-4 cytoplasmic domain regulates cell proliferation and survival in an FGF2-independent manner.

Key Words: turkey, muscle satellite cell, growth and development

107 Comparative phylogenetic analysis of gut microbiota of broilers fed with and without antibiotics. P. Singh*[1], A. Karimi[2], P. W. Waldroup[1], and Y. M. Kwon[1], [1]*University of Arkansas*, *Fayetteville,* [2]*University of Kurdistan*, *Sanadaj, Kurdistan, Iran*.

Antibiotics growth promoters (AGP) have been used for growth promotion of chickens in poultry industry since 1950. Recently, concerns have been raised to the use of AGP in livestock due to development of antibiotic resistance in bacteria. The objective of our study is to investigate the effect of AGP in cecal microbiota of broiler chickens. Two groups (n = 30) of chickens were fed corn-soybean meal diets with (ANT) and without supplementation of Penicillin (CON) at the concentration of 55 mg/kg. At 18 d of age, ANT group had significantly ($P < 0.05$) higher mean body weight than CON group (668.6 vs. 570.0 g). Cecal samples of 5 randomly selected birds were pooled from each group and used for genomic DNA isolation and PCR amplification of 16S rRNA gene. 454 pyrosequencing of the amplicons resulted in 7,881 and 11,214 sequence reads for CON and ANT groups, respectively. BLAST and phylogenetic analysis using MEGAN-3 indicate that AGP supplementation in ANT group resulted in elevated proportion of phylum Firmicutes from 16.67% to 17.47% and a decreased proportion of phylum Bacteriodetes from 15.71% to 0.14% as compared with CON group. Recent studies conducted in humans, pigs and mice have shown a similar shift in gut microbiota in obese individuals as compared with lean ones, indicating that this shift could be responsible for increase in energy harvest and body weight. The results of this study suggest that the growth promoting effect of AGP supplementation in broilers may be mediated by a similar microbial process. Hence, new and alternative methods for promoting the growth of the birds need to be sought for that may alter gut microflora in a similar pattern.

Key Words: antibiotics growth promoter, 16S rRNA gene, cecal microbiota

108 Impact of feeding raw materials on intestinal viscosity and performance of broilers. F. Nuyens[1], I. Somers[1], S. Van De Craen[1], W. Röser[1], C. Chudaske[2], and S. Van Dyck*[1], [1]*Kemin AgriFoods Europe*, *Herentals, Belgium*, [2]*Südzucker AG Mannheim/Ochsenfurt*, *Ochsenfurt, Germany*.

Alternative cereals and cereal by-products can be used to reduce the costs of poultry diets. However, the application of these new raw materials may call for an evaluation of their effect on gut viscosity. This paper evaluates the changes that appear in fiber analysis and in vitro viscosity for diets including 10% of wheat-based distillers dried grains with solubles (DDGS). It is the objective of this paper to assess the impact of feed viscosity changes on broiler performance and intestinal viscosity. Furthermore, the beneficial effect of feed enzymes will be demonstrated. A broiler growth trial was performed with 200 birds divided over 4 treatments (see Table 1) in a randomized block design. On d 21 of the trial, 9 broilers were sacrificed per treatment and viscosity of jejunum and ileum contents was measured (Dusel et al., 1997). The use of feed enzyme in the diet had significant effects ($P < 0.05$) on the intestinal viscosity (Table 1). By use of the feed enzyme in the diets that included

DDGS, the intestinal viscosity was decreased by 40% in the jejunum and 24% in the ileum. The results show that the fiber content in DDGS is much greater than in regular wheat. The DDGS did not induce a greater viscosity than regular wheat. The bioethanol production process might have reduced part of the soluble, long-chain arabinoxylan fibers that are responsible for the viscosity effect. The low viscosity values of both wheat and DDGS after treatment with a feed enzyme indicate the potential to control intestinal viscosity when wheat or DDGS are used in the feed formulation. The treatment with highest intestinal viscosity showed poorest daily gain and feed conversion ratio (FCR), while the group with lowest intestinal viscosity showed the best zootechnical performance (Table 1, $P < 0.05$).

Table 1. Intestinal viscosities and FCR for broilers fed a regular wheat diet and a modified wheat diet with 10% DDGS. The Feed Enzyme was supplemented at a dosage of 500 g/tonne.

Treatment	Jejunum	Ileum	FCR
Control	3.73^{a}	5.28^{ab}	1.83^{ab}
Control + DDGS	4.67^{b}	6.50^{b}	1.89^{b}
Control + Feed Enzyme	2.60^{c}	4.14^{a}	1.75^{a}
Control + DDGS + Feed Enzyme	2.81^{c}	4.95^{a}	1.85^{b}
SEM	0.048	0.018	0.001
p-value	0.0001	0.0039	0.0006

Means in same column with different superscripts are significantly different ($P < 0.05$).

Key Words: DDGS, Feed enzyme, intestinal viscosity

109 Ontogenic changes in the activation of translation initiation factors post feeding are not seen in adolescent Thoroughbred mares. A. L. Wagner*, J. C. Gould, R. B. Ennis, and K. L. Urschel, *University of Kentucky*, *Lexington.*

Following consumption of a protein meal, signaling proteins associated with the mTOR pathway are activated, triggering muscle protein synthesis due to increases in both insulin and amino acid (AA) concentrations. In neonates, the activation of the mTOR pathway decreases with age resulting in lower skeletal muscle protein synthesis. The slower growth seen during the adolescent age has not been studied with regards to mTOR-related signaling in any species. The purpose of this study was to determine the effects of an 18h feed witholding period, either with (postprandial; PP) or without (post-absorptive; PA) the re-feeding of a protein meal ($t = 0$ min), on the activation of translation initiation factors in gluteal muscle of yearling, 2y old, and mature Thoroughbred mares (n = 18). Blood samples were taken during the experimental protocol to measure plasma AA via HPLC. A gluteal muscle biopsy was taken after the last blood sample ($t = 90$ min) to measure the phosphorylation (P) of Akt at Ser^{473} and Thr^{308}, 4EBP1 at Thr$^{37/46}$, rpS6 at Ser$^{235/236;240/244}$, and p70 S6 Kinase at Thr^{389} using Western blotting. For all horses, indispensible plasma AA were ~25- 110% higher in the PP versus PA period ($P < 0.01$). There was a significant increase in Akt P-Ser^{473} ($P < 0.01$), 4EBP1 P-Thr$^{37/46}$ ($P < 0.01$), rpS6 P-Ser$^{235/236}$ ($P < 0.01$), rpS6 P-Ser$^{240/244}$ ($P < 0.01$), and p70 S6 Kinase P-Thr^{389} ($P < 0.01$), and a trend for higher AktP-Thr^{308} ($P = 0.10$) in the PP versus PA state. There was an interaction of age and treatment on the P of 4EBP1 ($P = 0.05$), and a trend for an interaction for the P of p70 S6 Kinase ($P = 0.08$). Age did not have an effect on the P of any protein ($P > 0.05$), although there was a trend for an age effect on AktP-Thr^{308} ($P = 0.10$). Consumption of a high protein meal, appeared to activate proteins associated with the mTOR pathway in adolescent and mature horses. However, growth of adolescent horses did not have a greater effect on the P of the proteins in the mTOR pathway compared with mature horses. More research is necessary to determine whether an effect of age is present in the rapidly growing equid neonate.

Key Words: mTOR pathway, growth, protein synthesis

110 Productive performance of pigs vaccinated against gonadotropin releasing factor compared to surgically castrated males and gilts from two different sire lines. J. I. Morales[1], M. P. Serrano*[2], L. Cámara[2], C. H. Zúñiga[2], J. P. López[1], and G. G. Mateos[2], [1]*Copiso S.A.*, *Soria, Spain*, [2]*Universidad Politécnica de Madrid*, *Madrid, Spain*.

A total of 360 pigs was used to study the influence of gender (immunocastrated males, IM; surgically castrated males, CM; intact females, IF) and terminal sire line (Top York; Tempo) on productive performance of pigs slaughtered at 125 kg BW. The female line used was Large White × Landrace in all cases. Improvac (Pfizer, Madrid, Spain) was used for active immunization against GnRH. The IM pigs received a first dose of Improvac at 76 d of age (16 d on trial) and a second dose at 124 d of age (64 d on trial; 7 wk before slaughter). There were 6 treatments (6 replicates of 10 pigs each) arranged factorially (3 × 2) with 3 genders and 2 terminal sire lines. From 60 to 76 d of age (IM were still entire males), IF and IM had lower ADG than CM (729 and 749 vs. 792 g/d; $P < 0.001$) but no differences were observed for feed intake. From 76 (injection of the first dose of the immune vaccine) to 124 d of age, IM had lower ($P < 0.001$) ADFI and ADG than CM with IF being intermediate. However, from 124 (injection of the second dose of the immune vaccine) to 172 d of age, IM recovered and in fact, they had better ($P < 0.001$) ADG and FCR than IF and CM. For the entire experimental period, IF and IM ate less feed than CM (2.43 and 2.43 vs. 2.59 kg/d; $P < 0.001$) whereas IM and CM had higher ADG than IF (952 and 945 vs. 913 g/d; $P < 0.01$). Also, IM had better FCR than CM with IF being intermediate (2.55 vs. 2.66 vs. 2.74 g/g; $P < 0.001$). From 60 to 172 d of age, crossbreds from Tempo sires had better ADG than crossbreds from Top York sires (952 vs. 922 g/d; $P < 0.001$) but no differences were observed for ADFI or FCR. We conclude that IM have better ADG and are more efficient than CM. Consequently, based on growth performance data, IM are a good alternative to CM for the production of 125 kg BW pigs. Also, the Tempo sire line is a good alternative to the Top York sire line for the production of heavy pigs.

Key Words: immunocastration and gender, sire line, pig performance

111 Effects of nutrient balance and implant status on IGF-1 and PUN concentrations of feedlot calves. T. Lee*, L. K. Mamedova, S. Guillossou, B. J. Bradford, C. D. Reinhardt, and D. U. Thomson, *Kansas State University*, *Manhattan*.

To simulate nutritional conditions in highly stressed feedlot calves with low nutrient intake, 16 predominantly English-breed calves (BW = 293.3 ± 5.41 kg) were used in a 2 × 2 factorial experiment to evaluate the main and interactive effects of poor vs. adequate nutrient intake and implant status on growth and PUN and serum IGF-1 concentrations. All calves were individually fed a common, pelleted, complete diet (15.3% CP; 1.44 Mcal NE_m /kg DM). After a 28-d period of adaptation to the Calan gates and the diet, 4 calves each were randomly assigned to receive either (1) implant + 2× maintenance energy intake; (2) implant + 1× maintenance energy intake; (3) no implant + 2× maintenance energy intake; or (4) no implant + 1× maintenance energy intake. Dietary NE_m content was estimated using dietary ingredient concentrations and NRC (1984) nutrient values. Animal NE_m requirement was determined based on d0 BW and NRC (1984) requirement tables; 1× maintenance calves

were fed to meet their NE_m requirement; 2× maintenance calves were fed twice their NE_m requirement; intake was subsequently adjusted based on d14 BW. Implanted calves were implanted (Revalor-XS; 40 mg estradiol-17β + 200 mg trenbolone acetate) on d0; all calves were weighed and processed through the chute on d0 and fed for 28 d. Blood samples were drawn on d0, d14, and d28 for analysis of serum IGF-1 (analyzed using ELISA) and plasma urea nitrogen (colorimetric assay). Data were analyzed as a repeated measures design using the MIXED procedure of SAS (v. 9.1). Diet affected ($P < 0.05$) ADG (1.65 vs. 0.04 kg/d for 2× vs. 1×), and d28 PUN (6.21 vs. 5.35 mM/L for 2× vs. 1×) but there was no effect of implant or any interaction between diet and implant on weight gain, PUN, or IGF-1 concentrations. These data suggest that nutrient restriction does not alter IGF-1 response or subsequent cellular nutrient uptake response due to implants.

Key Words: diet, feedlot, implant

112 Growth hormone and insulin-like growth factor I have different effects on bovine myoblasts and myotubes in culture. X. Ge* and H. Jiang, *Virginia Polytechnic Institute and State University*, *Blacksburg*.

Growth hormone (GH) and insulin-like growth factor I (IGF-I) are 2 major regulators of skeletal muscle growth in animals. The objective of this work was to compare the effects of GH and IGF-I on proliferation and fusion of primary bovine myoblasts, and their effects on protein synthesis and degradation in cultured bovine myotubes. Myoblasts were isolated from extensor carpi radialis of adult cattle by Pronase digestion and were allowed to proliferate or induced to form myotubes in culture. Recombinant bovine GH at the concentrations of 10 ng/mL and 100 ng/mL did not affect myoblast proliferation and fusion. However, both concentrations of GH increased protein accumulation by 15% compared with no-GH control ($P < 0.01$) without changing protein degradation. Although IGF-I at concentrations of 50 ng/mL and 500 ng/mL had no effect on myoblast fusion, IGF-I at concentration of 500 ng/mL increased myoblast proliferation by 20%, compared with no-IGF-I control ($P < 0.05$). Both concentrations of IGF-I increased protein accumulation in bovine myotubes by more than 75% ($P < 0.01$) and decreased protein degradation by 30% ($P < 0.05$), compared with no-IGF-I control. These data indicate that GH and IGF-I have largely different effects on proliferation and fusion of bovine myoblasts and on protein synthesis and degradation in bovine myotubes. These results suggest that GH and IGF-I might stimulate skeletal muscle growth in cattle through different mechanisms.

Key Words: GH, IGF-I, muscle

113 Trenbolone regulates myogenic differentiation via inducing androgen receptors and β-catenin interaction in muscle derived stem cells of cattle. J. X. Zhao*, J. Hu, M. J. Zhu, W. J. Means, and M. Du, *Department of Animal Science, University of Wyoming*, *Laramie*.

Anabolic steroid hormones have been widely used in the beef cattle industry for more than 50 years. Trenbolone is a synthetic analog of anabolic steroid hormone which can promotes both skeletal muscle and bone growth; however the underlying mechanisms remain obscure. Because canonical Wingless and Int (Wnt)/β-catenin signaling is known to promote myogenesis, we hypothesized that trenbolone regulates myogenesis through promoting the interaction of androgen receptor with β-catenin, increasing the transcription of β-catenin targeted genes. Muscle derived stem cells were prepared from male fetal skeletal muscle of cattle at mid-gestation, and treated with or without trenbolone (10 n*M*) in a myogenic medium consisting of DMEM plus 2% horse serum. Results showed that trenbolone treatment increases the protein contents of MyoD (0.72 ± 0.18 vs. 1.45 ± 0.19 arbitrary units, $P < 0.05$), myosin heavy chain (0.22 ± 0.03 vs. 0.38 ± 0.02 arbitrary units, $P < 0.05$), and androgen receptor (0.92 ± 0.04 vs. 1.18 ± 0.03 arbitrary units, $P < 0.05$) compared with the control group. The myogenic effect of trenbolone was blocked by cyproterone acetate, a specific inhibitor of androgen receptor, showing that the myogenic effect of trenbolone is mediated by androgen receptor. Immunoprecipitation showed that androgen receptor and β-catenin formed a complex; addition of trenbolone increased interaction between androgen receptor and β-catenin. Both cytoplasmic and nuclear β-catenin levels were increased following trenbolone treatment. The enhanced translocation of β-catenin to the nuclei following trenbolone treatment was correlated with higher β-catenin/T-cell transcription factor 1 (TCF) mediated transcriptional activity compared with that of control group (11.7 ± 1.6 vs. 6.9 ± 0.9 relative luciferase activity, $P < 0.05$). In conclusion, these data provide evidence that trenbolone promotes the interaction between androgen receptor and β-catenin, which promotes the expression of β-catenin targeted genes and myogenesis in the muscle derived stem cells of cattle.

Key Words: catenin, beef, androgen

114 Increasing days on the finishing diet equalizes carcass grade distributions of zilpaterol-HCl fed heifers. B. C. Bernhard*[1], R. S. Swingle[2], T. E. Lawrence[3], W. T. Nichols[4], D. A. Yates[4], J. P. Hutcheson[4], M. N. Streeter[4], J. C. Brooks[1], M. F. Miller[1], B. J. Johnson[1], and R. J. Rathmann[1], [1]*Texas Tech University*, *Lubbock*, [2]*Cactus Research Ltd.*, *Amarillo, Texas*, [3]*West Texas A&M University*, *Canyon*, [4]*Intervet Schering Plough Animal Health*, *DeSoto, Kansas*.

British × Continental heifers (n = 3,382; 307 kg) were serially slaughtered to determine if increasing days on the finishing diet (DOF) mitigates negative consequences of zilpaterol-HCl (ZH) on quality grade and tenderness. A 2 × 3 factorial arrangement of treatments in a completely randomized block design (36 pens; 6 pens/treatment) was used. Zilpaterol-HCl (8.33 mg/kg DM) was fed 0 and 20–22 d before slaughter plus a 3–5 d withdrawal to heifers spending 127, 148, and 167 DOF. Feedlot and carcass performance data was collected in addition to Warner-Bratzler shear force (WBSF) of strip loin steaks aged for 7, 14, and 21 d. No ZH × DOF interactions were detected ($P > 0.05$). Feeding ZH increased ADG, G:F, carcass ADG, carcass G:F, carcass ADG:live ADG, HCW, dressing percent, LM area and WBSF at 7, 14, and 21 d; decreased 12th-rib fat, YG ($P < 0.01$) and KPH ($P = 0.05$); and tended to decrease marbling score ($P = 0.10$). Feeding ZH decreased empty body fat percentage (EBF) and increased 28% EBF adjusted final BW ($P < 0.01$). Analysis of interactive means indicated that the ZH × 148 DOF group had a similar percentage of USDA Prime, Premium Choice, Low Choice and YG 1, 2, 3, 4, and 5 carcasses ($P > 0.10$); an increased percentage of total Choice ($P = 0.02$); and decreased percentage of Select ($P = 0.03$) and Standard ($P = 0.05$) compared with the Control × 127 DOF group. The ZH × 148 DOF group was tougher than the Control × 127 DOF group, but more tender than the ZH × 127 DOF group ($P < 0.01$) at 21 d. As a result of ZH shifting body composition, an additional number of DOF equalizes carcass grade distributions, but ZH mediated advantages in feedlot and carcass weight gain are sustained.

Key Words: zilpaterol-HCl, beef heifers, serial slaughter

115 Mitochondrial complex I protein is correlated to residual feed intake in beef cattle. M. H. Ramos* and M. S. Kerley, *University of Missouri*, *Columbia*.

Crossbred beef steers (310kg, n = 48) were fed over a 100 d period where daily feed intake and weight gain were measured. Diet fed to steers consisted of corn (62.5%), soyhulls (15%), distillers grain (10%), glycerol (10%) and mineral/vitamin supplements (2.5%). Dry matter intake and body weight was measured daily using Growsafe feed intake system. Intake was regressed on average metabolic body weight (MBW) and average daily gain (ADG) and resultant coefficients used to calculate predicted feed intake. Difference between actual and predicted intake was residual feed intake (RFI). Efficient animals (- RFI) had lower actual intake than predicted while inefficient animals (+ RFI) had higher actual intake than predicted. Blood was collected via jugular vein puncture and mitochondria isolated from lymphocytes. Mitochondria were processed to measure complex I quantity (CI), complex I enzyme activity (CIE) and pyruvate dehydrogenase quantity (PDH, as a mitochondria marker). Efficient animals had higher (P = 0.006) CI compared with average and inefficient animals (68.4, 39.2 and 28.5, respectively). Correlation between RFI and CI was −0.37 (P = 0.03) We concluded that efficient animals had higher CI. These results agree with previous research showing that efficiency is correlated to differences among animals in mitochondrial protein concentration.

Key Words: RFI, efficiency, mitochondria

116 Bone tissue-specific over-expression of growth differentiation factor 11 propeptide transgene causes homeotic transformation of the seventh cervical vertebra into a thoracic vertebra in mice. Z. Li*, M. Kawassumi, B. Zhao, S. Moisyadi, and J. Yang, *University of Hawaii at Manoa*, *Honolulu*.

Skeletal formation is highly dependent upon sequential switching on and off specific gene activities that control cellular events. Growth differentiation factor 11 (GDF11), also known as bone morphogenetic protein 11 (BMP11), is one of the significant genes that control skeletal formation and development. Complete deficiency of GDF11 function by gene targeting caused abnormal patterning of the anterior/posterior axial skeleton. However, all the GDF11-deficient mice died at birth because of serious kidney defect. To obtain live animals with disrupted GDF11 function, we developed a novel strategy to block the function of GDF11 through its propeptide. Using the intracytoplasmic sperm injection (ICSI) technique in combination with piggyBac transposon-mediated gene transfer, we produced viable transgenic mice overexpressing GDF11 propeptide under the control of a bone tissue-specific promoter, 2.3kb alpha1 type 1 collagen promoter. The transgenic mice exhibited skeletal abnormalities that appeared to represent homeotic transformation of the seventh cervical vertebra into a thoracic vertebra. The GDF11 propeptide transgene was detected as early as at 12.5 dpc in embryonic skeleton. Over 80% of the transgenic mice from a line expressing high level of transgene showed ectopic ribs on the seventh cervical vertebra. The transgene caused expression shifts of Hoxa-4 and 5 genes from their normal prevertebra locations in embryos. These results strongly suggest that the GDF11 function in the transgenic mice is suppressed in bone tissue. The transgenic mice with overexpressed GDF11 propeptide are useful animal models for investigating the role of GDF11 in skeletal formation and bone metabolism during late embryonic and postnatal growth.

Key Words: GDF11 propeptide, cervical rib, Hox gene

117 Soaking hay in water to reduce soluble carbohydrate concentrations prior to horse feeding. K Martinson*[1], C Sheaffer[1], and H Jung[1,2], [1]*University of Minnesota*, *St. Paul,* [2]*USDA-ARS*, *St. Paul, MN*.

Administering high concentrations of fructan to horses has resulted in laminitis. Cool season grasses accumulate fructan, which is estimated as the difference between water soluble carbohydrates (WSC; sucrose, fructose, glucose, fructans) and ethanol soluble carbohydrates (ESC; sucrose, fructose, glucose). Reducing fructan content in hay is critical for susceptible horses. The objective was to determine loss of WSC, ESC, and fructan from different hay types soaked in warm or cold tap water for various lengths of time. Five hays were evaluated; early bud (AB) and full flower (AF) alfalfa, mixed alfalfa orchardgrass (AO), and vegetative (VO) and mature (MO) orchardgrass. Soaking treatments included cold (22°C) and warm (39°C) water for 15, 30, and 60 min; cold tap water for 12 h; and a non-soaked control. One ′flake′ from each of 6 bales was randomly assigned to treatments. Hays were weighed, placed in mesh bags, and submerged in 25 L of fresh tap water. After soaking, flakes were drained for 30 min before drying at 60°C for 72 h. Each flake was ground and sent to a forage testing laboratory for WSC and ESC analysis. Data was analyzed using Proc Mix in SAS. Hays contained 81, 73, 114, 134, 129 g/kg WSC; 57, 48, 88, 68, and 66 g/kg ESC; and 24, 25, 27, 66 and 63 g/kg fructans (AB, AF, AO, VO, and MO, respectively). However, alfalfa does not contain fructan and AB and AF results probably reflect WSC extracted pectin. Soaking reduced WSC, ESC and fructan content in all hays ($P < 0.001$), except AO fructan. Except AB WSC and AO fructan, 15 min cold water soaking resulted in the least reduction of WSC, ESC, and fructan ($P < 0.001$), while the 12 h cold soak had the greatest reductions ($P < 0.001$). Soaking AF, AO, MO, and VO in warm water for 60 min had greater reductions in WSC compared with 60 min in cold water ($P < 0.001$). Reductions in MO fructan content were greater after soaking in warm vs. cold water for 60 min ($P < 0.001$). Forage type, soaking length, and water temperature all affected reductions in WSC, ESC, and fructan. Hay soaking is a viable method to reduce WSC, ESC, and fructan in hays.

Key Words: WSC, ESC, fructan, horse, hay soaking

118 Fasting length and hay type on metabolic parameters in the horse. A. M. Bruce* and E. L. Wagner, *Auburn University*, *Auburn, AL*.

Several metabolic disorders in the horse have been associated with postprandial fluctuations of insulin and glucose in response to the composition of feedstuffs consumed. Many studies have been conducted on altering grain form, type or feeding method to minimize the glycemic response to a meal; however there is a lack of research focusing on hay feeding protocols. The objectives of this study were 1) to examine changes in blood glucose and insulin in response to different fasting intervals and 2) to compare the effects of warm season and cool season hays on those same blood parameters. Six mature geldings were utilized in a 2 × 3 factorial design experiment. The horses were fed either bermudagrass hay (warm season) or fescue hay (cool season) during each of the fasting treatments. The 3 fasting periods consisted of a no fast where the horses would be offered ad libitum hay throughout the night, a short fast where the animals would receive hay until 2200 h with hay re-introduced at 0600 h, and a long fast where the animals would be offered hay until 2200 h and not offered any hay until the 0700 h morning feeding. All horses received concentrate and additional hay at 0700 h. Following a 6 d treatment adaptation, horses were fitted with an indwelling jugular catheter to facilitate a 7 h serial blood draw in conjunction with the morning feeding. Area under the curve (AUC) was calculated by the trapezoidal method for blood insulin and blood glucose concentrations. Insulin and glucose AUC were compared using the GLM procedure of SAS. No significant differences ($P < 0.05$) in AUC for blood glucose or insulin concentrations were seen between warm season and cool season hay. Fasting length did not alter blood glucose or insulin AUC concentrations. Fasting length and hay type do not significantly alter the blood insulin and glucose values in the horse; allowing the horse owner to use the method that is most convenient.

Key Words: horse, fasting length, hay type

119 Effects of endophyte-infested fescue seed consumption on post exercise recovery of horses in humid climates. J. A. Ford*, G. W. Webb, S. P. Webb, H. M. Hurshman, E. L. Walker, and B. Onyango, *Missouri State University*, *Springfield*.

The objective of this study was to determine the effect of endophyte consumption on horses subject to a standardized exercise test (SET) in humid conditions. Nine quarter horses (422–568 kg) were assigned into 2 groups of 5 and 4 to equalized skill level. During the first of 2 28 d periods, the groups were randomly assigned to E+ (endophyte-infested seed) or E- treatments (endophyte-free KY-31 seed) and exposed to the opposite treatment during the second 28 d, which followed immediately after the first. Horses were fed alfalfa hay, commercial sweet feed and either E+ or E- ground fescue seed. A molasses-water solution was used to mix the seed with the grain and encourage intake. Diets contained 12% seed, resulting in 459 ppb ergovaline for the E+ diet. Three days a week horses were subjected to a 25 min conditioning program: walk, trot, lope, stops, turns, and suppling exercises. Two days a week horses were trained on a mechanical cow for 5 min (20–25 turns) except on d 14, 28, 42, and 56 when they were ridden on the SET. The SET consisted of 40 turns in 4 min and was designed to raise the horse's heart rate (HR) beyond the anaerobic threshold (~150 bpm). During the SET, humidity averaged 80.3% and temperature averaged 27.3°C. Parameters measured on SET days were HR, respiration rate (RR), rectal temperature (RTemp), and blood lactate (Lac). Data were analyzed by ANOVA with treatment considered a fixed effect and all other effects considered random. Post SET values for Lac confirmed the horses were performing anaerobic work. Treatment had no effect on Lac, RTemp or HR at any time measured. There was a horse effect ($P \leq 0.05$) on post SET RR, HR, and Lac but not RTemp. There was no horse x treatment interaction for these variables. RR did not vary by treatment at rest or 1 min post SET. During the periods when horses consumed E+ seed, RR were higher at 5 and 10 min post SET ($P \leq 0.005$). There was no period effect, period x treatment or period x horse interaction. Horses that consumed E+ versus E- seed maintained higher respiration rates after a SET in which they were subjected to anaerobic work in humid conditions.

Key Words: horse, fescue, exercise

120 Digestibility of oats in horses using the substitution approach. A. D. Woodward*[1], A. Willyard[1], A. Buckley[1], J. Liesman[1], C. F. M. de Lange[2], and N. L. Trottier[1], [1]*Michigan State University*, *East Lansing*, [2]*University of Guelph*, *Ontario, Canada*.

Limited published information regarding apparent whole tract N digestibility of oats fed as a single protein source is available in horses due to the dietary obligate requirement for forages. The objective of the study was to estimate the apparent whole tract N digestibility of oats using the substitution approach. Six mature Arabian geldings (450 kg) were allocated to 6 diets over 6 time periods in a 6 × 6 Latin square design. Diets were composed of varying ratios of timothy grass hay and oats fed at 1.6% BW (DM basis), i.e., 1.6:0, 1.45:0.15, 1.3:0.3, 1.15:0.45, 1:0.6, and 0.85:0.75. Diets were formulated and fed to provide equal amounts of CP per kg BW (DM basis); percentage dietary CP contribution from hay and oats were 100:0, 91:9, 83:17, 74:26, 66:34, and 55:45, respectively. Each period consisted of 11-d adaptation to the diet followed by collection of all feces and urine every 8 h over 3 d. Feed, fecal and urine samples were analyzed for N. Apparent whole tract N digestibility was regressed against the contribution level of CP from oats to the total diet, i.e., 0, 9, 17, 26, 34, and 45%. As the level of oats inclusion and contribution of CP from oats increased, apparent whole tract N digestibility tended to increase ($P = 0.08$). The relationship was defined as y = 0.15 (±0.05)x + 51.90 (±1.45) ($R^2 = 0.72$, $P < 0.001$), where y is the intercept and represents the apparent N digestibility of timothy grass hay and x represents the level of CP contribution from oats to the diets. The apparent N digestibility of oats, estimated with x = 100, was 67%, and timothy grass hay, with x = 0, was 52%. In conclusion, apparent whole tract N digestibility of oats is 67%. The oats N digestibility value estimated using the substitution approach will allow the formulation of equine diets on a digestible protein basis to more efficiently meet protein requirements of horses receiving oats in addition to forages.

Key Words: horse, oat nitrogen digestibility, substitution approach

121 Effect of dietary energy manipulation on mares and their foals: Performance and hormones of mares in late gestation. K. N. Winsco*[1], J. A. Coverdale[1], and C. J. Hammer[2,3], [1]*Department of Animal Science, Texas A&M University*, *College Station,* [2]*Department of Animal Sciences, North Dakota State University*, *Fargo,* [3]*Center for Nutrition and Pregnancy*, *Fargo, ND*.

To investigate the effect of dietary DE manipulation on performance and reproductive hormones of mares in the last third of pregnancy, 30 Quarter Horse mares (538 to 695 kg of BW and 4 to 19 yrs of age) were blocked by expected foaling date. All mares were allowed ad libitum access to coastal bermudagrass pasture and randomly assigned within block to one of 2 dietary treatments: pasture (P) or pasture + concentrate (PC; concentrate fed at 0.75% BW on an as-fed basis). Treatments began 110 d before expected foaling date and terminated at parturition. Blood samples were collected every 14 d until parturition and analyzed for progesterone (P4), estradiol (E2), and cortisol (CORT) concentrations. Mare performance parameters (BW, BCS, and rump fat (RF)) were also recorded every 14 d. Data were analyzed using the PROC MIXED procedure of SAS. There was no influence of dietary treatment on mare BW. However, RF and BCS decreased ($P \leq 0.01$) in mares fed P compared with PC. There was no effect of dietary treatment on P4, E2, or CORT concentrations ($P \geq 0.10$). Regardless of diet, plasma P4 concentrations increased steadily over time ($P < 0.01$) from d 70 to d 112 (2.26 to 8.61 mg/ml). There was a tendency for a treatment by time interaction ($P < 0.10$) with plasma P4 concentrations rising sharply in PC mares beginning at d 70 and being greater ($P < 0.05$) than P mares at d 84. Serum CORT was also influenced by time ($P < 0.01$) with concentrations rising sharply before parturition. In addition, there was a treatment by time interaction ($P < 0.05$) with P mares having a rapid decline in plasma CORT until d 42. Serum E2 concentrations decreased sharply over time ($P < 0.01$) from d 42 to d 70 (311.23 to 223.98 pg/ml). In addition, there was a treatment by time interaction ($P < 0.05$) with PC mares having lower ($P < 0.05$) E2 concentrations than P mares at d 56 and 70. In summary, these data indicate that dietary DE manipulation of mares in late gestation influenced BCS and rump fat values, but not mare BW. Furthermore, dietary manipulation of DE altered mare hormonal response before parturition.

Key Words: mares, energy, pregnancy

122 Evaluation of the capacity for maternal transfer and foal synthesis of long-chain polyunsaturated fatty acids. L. K. Warren*, J. Kivipelto, and E. Gettinger, *University of Florida*, *Gainesville*.

Long-chain polyunsaturated fatty acids (LCPUFA), particularly 20:4ω6 and 22:6ω3, are necessary for normal neural development and are important regulators of cell function. Equine diets typically lack LCPUFA, thus foals presumably acquire LCPUFA via placental transfer, milk or through bioconversion of 18:2ω6 and 18:3ω3 precursors. Eighteen Thoroughbred (n = 11) and Quarter horse (n = 7) mares and foals were used to assess the capacity for maternal transfer and foal synthesis of LCPUFA. Mares were offered Coastal bermudagrass hay *ad libitum* and individually fed 1.5% BW/d of concentrate (16.7% CP, 3.8% fat, 10.2% ADF). Fatty acid (FA) composition of colostrum and umbilical cord plasma collected at foaling and milk, plasma and red blood cells (RBC) collected from mares and foals at 5 and 50 d of age was determined. Capacity for LCPUFA bioconversion was estimated as the ratio of 20:3ω6/18:2ω6 (Δ5-desaturase activity) and 20:4ω6/20:3ω6 (Δ6-desaturase) in plasma. Data were evaluated using the mixed procedure of SAS (v. 9.2). Mare diets were devoid of LCPUFA. LCPUFA were not detected in colostrum, but were present as <1 g/100 g FA in milk. Cord plasma was higher ($P < 0.01$) in LCPUFA, and lower ($P < 0.01$) in18:2ω6, total ω6, 18:3ω3, and total ω3 than foal and mare plasma at d 5 and 50. Foal plasma and RBC were higher ($P < 0.01$) in LCPUFA, total ω3 and 18:3ω3, and lower ($P < 0.01$) in total ω6 and 18:2ω6 than mare plasma and RBC at d 5 and 50. Foal and mare plasma were higher in Δ5-desaturase activity ($P < 0.01$) and lower in Δ6-desaturase ($P < 0.01$) than cord plasma. Higher LCPUFA in cord plasma indicates capacity for synthesis by the mare and selective placental transfer to the foal. Higher LCPUFA in foal plasma compared with mare plasma likely reflects mobilization of FA deposited in utero, intake from milk, and synthesis of LCPUFA from precursors consumed in milk. Greater Δ5-desaturase activity in foal compared with cord plasma indicates capacity for 20:4ω6 and 20:5ω3 synthesis by the foal. However, low Δ6-desaturase activity in foal plasma suggests fetal stores of LCPUFA are critical to support pre- and postnatal development of neural tissues.

Key Words: DHA, essential fatty acids, horse

123 Profiling the change in fecal microbial populations of mares and foals over time. J. E. Earing*[1], A. C. Durig[1], G. L. Gellin[2], M. D. Flythe[2], and L. M. Lawrence[1], [1]*University of Kentucky*, *Lexington*, [2]*USDA-ARS*, *Lexington, KY*.

The gastrointestinal tract of the mature horse contains a complex community of microorganisms, many of which aid in digestion. Little information is available concerning the establishment of these microbial populations in young horses. The limited research that has been conducted has utilized culture-dependant methods, but culture-independent methods have revealed that cultivation underestimates species diversity. Polymerase chain reaction-denaturing gradient gel electrophoresis (PCR-DGGE) is a molecular technique that can be used to evaluate diversity in microbial communities. The objective of this study was to compare the microbial profiles of the feces of mares and foals using

PCR-DGGE in an attempt to describe bacterial colonization in the equine gut. The hypothesis was that foals would be born sterile, and would be indistinguishable from mares by 12 wk of age. Nine mare/foal pairs were used for the study. Fecal samples were collected from each mare and foal as the foal matured; samples were subjected to PCR-DGGE. Comparisons between mares and foals were made using UPGMA cluster analysis and reported as percent similarity. The mean similarity between mares and their foals was 11% on the day of parturition (d 0; n = 2), 51% on d 1 (n = 4), 52% on d 4 (n = 3), 67% at wk 2 (n = 4), 71% at wk 6 (n = 5), and 70% at wk 12 (n = 5). These results indicate that most of the colonization events occurred within the first few days of the foal's life, which is consistent with a study utilizing culture-based techniques. By wk 2, the mean similarity between mares and foals was numerically higher than the mean similarity among mares (61%), suggesting that by 2 wk of age the bacterial species found in the foal's gut are similar to those found in the mature horse. While PCR-DGGE can be used to examine the diversity of bacteria present in the gut, it does not estimate the relative abundance of the bacterial populations. Also, the presence of bacterial DNA in feces suggests, but does not prove, colonization of the gut by the respective bacterial populations.

Key Words: DGGE, horse, microbes

124 Stallion spermatozoal parameters of motility and conception rates on a large commercial ranch. A. L. Garcia[1], H. A. Brady*[1], M. A. Ballou[1], D. D. Varner[2], C. C. Love[2], and G. Blodgett[3], [1]*Texas Tech University*, *Lubbock,* [2]*Texas A&M University*, *College Station,* [3]*6666 Ranch*, *Guthrie, TX*.

Stallion ejaculate values and variability over a breeding season based large numbers are not available for clinical and research use. Further, there are conflicting reports on the predictive value of motility for fertility in the horse. The objectives of this study were to evaluate ejaculates from a large number of stallions over an entire breeding season with advanced techniques and to evaluate the relationships of motility to conception rates of mares. Semen collections (n = 602) from a total of 19 stallions at a ranch in Guthrie, Texas, were evaluated over the 2008 breeding season. Ejaculates were evaluated using a new advanced system, the NucleoCounter (Chemometic, Allerød, Denmark) and the IVOS system (Hamilton Thorne, Beverly, USA). The mean total sperm, concentration, and gel-free volume were 11.25 billion (±2.5), 247.6 million/ml (±72.1) and 50.42 mL (±15.1), respectively. It was determined there were high inter- and intra-stallion variability in parameters of motility studied. Highest intra-stallion variables were moderately progressive cells (cv = 42.7) and total concentration (cv = 37.7) and the least variable parameters were flagellar beat frequency (BCF) (cv = 5.7) and % linearity (cv = 8.0). Highest inter-stallion variables included mount attempts (cv = 47.5) and % moderately progressive cells (cv = 30.5), and the least variable parameters included the BCF (cv = 7.6) and % straightness (cv = 9.6). An odds-ratio procedure and backward logistical regression procedure was used to calculate the influence of motility and concentration parameters on the pregnancy outcome. A total of 328 on-the farm mares were bred by A.I. with a 91% pregnancy rate. No correlation between motility parameters and the pregnancy binomial status was found; however, all stallions were very fertile and the on-site breedings were under consistent management. In summary, this study has provided important clinical standards on ejaculate values based on a large group of ejaculates using advanced techniques. These values have important clinical implications for more accurate standards within the breeding soundness examination of the stallion.

Key Words: stallion, spermatozoa, motility

125 Weight estimation in miniature horses and Shetland ponies. AM Bruce*, EL Wagner, and PJ Tyler, *Auburn University*, *Auburn, AL*.

Reliable weight estimation in the small breeds of horses is critical to the animals' well-being. To properly feed or medicate, bodyweight needs to be as accurate as possible to reduce the risk of error. The 2 common weight estimation practices used for average sized horses are commercially available weight tapes and an established formula, where estimated weight (lbs), (kg) = (heartgirth^2 × body length)/(330 in^3), (11880 cm^3). The objectives of this study were 1) evaluate the accuracy of the weight tape and current formula in estimating body weight of the small breed horse and 2) calculate a more exact formula for miniature horses and Shetlands. Fifty-four miniature horses and 15 Shetland ponies of varying ages were measured. Actual weight was determined via a calibrated electronic livestock scale. Other measurements included height at the withers, body length as measured from the point of the shoulder to the point of the buttock, heart girth, and weight tape. Mean age of the animals was 4.23 ± 3.47 years, with a mean height of 92.21 ± 10.36 cm, and a mean body condition score of 6.3 ± 0.85 based on a 9 point scale. Paired *t*-tests were used to compare the tape weight and formula weight with the actual weight. There was a significant difference ($P < 0.05$) between the tape weight (112.66 ± 33.99 kg) and the actual weight (108.71 ± 31.44 kg). The difference between actual weight and the formula estimated weight (100.52 ± 30.83 kg) was also significant. Linear regression was used to determine a more accurate denominator for the formula. Using the new denominator of 11061 cm^3 (307 in^3) a new mean estimated weight of 108.12 ± 33.16 kg was calculated, which was significantly different from weight calculated by the previous equation. The new denominator appears to be a more accurate method of estimating weight in miniature horses and Shetland ponies. To validate the new equation more miniature horses and Shetland ponies need to be evaluated.

Key Words: weight estimation, body measurements, miniature horse

126 Evaluation of body weight estimation methods in horses. E. L. Wagner* and P. J. Tyler, *Auburn University*, *Auburn, AL*.

Weight tapes and body weight estimation formulas are routinely used to help determine the body weight of a horse when a scale is not available. The formula incorporates measurements of body length and heart girth circumference to estimate body weight in mature horses, where estimated weight (lbs), (kg) = (heartgirth^2 × body length)/(330 in^3), (11880 cm^3). Two variations of the body length measurement have been published. One measures the distance from the point of the shoulder to the ischial tuberosity (point). The other measures the distance from the point of the shoulder to the midpoint of the distance between the widest part of the stifle and the tail when viewed from the rear (stifle). The objective of this study was to evaluate the accuracy of a commercial weight tape and the body weight estimation formula using both body length measurements in estimating weight of adult horses. Seventy-one horses of various breeds were weighed on a portable livestock scale. Horses were measured for height at the withers, heart girth circumference and body length using the point and stifle measurements. A commercial weight tape was used to estimate body weight on 36 of the horses. Statistical analysis was performed by paired *t*-tests and simple linear regression using STATA statistical software with significance set at $P < 0.05$. Mean height was 159.34 ± 9.27 cm with a mean scale weight of 516.94 ± 81.93 kg. Point body length was significantly longer than stifle body length (170.56 ± 9.27 cm and 161.99 ± 8.14 cm, respectively).This resulted in a significant difference between the formula estimated weights using the 2 length measurements. The 2 formula weight estimations (n = 71)

and the weight tape estimation (n = 36) were significantly different from the actual weight and from each other. The mean difference between actual weight and tape weight (n = 36) was 65.35 ± 46.23 kg, whereas the differences between actual weight and the formula estimations (n = 71) were 19.83 ± 38.99 kg for the point measurement and 43.44 ± 39.74 kg for the stifle measurement. The estimation formula using body length measurement with the ischial tuberosity endpoint most closely estimates the actual body weight of the horses.

Key Words: horse, weight estimation

National ADSA Dairy Foods Oral: Dairy Foods Oral Student Competition

127 The effect of sodium gluconate on pH, lactose, lactic and, and water soluble Ca changes during Cheddar cheese ripening. C. Phadungath*[1] and L. E. Metzger[2], [1]*Midwest Dairy Foods Research Center, University of Minnesota*, *St Paul,* [2]*Midwest Dairy Foods Research Center, South Dakota State University*, *Brookings*.

Sodium gluconate increases the solubility of calcium late in model solutions by forming soluble sodium-lactate-gluconate complexes. However, its effect on the main components responsible for calcium lactate crystals in Cheddar cheese, which are lactic acid and water soluble calcium, has not been reported. The objective of this study was to determine the effect of sodium gluconate on pH, lactose, lactic acid, and water soluble Ca changes during Cheddar cheese ripening. Six Cheddar cheeses with 2 salting levels (2 and 2.5%) and 3 sodium gluconate levels (0, 0.5 and 1%) were manufactured in triplicate. Composition and chemical analysis was performed at 1 week of ripening, and at 1 week, 3, 6, 9, and 12 mo of ripening. Cheeses were analyzed for pH, lactose and lactic acid, and water soluble calcium (WSC). Compositional analyses at 1 week indicated that sodium gluconate addition had a significant effect on cheese pH, moisture, Na, lactose, and lactic acid. Cheddar cheeses from both 2% and 2.5% salt levels with higher concentration of sodium gluconate exhibited higher pH than the control cheeses throughout the ripening time, which corresponded to the concentration of lactic acid in the cheeses. HPLC results from Cheddar cheeses from both 2% and 2.5% salt levels indicated that cheeses with higher concentration of sodium gluconate addition had higher concentration of lactose, but lower concentration of lactic acid when compared with the control cheeses throughout the ripening time. WSC results indicated that Cheddar cheeses from both 2% and 2.5% salt levels with higher concentration of sodium gluconate addition had lower WSC concentration when compared with the control cheeses throughout the ripening time. From the results, we concluded that sodium gluconate could have an effect on starter culture activity and could also act as buffering agent, which would cause a higher cheese pH. A higher cheese pH resulted in less soluble of calcium in the cheese serum; thus, resulting in less calcium and lactate ions in the cheese serum.

Key Words: calcium lactate crystal, water soluble calcium, sodium gluconate

128 The impact of starter culture and annatto on the flavor and functionality of whey protein concentrate. R. E. Campbell*, R. E. Miracle, and M. A. Drake, *North Carolina State University*, *Raleigh*.

The flavor of whey protein can carry through into ingredient applications and negatively influence consumer acceptance. Understanding sources of flavors in whey protein is crucial to minimize flavor. The objective of this study was to evaluate the impact of annatto color and starter culture on flavor of whey protein concentrate (WPC). Cheddar cheese whey with and without annatto (15mL/454kg with 3% norbixin content) was manufactured using a mesophilic lactic starter culture or by addition of lactic acid and rennet (rennet-set). Pasteurized fat-separated whey was then ultrafiltered and spray dried into WPC62. The experiment was replicated 4 times. Flavor of liquid wheys was evaluated by sensory and instrumental volatile analyses, and sensory and instrumental analyses, color analyses (Hunter Lab and norbixin extraction) and functionality (solubility and heat stability) were performed on WPC. Both main effects (annatto, starter) and interactions were investigated. No differences in sensory properties or functionality were observed among WPC ($P > 0.05$). Lipid oxidation compounds were higher ($P < 0.05$) in WPC manufactured from whey with starter culture compared with WPC from rennet-set whey. WPC with annatto had higher concentrations of p-xylene, diacetyl, pentanal, and decanal ($P < 0.05$) compared with WPC without annatto. Interactions ($P < 0.05$) were observed between starter and annatto for hexanal, suggesting that annatto may have an antioxidant effect when present in whey made with starter culture.

Key Words: whey, antioxidant, flavor

129 Exopolysaccharides modify the functional properties of whey protein concentrate. G. Deep* and A. Hassan, *Midwest Dairy Foods Research Center, Dairy Science Department*, *South Dakota State University, Brookings*.

The objective was to study the effect of exopolysaccharides (EPS) on the functional properties of whey protein concentrate (WPC). Exopolysaccharides producing cultures are used to improve the physical properties of reduced fat cheeses. It was hypothesized that EPS released in the whey would modify the functional properties of WPC due to their interaction with whey proteins. An EPS-producing culture of *Lactococcus lactis* ssp. *cremoris* (JFR), an EPS-producing culture of *Streptococcus thermophilus* (DP) and an EPS-nonproducing commercial cheese culture (DVS 850) were used in this study. Cultures were grown overnight in reconstituted WPC (10% w/w) which was then added, directly or after overnight cooling, at 2% to rehydrated dry whey (6% w/w). This gave a level of EPS similar to that found in whey from cheese made with EPS-producing cultures. Whey was then pasteurized at 75°C for 35 s and ultrafiltered 5 times. Ultrafiltered whey (retentate) was spray dried at inlet and outlet air temperatures of 200°C and 90°C, respectively. The protein level in WPC was about 32%. Results showed that EPS decreased ($P < 0.05$) the minimum gelling concentration and protein denaturation, and increased emulsifying capacity and gel hardness of WPC. Exopolysaccharides from DP culture showed more pronounced changes in functionality of WPC than did EPS from the JFR culture. Cooling of the fermented medium containing EPS, before its addition to whey, increased ($P < 0.05$) gel hardness and emulsifying capacity of WPC. This is possibly due to effect of cooling on interactions within EPS molecules and between EPS and proteins. This study demonstrated that application of EPS-producing cultures in cheese making modified the functional properties of WPC. Further studies will be directed toward understanding the effect of EPS structure and their interaction with whey protein on WPC functionality.

Key Words: exopolysaccharides, whey protein concentrate, functional properties

130 Evaluation of the effects of cheese milk fat content on the lipid composition and flavor of liquid whey and whey protein concentrate. A. E. Croissant*[1], L. Dean[2], and M. A. Drake[1], [1]*North Carolina State University*, *Raleigh,* [2]*USDA-ARS, North Carolina State University*, *Raleigh.*

Lipid oxidation is generally considered the most important degradation process to food products, and whey products are no exception. Ongoing research has established that lipid oxidation is initiated during the cheese make process. A relationship between lipids and phospholipids and flavor and flavor stability of WPC80 has not been established. The objective of this study was to evaluate the effect of 3 milk fat levels in cheese milk on the lipid composition of fluid whey and WPC80 and subsequent effects on flavor and flavor stability. WPC80 was manufac-

tured from uncolored Cheddar whey in triplicate. For each replication, pasteurized whole, low fat, and skim milk (3.25, 1, and 0.25% milk fat, respectively) were acquired from a single batch of milk. Spray dried WPC80 was produced from each milk on successive days and order was balanced between replications. WPC80 were evaluated by sensory and instrumental analyses as well as proximate analyses. Lipid concentrations in WPC80 from whole, low fat, and skim milk were 5.03, 3.90, and 3.45%, respectively. Whole milk WPC80 was higher in cardboard flavor ($P < 0.05$) compared with low fat and skim WPC80. WPC80 from whole milk also had higher relative abundances of oxidation reaction products including heptanal, hexanal, octanal, nonanal, and 1-octen-3-one ($P < 0.05$) compared with low fat and skim WPC. Results indicate that cheese milk lipid concentration does impact the lipid composition of WPC as well as the flavor and volatile compounds associated with lipid oxidation. Currently, low and reduced-fat cheese whey streams are combined with full-fat cheese whey streams in WPC manufacturing. Reduced-fat cheese production is situated to increase greatly given the growing consumer and governmental interest in fat reduction. The examination of the impact of reduced-fat cheese production on the flavor and lipid composition of whey protein concentrates has the potential to influence the creation of a value-added whey protein product.

Key Words: WPC, lipids, low fat

131 Growth and production of volatile compounds by *Lactobacillus casei* in Cheddar cheese extract under cheddar cheese ripening condition. H. Cai*[1], M. Budinich[1], W. Tan[1], E. Miracle[2], J. Broadbent[3], M. A. Drake[2], and J. Steele[1], [1]*University of Wisconsin*, *Madison*, [2]*North Carolina State University*, *Raleigh*, [3]*Utah State University*, *Logan*.

Lactobacillus casei are commonly used as adjunct cultures for the control of off-flavors, as well as the intensification and acceleration of beneficial flavors in bacterial-ripened cheeses. In this study, 22 *Lb. casei* strains were screened in a model system for attributes likely to influence their potential to serve as adjunct cultures for the manufacture of Cheddar cheese. The model system used was 4-mo-old Cheddar cheese extract supplemented with citrate (4mCCE–cit) and the experiment was conducted under Cheddar cheese ripening condition (pH5.1, 3.1% NaCl, and 8°C). The attributes screened for were the ability to dominate the NSLAB microbiota, produce volatile flavor compounds, and hydrolyze bitter peptides. None of the *Lb. casei* strains examined could degrade the model bitter peptide β-CN(f193–209) under the condition examined. Six strains (A2-309, CRF28, L9, M36, UW1 and UW4) exhibited growth parameters in the model system, relatively short lag phase, rapid growth rates, and high final cell densities, likely to be associated with the ability to dominate the NSLAB microbiota of Cheddar cheese. Significant increases in 2,3-butanedione accumulation was observed with 7 of the *Lb. casei* strains examined; 2,3-butanedione is strongly associated with the beneficial buttery note in young Cheddar cheese. Significant decreases in phenylethanal concentrations were observed for 9 strains and significant increases in phenylethanol concentrations were also observed for 9 strains. The use of culture adjuncts that reduce the level of phenylethanal would likely result in Cheddar cheese with a reduced rosy note. The results of this study provided a starting point for the rational selection of culture adjuncts to control cheese flavor development in Cheddar cheese.

Key Words: *Lactobacillus casei*, volatile, Cheddar cheese ripening

132 Interaction between casein micelles and serum protein/κ–casein complexes during renneting of heat–treated skim milk. P. Kethireddipalli*, A. R. Hill, and D. G. Dalgleish, *University of Guelph*, *Guelph, ON, Canada*.

Heat-induced complexes of whey protein (WP) and κ-casein (κ-CN) can impair rennet clotting of native casein micelles; coagulation can be mostly restored by dialyzing the complex–laden serum against unheated milk (to be published). The present study investigated the mechanism of interaction between casein micelles and WP/κ-CN complexes during renneting of heat-treated milk. Native casein micelles were separated from unheated skim milk and re–suspended in the serum of heated (90°C, 10 min) milk, with and without dialysis of the serum against unheated milk. Using size exclusion chromatography, it was found that in both milk systems, the WP/κ-CN complexes progressively bind to the casein micelles as renneting proceeded. At about 85% κ-CN cleavage (caseinomacropeptide was quantified), the protein complex peak area decreased by 30 ± 5% and at 90% cleavage (prior to onset of clotting), peak area reduction was 50 ± 4%. In the absence of micelles, renneting of protein complexes in isolation showed no significant self aggregation, even when 90% κ-CN had been proteolyzed. Enzyme treatment of the dialyzed serum, however, resulted in significant aggregation of complexes (20 ± 2% at about 90% κ-CN cleavage), but to a much lesser extent than when casein micelles were present. Similar trends were noted when casein micelles from milk heated at native pH 6.7 (some surface-bound WP/κ-CN complexes), pH 7.1 (nearly complex-free micelle surface) or pH 6.3 (complex-saturated surface) were suspended in the serum of heated milk. No matter what the micelle surface was, all micelles were capable of binding more serum protein complexes in the course of renneting. These results are strong evidence that impaired rennet clotting of native casein micelles suspended in the serum of heated milk is due to the binding of WP/κ–CN complexes to the micelle surface prior to the onset of micelle aggregation, thereby sterically impairing the aggregation process. For reasons possibly related to ionic equilibria, heat-induced protein complexes in serum dialyzed against unheated milk are less detrimental to micelle fusion.

Key Words: whey protein/κ-casein complexes, heated milk, rennet

133 Starter cultures and cattle feed manipulation enhance conjugated linoleic acid levels in Cheddar cheese. M. S. Mohan*, S. Anand, K. F. Kalscheur, and A. N. Hassan, *Midwest Dairy Foods Research Center, South Dakota State University*, *Brookings*.

Conjugated linoleic acid (CLA) is a fatty acid that provides several health benefits to humans. In our previous research, a CLA-producing starter culture of Lactococcus lactis (CI4b) increased the CLA content in Cheddar cheese. Addition of fish oil to cattle diets has also been reported to increase the CLA content in milk. Thus, it was hypothesized that the use of the CLA-positive starter (CI4b) along with high CLA milk (obtained through dietary manipulation in cattle) would enhance the CLA content in Cheddar cheese. A diet containing fish oil (0.75% of dry matter) was fed to 32 dairy cows grouped in a pen for 15 d. This increased the CLA cis-9, trans-11 (CLA1) and CLA trans-10, cis-12 (CLA2) content from 0.8 and 0.13 g/100 g of fatty acids in the normal milk to 1.22 and 0.27 g/100g fatty acids in the treatment milk, respectively. A 2 × 2 factorial treatment design was used to test the effect of culture (DVS vs. CI4b) and type of milk (normal vs. treatment milk) on CLA content in Cheddar Cheese. A commercial cheese starter (DVS) was selected as the CLA nonproducing culture. Chemical composition (moisture, salt, fat, protein) of cheese was not affected by the type of culture used ($P > 0.05$). The textural properties (hardness, gumminess, chewiness) showed an interaction between milk and culture ($P < 0.05$) in the 1 mo old cheese. The 1 mo old cheese made from normal milk with DVS culture, normal milk with CI4b culture, treatment milk with

DVS culture and treatment milk with CI4b culture contained 0.34, 0.39, 1.03, 1.10 (±0.09) of CLA1 concentration and 0.06, 0.10, 0.18, 0.21 (±0.13) of CLA2 concentration (g/100 g of fatty acid), respectively. The treatment milk resulted in increased ($P < 0.01$) CLA1 and CLA2, while the CI4b culture increased only CLA2 levels ($P = 0.03$) in cheese. The results indicated that the combination of a CLA producing starter culture and dietary manipulated milk could enhance levels of CLA (CLA1 + CLA2) in Cheddar cheese by up to 3.3 times.

Key Words: conjugated linoleic acid, fish oil, cheddar cheese

134 Transcriptional stress responses to hydrogen peroxide in *Bifidobacterium longum*. T. S. Oberg*[1], J. L. Steele[2], S. C. Ingham[2], and J. R. Broadbent[1], [1]*Utah State University*, *Logan,* [2]*University of Wisconsin*, *Madison*.

Commercial application of bifidobacteria probiotics in function foods has increased dramatically in recent years. Due to the anaerobic nature of bifidobacteria, however, oxidative stress can significantly diminish viability of bifidobacteria during food production and storage. To better understand mechanisms for oxidative stress resistance in these cells, we examined the transcriptional stress responses to hydrogen peroxide (H_2O_2) of *Bifidobacterium longum* NCC2705, a strain that exhibits oxidative stress resistance, and *B. longum* D2957, a strain that does not. Bacteria were grown in MP5 medium to late logarithmic phase under anaerobic conditions with pH control, then suspended in MP5 with 0.625 mM H_2O_2 and incubated 5 or 20 min (NCC2705) or for 5 or 60 min (D2957). mRNA was isolated from each sample, converted to cDNA, and hybridized to a custom made Affymetrix DNA array. Three biological replicates of each treatment were performed. The microarray data was preprocessed using the RMA-MS method, filtered to only include genes with high signal intensity and a low coefficient of variation, then tested for differential expression using the limma/eBayes method (P value <0.05). Results showed *B. longum* NCC2705 had 316 genes that were differentially expressed after the 5-min treatment and 131 differentially expressed genes after the 20-min treatment. In contrast, D2957 had only 24 and 116 differentially expressed genes after the 5-and 60-min treatments, respectively. Both strains showed upregulation of genes associated with an oxidative stress response, including thioredoxin reductase, peroxiredoxin, ferridoxin and glutaredoxin. However, NCC2705 showed more extensive upregulation of genes involved in transcription regulation, a greater number of downregulated genes involved in sugar transport and metabolism, and several other differences. These observations provide a platform for future functional genomics research to determine the molecular basis for differences that are observed in oxidative stress resistance among strains of *B. longum*.

Key Words: probiotics, bifidobacteria, oxidative stress

135 Positive influence of milk on the expression of some stress-induced genes in *Bifidobacterium longum*. W. Dominguez* and D. J. O'Sullivan, *University of Minnesota*.

The objective of this study is to define the genes encompassing the yogurt fermentation stress regulon in *B. longum* DJO10A. A genome-wide microarray analysis was conducted on total RNA from samples taken at different time points during a yogurt fermentation with *B. longum*DJO10A. A control yogurt fermentation revealed that cross-hybridization of the yogurt starter culture transcripts with the microarray was essentially negligible under these fermentation conditions. During the fermentation, a set of genes located in 5 clusters, some of which have previously been associated with stress protection, were significantly expressed. These consisted of the *dnaK* and ibpA gene clusters, *groL*, a predicted gene BLD_1532, and genes encoding the F_0F_1-type ATP synthase. These 5 gene clusters were defined as the bifidobacteria stress regulon for yogurt fermentation and 4 genes were selected for further analysis using real-time PCR. Primers and TaqMan probes were designed to monitor the expression of these genes when the culture was exposed to milk and media supplemented with glucose or lactose and when the pH was decreased to 4.5. As the pH dropped in the media, low upregulation (<2 times) was observed in all the tested genes, except for *ibpA*, which was 8 times higher at the final pH (4.5) compared with the initial pH (6.4). However, when the cells sensed the pH drop in milk, they responded by upregulating *ibpA* and BLD_1532 by 30 and 5 times respectively. The expression of *ibpA* is induced by acid stress and milk components, other than lactose. A low pH in milk upregulates *ibpA* at a higher level than the presence of acid by itself and BLD_1532 expression is upregulated at low pH only when milk components are present. This suggests that the higher expression of these stress-induced genes in milk may afford a protective effect on bifidobacteria from acid or other stresses.

Key Words: bifidobacteria, probiotics, microarray

136 Impact of color of low fat Cheddar cheese on consumer preference. R. Wadhwani*, D. J. McMahon, and C. Maughan, *Utah State University*, *Logan*.

To observe if color impacts low fat cheese consumer preference, 9 batches of low fat Cheddar cheeses were manufactured at USU with 3 different levels of annatto (0, 7.34, and 22 g/100 kg) and TiO_2 (0, 7.67, and 40 g/100 kg) in a 3 × 3 completely randomized block design and aged 60 d before consumer liking assessment. The IRB approved consumer panel was conducted with 120 panelists recruited from the vicinity through newspaper advertisements, emails, and flyers. Panelists evaluation and responses were recorded anonymously in computers using SIMS 2000 program. Population studied were 18 to 35 years of age with >60% were frequent cheese consumers. Among 9 combinations, cheese with no color, intermediate and maximum level of annatto and TiO_2 combination were rated significantly higher for overall liking than other combinations ($P < 0.05$) on a 9-point hedonic scale of degree of liking. Interestingly, maximum level of TiO_2 when added singly, was rated higher (6.27) along with the combination of both TiO_2 and annatto, however, annatto when added singly, was rated significantly lower (4.82). Regarding the flavor and appearance liking, exactly same responses were observed and both intermediate and maximum levels of both colors in combination and maximum level of TiO_2 were rated significantly higher than other levels tested. However, texture rating was slightly different than previous attributes. For texture liking, consumers did not prefer the maximum level of TiO_2 and rated significantly lower (5.52) than intermediate and maximum levels. Panelists were also asked to evaluate these samples for the sharpness level on a 4-point scale where 1 = mild and 4 = extra sharp. The panelists rated maximum level of TiO_2 as significantly milder (1.48) and maximum level of annatto as significantly sharper (2.76) than other levels of color ($P < 0.05$). All panelists unanimously responded that these samples contained 24–26% fat when asked to assume the fat level wherein reality they all contained 6% fat. This study clearly indicated a significant impact of color on overall liking of Cheddar cheese and consumers' responses were driven by the appearance of cheese.

Key Words: color, Cheddar, liking

Nonruminant Nutrition: Amino Acids 1

137 Dietary supplementation of L-glutamine and L-glutamate to newly hatched broiler chickens. Y. Zhao*[1], P. R. Ferket[1], G. Wu[2], K. Nakagawa[3], and S. W. Kim[1], [1]*North Carolina State University*, *Raleigh*, [2]*Texas A&M University*, *College Station*, [3]*Ajinomoto Co. Inc.*, *Tokyo, Japan*.

This study was conducted to evaluate effects of supplemental L-glutamine (Gln) and L-glutamate (Glu) on growth and physiological responses in broiler chickens. Within 8 h after hatching (36.1 ± 1.1 g BW), 480 broiler chickens were allotted randomly to 6 dietary treatments: NC (without Gln or Glu), GN5 (with 0.5% Gln), GN10 (with 1.0% Gln), GU5 (with 0.5% Glu), GU10 (with 1.0% Glu), and AG10 (with 1.0% AminoGut, consisting of L-Gln >10% & L-Glu >10%, Ajinomoto). Each treatment had 8 replicates with 10 birds per cage. Diets were fed ad libitum for 6 wk. Body weight and feed intake were measured weekly. At the end of wk 1 and 6, one bird per cage was selected randomly to measure the weights of gut, breast muscle, thigh muscle, liver, and abdominal fat pad, and to obtain blood samples. Jejunum samples from wk 1 were used to measure villus height and crypt depth. Blood samples from wk 1 and 6 were used to measure plasma IgG and IgA concentration. Initial BW did not differ among treatment groups. During the entire period, weight gain of GN10 was greater ($P < 0.05$) than those of GN5, GU5, and NC. The weight gain of AG10 was greater ($P < 0.05$) than that of NC. Feed intake of birds did not differ among treatment groups during starter, grower, and finisher phases. There was no difference in feed:gain among treatment groups during the entire period. At the end of wk1, villus height or crypt depth of birds did not differ among treatment groups. There were no difference in the % weight of each tissue among treatment groups when measured at the end of wk 1 and wk 6. Plasma IgA concentration of AG10, GN5, and GU5 were greater ($P < 0.05$) than that of NC at wk 6. Plasma IgG concentration of AG10 was greater ($P < 0.05$) than that of other treatment groups at wk 6. This study shows potential benefits of supplemental glutamine or AG to broiler chickens.

Supported by US Poultry and Egg Association and Ajinomoto Co., Inc.

Key Words: broilers, glutamate, glutamine

138 The digestible lysine requirement of Cobb 500 x Hubbard M99 male broilers from 35 to 49 days. M. D. Dimova*[1], R. B. Shirley[2], J. L. Usry[2], P. B. Tilman[2], M. E. Freeman[1], and A. J. Davis[1], [1]*University of Georgia*, *Athens,* [2]*Ajinomoto Heartland, LLC*, *Chicago, IL*.

An experiment was conducted to determine the digestible lysine (dLys) requirement of the male, Cobb 500 fast-feathering female × Hubbard M99 male cross during the withdrawal period (35 to 49 d of age). Day-of-hatch birds were randomly allotted to 96 floor pens (4 rooms, 24 pens per room, 50 chicks per pen) and reared on used litter from 3 previous flocks. All chicks were fed the same starter (0 to 7 d), grower (7 to 21 d), and finisher (21 to 35 d) diets and these diets were formulated to exceed the Cobb 500 guidelines. On d 35 the number of birds was adjusted to 42 birds per pen and the 96 pens were assigned to one of 8 dietary treatments (12 replicates per treatment, 3 replicate pens per treatment in each room). The treatment diets were derived from a common base diet and common summit diet. The common base diet supplied 3,215 kcal/kg, 13.71% crude protein (CP) and 0.62% dLys, and the common summit diet supplied 3,215 kcal/kg, 23.59% CP and 1.24% dLys. By blending the base and summit diets, 6 intermediate levels of dLys were produced (0.71, 0.80, 0.89, 0.97, 1.06, and 1.15%). The minimum ideal essential amino acid ratios were maintained between the 8 diets; however, the dietary CP changed by an increment of 1.41% as the level of dLys changed. Broken-line regression analyses estimated the dLys requirement per bird in the withdrawal phase to be 24.45 g for body weight gain, 28.56 g for feed consumption, 25.61 g for feed conversion, and 25.28 g for total white meat yield (Pectoralis major and minor). The dLys requirement as a % of diet for body weight, feed consumption, feed conversion and total white meat was 0.86, 1.07, 0.91 and 0.90, respectively. This study aids in further defining the dLys requirement of the 35–49 d-old male, Cobb 500 fast-feathering female × Hubbard M99 male cross.

Key Words: broiler performance, meat yield, amino acid requirement

139 The effect of dietary pea and amino acid levels on the performance of broiler chickens. S. M. Ebsim*[1], T. D. Warkentin[2], and H. L. Classen[1], [1]*Department of Animal and Poultry Science, University of Saskatchewan*, *Saskatoon, Saskatchewan, Canada*, [2]*Crop Development Centre, University of Saskatchewan*, *Saskatoon, Saskatchewan, Canada*.

Pea is an important crop in Western Canada with considerable potential as a feed ingredient for broilers. Pea has also been recognized for its slowly degraded starch, which has been suggested to reduce the amino acid requirement of broilers. Therefore, an experiment was designed to investigate maximum inclusion levels of pea in broiler diets and the interaction of dietary pea and amino acid inclusion. A growth trial with 3,480 broiler chickens was conducted in a 6 × 2 factorial arrangement evaluating 6 levels of pea inclusion (0, 150, 300, 450, 600, 750 g/kg) and 2 levels of amino acids (100% and 85% of Ross × Ross 308 requirement). Each treatment was offered to 5 pens of 58 males from 0 to 35 d. No interactions were found between pea inclusion and amino acid level for all studied parameters. The higher level of amino acids increased breast meat ($P = 0.0267$) and improved mortality corrected feed efficiency ($P = 0.0437$). Pea inclusion level affected performance in an age dependent manner. Body weight gain from 0 to 10, 10 to 25 and 25 to 35 d decreased when pea level exceeded 300, 600 and 600 g/kg, respectively. Mortality corrected feed to gain ratio was increased by pea inclusion when values exceeded 600 and 300 g/kg for 0 to 10 and 10 to 25 d periods but was unaffected by pea level from 25 to 35 d. Broilers fed pea levels above 450 g/kg had reduced carcass and breast weight ($P = 0.0001$) as a proportion of live weight. High levels of pea inclusion decreased proportional breast (600 and 750 g/kg) and drum skin (750 g/kg) weight. In conclusion, maximum pea inclusion levels increase with broiler age and no interactions were found between dietary treatments at the levels of amino acids used in this research.

Key Words: broilers, pea, starch, amino acid

140 Effect of a mono component protease on true amino acid digestibility of full fat soy for broiler chickens using different methods. R. K. G. Messias[1], L. F. T. Albino[1], J. O. B. Sorbara*[2], and H. S. Rostagno[1], [1]*Universidade Federal de Viçosa*, *Viçosa, MG, Brazil*, [2]*DSM Nutritional Products*, *São Paulo, SP, Brazil*.

Different methods have been used to determine the true amino acid digestibility (TAAD) of feed ingredients. All methods were always used to estimate the TAAD of only one ingredient and were not developed to determine the effect of an additive (ex. enzymes) on a single ingredient.

Based on this, a digestibility trial was conducted to determine the effect of 2 different methods on TAAD of full fat soy (FFS) when using a mono component protease. The trial was conducted with 336 broiler chicks from 12 to 22 d of age placed on wire cages, in a complete randomized experimental design with 8 treatments and 6 replicates of 7 birds each. The first 4 treatments were used to evaluate the classic method using a protein free diet (PFD) where FFS replaced 30% of starch in the PFD with and without the protease addition. Treatments 5 to 8 were used to evaluate a second method. Treatment 5 was a corn soy basal diet with 30% starch and treatment 6 was the basal diet (T5) but FFS replaced the starch. Treatments 7 and 8 were the same T5 and T6 with protease addition. The mono component protease used (dose 200 ppm) was RONOZYME ProAct with 75000 Prot Units/g. At 22 d all birds were sacrificed and ileal digesta collected. Acid insoluble ash (Celite) was used as inert marker. Feed and water were provided ad libitum. At 22 d of age all birds were sacrificed and ileum content collected. The samples were freeze-dried at −40°C for 72 h. No interaction was observed between method and protease addition. Protease addition increased ($P < 0.05$) TAAD of FFS by 3%, 3%, 9%, 7%, 2%, 7%, 4%, 5%, 6%, 12%, 8%, 7%, 8%, 8% for Lys, Met, M+C, Thr, Val, His, Arg, Phe, Gly+Ser, Asp, Glu, Ala, Pro, Tyr, respectively. The method with the basal diet plus FFS showed 18% lower TAAD (mean sum of AAs) as compared with the PFD method. In conclusion the protease supplementation improved TAAD of FFS on average 6% independently of the method used.

Key Words: enzyme, nutrition, method

141 Ileal digestibility of the amino acids of soybean meals of different origin in broilers. M. Frikha[1], M. P. Serrano[1], D. G. Valencia[2], C. Centeno[3], R. Lázaro[1], and G. G. Mateos*[1], [1]*Universidad Politécnica de Madrid*, *Madrid, Spain*, [2]*Nutral S.A.*, *Madrid, Spain*, [3]*CSIC*, *Madrid, Spain*.

A trial was conducted to determine the apparent (AID) and standardized (SID) ileal digestibility of CP and AA of 22 soybean meals (SBM) from 3 different origins; USA, Brazil (BRA), and Argentina (ARG) in 21-d-old broilers. There were 7 to 8 samples of SBM per origin and 6 replicates (6 chicks each) per each SBM sample. On DM bases, the average CP was 53.5, 55.3, and 52.3% for USA (n = 8), BRA (n = 7), and ARG (n = 7) meals, respectively. The concentration of Lys and Met per unit of protein was highest ($P < 0.01$) for the USA meal and lowest for the BRA meal with ARG meal being intermediate. The KOH solubility was higher for USA than for BRA and ARG meals (86.5, 82.8, and 80.0%; ($P < 0.05$) but trypsin inhibitor activity (TIA) was similar for all origins (3.0 mg/g DM). Chicks were fed a commercial corn-soybean meal diet from 1 to 17 d and then, their respective experimental diets, with the SBM tested as the only source of CP (20%), from 18 to 21 d of age. In addition, a N-free diet was used to estimate ileal endogenous losses of the AA in 6 extra replicates. The AID of the 22 SBM samples ranged from 82.9 to 88.0 for CP, from 85.0 to 90.5 for Lys, and from 66.4 to 75.0 for Cys. In general, the AID of CP and of most indispensable AA were similar for USA and BRA SBM meals and for both higher (($P < 0.01$) than for ARG meal (i.e., 88.2 and 88.1 vs. 86.7 for Lys and 88.0 and 89.1 vs. 86.6 for Met, respectively). The SID values of the 22 SBM samples ranged from 89.3 to 94.6 for CP, from 90.1 to 94.9 for Lys, and from 78.5 to 85.4 for Cys. The SID values of most indispensable AA were similar for USA and BRA meals and higher for both (($P < 0.05$) than for the ARG meal (i.e., 93.0 and 92.7 vs. 91.8 for Lys and 95.6 and 96.9 vs. 94.9 for Met). It is concluded that the ileal digestibility of CP and AA varies considerably among commercial SBM samples. In fact, in this study, USA and BRA SBM had a higher AID and SID than ARG SBM.

Key Words: soybean meal origin, ileal amino acid digestibility, broilers

142 Nutrient density and balanced amino acids to ME ratio are drivers of growth, feed efficiency and carcass yield in broiler chickens. L. F. Romero*[1] and V. Ravindran[2], [1]*Danisco Animal Nutrition*, *Marlborough, UK*, [2]*Massey University*, *Palmerston North, New Zealand*.

Broiler nutritionists typically consider ME, CP (%), and essential amino acids (%) as criteria for diet formulation based on a set of recommended values per unit of feed mass. However, nutrient density, and balanced amino acids to ME ratio may be better explanatory variables of animal performance. Two 42-d performance trials, each with a total of 480 male broilers (Ross 308) were conducted to evaluate growth, feed efficiency, and carcass yield in response to 2 levels of nutrient density (Starter: 2,875 or 3,200 kcal ME/kg; Finisher: 3,020 or 3,315 kcal ME/kg; other nutrients proportional to ME), and 3 levels of digestible lysine (dlys) to ME ratios (Starter: 3.5, 3.9, 4.3 g dlys/Mcal ME; Finisher: 3.0, 3.5, 3.9 g dlys/Mcal ME). Diets were based on corn, soybean meal, corn gluten (= <5%), wheat middlings (= <5%), and A/V fat blend (0.5–7.5%). Other amino acids were balanced relative to lysine. Data were analyzed as a factorial design using the Mixed Procedure of SAS. Significance was evaluated at $P < 0.05$. Birds fed the low density diet exhibited a lower BW gain from 0 to 42 d compared with birds on the high density diet (3,252 g vs. 3,346 g; $P < 0.05$). Increments of dlys:ME resulted in significant increments of BW gain from 3,133 to 3,328 and 3,435 g. Increasing dlys:ME resulted in linear reductions of feed per gain, both in high and low density diets, ranging from 1.66 g/g in low dlys:ME x low ME to 1.44 g/g in high dlys:ME × high ME diets. High density increased caloric intake (16.22 Mcal/bird) versus low density diets (15.29 Mcal/bird). Low density diets had reduced caloric conversion (4.71 kcal/g BW) compared with high density diets (4.85 kcal/g BW). Caloric conversion linearly decreased with increments in dlys:ME (4.97, 4.77 and 4.60 kcal/g BW). Carcass and breast yields increased, and abdominal fat yield decreased with increasing dlys:ME ratios, in both low and high ME diets. More predictable responses of broiler performance by the use of nutrient density and dlys:ME as flexible criteria in diet formulations will enable accurate profit optimization of broiler operations.

Key Words: amino acid, broiler chicken, diet optimization

143 Digestible lysine requirements of Cobb × Cobb 700 male broilers from twenty-eight to forty-two days of age. W. A. Dozier III*[1], A. Corzo[2], M. T. Kidd[2], and P. B. Tillman[3], [1]*Auburn University*, *Auburn, AL*, [2]*Mississippi State University*, *Mississippi State,* [3]*Ajinomoto Heartland LLC*, *Chicago, IL*.

Research addressing digestible (dig) Lys requirement data of modern broilers from 4 to 6 wk of age is limited. This study examined growth and meat yield responses of broilers provided experimental diets varying in dig Lys, to determine the dig Lys requirements, from 28 to 42 d of age. Three-thousand male Cobb × Cobb 700 chicks were randomly distributed into floor pens at 1 d of age and were fed common starter and grower diets until 28 d of age. At 28 d of age, all pens were equalized with 23 birds (0.09 m^2/bird) and fed the experimental diets until 42 d of age. Two diets (dilution and summit) consisting of corn, soybean meal, meat and bone meal, and peanut meal were formulated to be adequate in all other amino acids. The dilution and summit diets were blended to create 7 intermediate diets, for a total of 9 titration diets. A control diet containing adequate dig Lys was used for comparison with the titration diets. Each treatment was represented by 12 replicate pens. Body

weight gain, feed intake, dig Lys intake, dig Lys intake/BW gain, feed conversion, mortality, carcass yields, and physiological parameters were assessed during experimentation. Dig Lys requirements were estimated using a quadratic broken-line model. Dig Lys requirement for male Cobb × Cobb 700 broilers ranged from 0.965 to 1.030% for BW gain, feed conversion, carcass weight, total breast meat weight, and total breast meat yield. Dig Lys requirements for male Cobb × Cobb 700 broilers were estimated at 0.995% based upon averages of live performance and meat yield responses. These data support a higher dig Lys requirement of male broilers from 28 to 42 d of age on a percentage basis than previous research as noted by less feed intake per unit of BW gain and a greater meat accretion rate.

Key Words: amino acid, broiler, lysine

144 Maximizing the use of supplemental amino acids in diets for 7-kg pigs. V. D. Naranjo*[1], T. D. Bidner[1], R. L. Payne[2], and L. L Southern[1], [1]*LSU Agricultural Center*, *Baton Rouge,* [2]*Evonik-Degussa Corporation*, *Kennesaw, GA*.

Three (14-d) experiments were conducted to determine the Lys requirement of 7-kg pigs and then to determine the maximum level of supplemental L-Lys along with DL-Met, L-Thr, and L-Trp that can be added in these diets. In all experiments, pigs were fed a common diet during wk-1 post-weaning. On d 7, pigs were blocked by initial BW and sex, and littermates were balanced across treatments. In Exp. 1 (5 reps of 3 or 4 pigs per pen; initial BW = 7.4 ± 1.2 kg), pigs were fed corn-soybean meal-peanut meal (C-SBM-PM) diets containing 0.754, 0.879, 1.004, 1.129, and 1.254% standardized ileal digestible (SID) Lys. A positive control (PC) diet without PM contained 1.254% SID Lys. Daily gain (257, 329, 364, 399, 440; 449 g/d), ADFI (620, 781, 700, 737, 804; 782 g/d), and G:F (0.42, 0.42, 0.52, 0.54, 0.55; 0.57) were linearly increased ($P < 0.01$) as SID Lys increased. Based on ADG, the SID Lys requirement was estimated at 1.221% ($P = 0.02$). In Exp. 2 (5 pens of 4 pigs per pen; initial BW = 6.30 ± 0.8 kg) and Exp. 3 (5 reps of 4 pigs per pen; initial BW = 6.9 ± 1.0 kg), C-SBM diets were formulated to contain 1.221% SID Lys. Only supplemental Met, Thr, and Trp were added to the diets to keep a constant ratio to Lys. In Exp.2, dietary treatments included 6 levels of supplemental L-Lys: 0, 0.049, 0.099, 0.149, 0.198, and 0.248%. There were no linear or quadratic effects ($P > 0.10$) in ADG (358, 361, 386, 357, 351, and 356 g/d), ADFI (861, 786, 856, 822, 819, and 893 g/d), or G:F (0.42, 0.47, 0.46, 0.44, 0.43, and 0.41) of supplemental L-Lys. In Exp. 3, dietary treatments included 5 levels of supplemental L-Lys: 0.198, 0.248, 0.298, 0.347, and 0.397%. Daily gain (376, 384, 379, 351, and 344 g/d; $P = 0.03$) and G:F (0.62, 0.54, 0.56, 0.52, and 0.50; $P < 0.01$) were linearly decreased, but ADFI (615, 718, 682, 675, and 696 g/d) was not affected. The results of this research indicate that up to 0.298% supplemental L-Lys along with supplemental Thr, Met, and Trp can be added in diets for 7-kg pigs without affecting ADG, but G:F is reduced at levels greater than 0.198% supplemental Lys.

Key Words: amino acids, pig, nursery

145 Well-fed piglets prefer amino acids that elicit umami taste. G. Tedo*[1], E. Roura[1], M. Reina[2], J. L. Ruiz-de la Torre[3], and X. Manteca[3], [1]*Lucta SA*, *Barcelona, Spain*, [2]*Celltec-University of Barcelona*, *Barcelona, Spain*, [3]*Autonomous University of Barcelona*, *Barcelona, Spain*.

Pigs perceive the umami taste via the pT1r1/pT1r3 receptor present in their tongue. In vitro studies, using a proprietary cell reporter system (CRS) that expresses this heterodimer, showed that it is tuned to detect amino acids (AA). The objectives of this work were (1) to evaluate preferences of piglets for AA and (2) to correlate preference data with outcomes from the CRS for the same AA. Forty-eight weaned piglets (10.7 ± 1.20 Kg of BW, mixed sexes) were distributed in pairs/pen, with ad libitum access to water and pelleted starter feed (2521Kcal NE/Kg, 19.1% CP, 1.32% Lys). Preferences were assessed using a double-choice model that consisted of 10-min training sessions conducted twice daily (9AM, 12PM) over 2 consecutive days followed by 2-min test sessions conducted twice daily (9AM, 12PM) over 5 d. During training, plain and sweetened (500mM sucrose) water were offered simultaneously in stainless steel containers (250g/container); whereas, in test sessions, water was offered along with water (control) and 50mM solutions of monosodium glutamate (MSG), D,L-Met, Gly, L-Ala, L-Gln, L-Glu, L-Lys, L-Thr and L-Trp. Preference (%) data [g test solution / (g test solution + g water) x 100] were analyzed using a mixed model approach that included the effects of pen (random), day, time, and treatment. Preferred solutions ($P < 0.01$) were MSG (79.6 ± 2.03), Glu (79.8 ± 2.45), Lys (77.2 ± 3.91), Gln (73.4 ± 3.37) and Ala (67.6 ± 4.46), whereas Trp (25.6 ± 4.40) was rejected. Additionally, solutions of Met (64.4 ± 9.58), Gly (59.9 ± 4.41) and Thr (49.5 ± 10.05) were not different from control (46.1 ± 3.18). Results from CRS were positively correlated ($R = 0.92$, $P < 0.05$) with preferences of Ala, Gln, Glu and MSG. Lys was also preferred but did not stimulate the umami receptor. In summary, well-fed piglets mainly preferred AA that stimulated the umami taste receptor expressed in the CRS. Therefore, the umami taste has a positive hedonic (pleasant) valence (value) for pigs.

Key Words: umami, amino acids, intake

146 Effect of fat source and levels, with lysophospholipids, on broiler performance, fatty acid digestibility and apparent metabolizable energy content in feed. B. K. Zhang*[1], H. T. Li[2], Y. M. Guo[1], and D. Q. Zhao[1], [1]*China Agricultural University*, *Beijing, China*, [2]*Kemin Industries Co. Ltd*, *Zhuhai, China*.

Three fat sources (soybean oil, tallow, and poultry fat), at 2 levels of addition (24 or 30 g/kg diet) with or without a lysophospholipid emulsifier (0 or 500 mg/kg) were incorporated into broiler feed. A total of 504 one day-old male Arbor Acres broiler chickens were randomly allocated to 12 treatments with 7 replicates of 6 birds each. The experimental period lasted 21 d. The lysophospholipid emulsifier (LPL) was a commercial powder preparation mainly containing lysophosphatidylcholine. The performance of the broilers, fatty acid digestibility and apparent metabolizable energy (AME) of the feed was studied. The source of fat had a clear effect ($P < 0.01$) on body weight gain and feed conversion ratio. Body weight gain was lower ($P < 0.01$) for broilers fed diets containing tallow than for those fed diets containing soybean oil or poultry fat. Levels of fat addition did not significantly influence the body weight gain of broilers. The addition of LPL increased the body weight gain of broilers ($P = 0.030$) and also increased the AME ($P < 0.05$) and AMEn ($P < 0.05$) of the diets. The LPL enhanced body weight gain for chickens fed the poultry fat diet (563 g vs. 539.5 g), and to a lesser extent with the tallow diet (532.5 vs. 514.5 g), but not for the birds given the soybean oil diet. The sources of fat had a clear effect ($P < 0.01$) on the digestibility of most fatty acids. Addition of LPL increased digestibility of C16:0, and C18:0 fatty acids in the starter period ($P < 0.05$), but had no effect on the digestibility of the other fatty acids under the conditions tested. The AME and AMEn of the diets were not significantly affected by sources of fat ($P > 0.05$), but were significantly improved by LPL ($P < 0.05$). The digestibility of CP and DM were not affected ($P > 0.05$) by LPL, fat sources or the levels of fat addition. There was no significant interaction between growth parameters, digestibility and AME of the diets ($P > 0.05$). These data indicated that the effect of LPL on broiler performance was dependent upon the types of dietary fat.

Key Words: lysophospholipids, fats, broiler

147 Effect of dietary fat on the production and composition of emu oil. D. C. Bennett*, W. E. Code, and K. M. Cheng, *University of British Columbia*, *Vancouver, BC, Canada*.

Emus (*Dromaius novaehollandiae*) are large flightless birds that are farmed for their meat and fat. The fat from both the subcutaneous and retroperitoneal adipose depots is rendered into oil, which is purported to have anti-inflammatory and anti-oxidant properties. Dietary fatty acid composition influences the fatty acid composition of the oil, but its affect on fat deposition or on the amount of oil produced after rendering has not been reported. Work on broiler chickens has shown that dietary fatty acid composition influences both the accumulation and fatty acid composition of abdominal fat. Therefore, the objective of the present study is to examine the effect of 2 dietary sources of fat on the amount and fatty acid composition of emu oil. Forty 3-year-old emus were fed a barley-alfalfa base diet that was supplemented with either tallow or canola oil at 2 levels (4% or 8%; 5 males and 5 females per dietary group); an additional 10 birds (5 males and 5 females) remained on the barley-alfalfa diet as controls. Birds were fed these diets for 6 mo before being slaughtered in October. Body weight and meat and fat yields were unaffected by the diet and averaged 44.2, 14.1 and 9.7 kg/bird, respectively. Females weighed more than males (45.6 and 42.9 kg, respectively), but fat yield did not differ between the sexes (9.4 and 10.0 kg/bird, respectively). Similarly, diet did not affect the total amount of oil produced after rendering, which averaged 6.8 kg/bird. Analysis of fatty composition of the oil is currently underway. These results indicate that, unlike chickens, neither the source nor the level of fat in the diet affected the amount of fat deposition in emus.

Key Words: emu, fat production, dietary fat

148 Whole body retention of highly unsaturated n-3 fatty acids (HUFA) and apparent conversion from 18:3n-3 are independent of body weight in pigs fed flaxseed diets. H. R. Martínez Ramírez*[1], J. K. G. Kramer[2], and C. F. M. de Lange[1], [1]*Centre for Nutritional Modeling, Department of Animal and Poultry Science, University of Guelph*, *Guelph, ON, Canada, N1G2W1*, [2]*Agriculture and Agri-Food Canada*, *Guelph, ON, Canada, N1G5C9*.

A total of 28 Yorkshire growing gilts were used in a serial slaughter study to determine the content of n-3 fatty acid (FA) and the apparent conversion (AC) of 18:3n-3 to HUFAs (18:4n-3, 20:3n-3, 20:5n-3, 22:5n-3, 22:6n-3) on a whole body basis, fed 3 feeding programs (n = 8). Four pigs were slaughtered at 25 kg BW to determine initial body composition. Corn-wheat-soy based diets were fed to growing gilts containing ground flaxseed (FS): T1, FS diet (10%) between 25 and 50 kg BW, and control diets (C, low in n-3 FA) thereafter until 110 kg BW; T2, C between 25 and 85 kg BW, and FS diet (6%) thereafter until 110 kg BW; and T3, C between 25 and 110 kg BW. Feed intake was fixed at 95% of the voluntary feed intake according to NRC (1998). Pigs on T1 and T2 consumed equal amounts of FS (5.1 vs. 5.2 kg, $P > 0.10$). The FA content in whole body was expressed as mg/100 g of empty BW. No treatment effect was observed for growth performance, composition of growth, and chemical and physical body composition across treatments ($P > 0.05$). Contents of 18:3n-3 and HUFA were larger in T1 and T2 than T3 ($P < 0.05$), except for 22:6n-3. Content of 18:3n-3 was lower in T1 than T2 (522 vs. 611; $P < 0.01$), whereas no such effect was observed for either total HUFA (136 vs. 140; $P > 0.10$) or n-6/n-3 ratio (4.5 vs. 4.0; $P > 0.10$). Expressed as a portion of 18:3n-3 intake, the largest AC among n-3 FA in T1 and T2 was to 20:3n-3 (9.1 vs. 10.3%) and 22:5n-3 (3.1 vs. 3.3%), whereas the total AC of n-3 FA was not affected by previous feeding program (8.7 vs. 13.6%; $P > 0.10$). These results suggest that the rate of AC of n-3 FA and HUFA content is independent of BW which provides flexibility as to when n-3 FA might be fed to produce n-3 enriched pork.

Key Words: apparent conversion, n-3 fatty acid, pigs

149 Effect of dietary conjugated linoleic acid on markers of intramuscular adipocytes in pork. K. M. Barnes*[1], N. Winslow[1], A. Shelton[1], and M. J. Azain[2], [1]*West Virginia University*, *Morgantown,* [2]*University of Georgia*, *Athens*.

Dietary conjugated linoleic acid (CLA) has been reported to decrease backfat and increase marbling in hogs. Our objective was to determine if the increased marbling was related to increased intramuscular adipocyte development. Barrows (n = 20, 53 kg) were penned in pairs and pens were randomly allotted to receive finishing diets containing 1% soybean oil (SBO) or 1% CLA oil (60% mixed CLA isomers) for 6 wks. Body weight and feed intake were determined weekly. At slaughter loin samples were obtained and flash frozen for RNA extraction and real time RT-PCR analysis of gene expression. Following a 24 h chill, carcasses

were ribbed and loin eye area (LEA) and backfat depth were measured, and subjective marbling and color scores were assigned. Loin, backfat, and belly fat samples were obtained for fatty acid analysis by gas chromatography. Dietary CLA did not affect body weight or feed intake at any point, nor did treatment groups differ in hot carcass weight, LEA, or color. CLA-fed pigs did have less ($P < 0.05$) backfat than SBO-fed pigs (25 vs. 30 mm, respectively) and had a non-significant ($P = 0.164$) increase in marbling score (3.1 vs. 2.4, respectively). The cis9,trans11 and trans10,cis12 CLA isomers were incorporated ($P < 0.001$) into backfat and belly fat but only trans10,cis12 CLA was increased ($P < 0.001$) in the loin of CLA-fed pigs. In all 3 tissues, the proportion of saturated fatty acids were increased ($P < 0.001$) by CLA. Relative gene expression for markers of preadipocytes (Pref-1), differentiating adipocytes (PPARγ), and mature adipocytes (Ap2 and Perilipin) were determined and normalized to the expression of acidic ribosomal phosphoprotein. No significant differences were detected but the expression of PPARγ (1.49 vs. 1.21, $P = 0.374$), Perilipin (1.81 vs. 1.44, $P = 0.485$), and Ap2 (1.75 vs. 1.21, $P = 0.205$) all were numerically greater in CLA-fed pigs than SBO-fed pigs. These preliminary results indicate that the increase in marbling in pigs fed CLA may be related to increased intramuscular adipocytes.

Key Words: conjugated linoleic acid, marbling, pork

150 Effects of dietary polyunsaturation level and genistein supplementation on performance and meat quality in quails reared under heat stress. N. Sahin* and C. Orhan, *Firat University Faculty of Veterinary Medicine Department of Animal Nutrition*, *Elazig, Turkey*.

This experiment was conducted to investigate the effects of dietary polyunsaturated fatty acids (PUFA) level (15 *vs*. 45%) and genistein supplementation (GS, 0, 400, and 800 mg/kg) on performance and muscle lipid profile in quails (*Coturnix coturnix japonica*, n = 360) reared under thermoneutral (TN, 22°C) and heat stress (HS, 34°C) conditions. Data were analyzed by 3-way ANOVA using the MIXED Procedure. Each treatment was replicated in 10 cages, each containing 3 birds, from d 10 to 42. HS condition decreased body weigh gain (BWG, 137 *vs*. 150 g) and cumulative feed intake (CFI, 657 *vs*. 708 g) and increased feed conversion ratio (FCR, 4.82 *vs*. 4.72) compared with TN condition ($P < 0.0001$ for all). Increasing dietary PUFA level was associated with decreases in BWG (5.26%; $P < 0.0001$) and CFI (6 g; $P < 0.01$) and an increase in FCR (4.61%; $P < 0.0001$). There were linear increases in BWG from 142 to 145 g and FCR from 4.83 to 4.73, with increasing GS ($P < 0.05$). Quails reared under TN condition had greater proportions (g/100 g fat) of PUFA (25 vs. 21), monounsaturated fatty acid (MUFA, 45 vs. 43), ω-6 (13 vs. 11), and ω-3 (12 vs. 10.38) and a less proportion of saturated fatty acid (SFA, 30 vs. 36) than quails reared under HS condition ($P < 0.0001$ for all). Quails fed diet containing 15% PUFA had greater MUFA (52 vs. 35) and SFA (36 vs. 31) and less PUFA (12 vs. 34), ω-6 (10 vs. 14), and ω-3 (2 vs. 20) than quails fed diet containing 45% PUFA ($P < 0.0001$ for all). Muscle FA profile did not vary by GS. Quails that were reared under HS condition (0.48 vs. 0.29 µg/g) and quails that were fed diet containing 45% PUFA (0.91 vs. 0.78 µg/g) had greater muscle malondialdehyde (MDA) content than their counterparts ($P < 0.0001$ for both). GS did not affect muscle MDA content. There were variable 2-way treatment interaction effects on response variables. In conclusion, increasing dietary PUFA level and GS may improve performance and meat quality in heat stress.

Key Words: PUFA, genistein, quail

151 Evaluating the efficacy of OptiCal under varying levels of dietary fat inclusion. J. D. Hamburg*[1], A. B. Batal[1], and S. D. Frankenbach[2], [1]*University of Georgia*, *Athens,* [2]*JBS United Inc.*, *Indianapolis, IN*.

Fat inclusion in diets has been shown to decrease gut transit which increases the energy availability of the diet. Thus, the objective of these studies was to determine the efficacy of OptiCal in diets with various levels of fat inclusion. Two 4 × 2 factorial studies were conducted in which a standard corn-soybean meal-distillers dried grains plus soluble diet was fed to broilers for performance and AME determination and also to roosters for TME_N determination. There were 4 levels of fat: 0, 1, 2, and 3% and 2 levels of Optical, 0 and 0.25lbs/ton. The diets were formulated to meet digestible amino acid requirements; however the ME of the diets varied with fat inclusion. The calculated ME of the control diet (0% fat and no Optical) was 2,900 kcal/kg and the ME increased 84 kcal/kg for every 1% inclusion of fat. To determine TME_N, a traditional precision-fed rooster assay in which 8 birds per diet were fasted for 24 h then crop intubated with 35 g of the test diets. Excreta were then collected for 48 h. For the chick assay 288 male broiler chicks were placed in Petersime battery brooders and fed a standard corn-soybean meal crumble diet. At 4 d of age, 9 replications of 4 chicks were weighed and assigned to one of the 8 dietary treatments. Body weight and feed intake were measured at 9 and 18 d of age. Excreta were collected at d 18 for AME determination. The TME_N values of the diets increased as the fat inclusion in the diets increased from 0 to 3% fat (3,036 to 3,234 kcal/kg, respectively). The efficacy of Optical on releasing energy, increasing the TME_N value improved as the inclusion of fat increased, on average the TME_N value of the diets with Optical were 57 kcal/kg higher than the diets without Optical. There was no effect of the addition of Optical on the diet without any fat inclusion. The inclusion of fat improved the feed:gain ratio as compared with the diets without fat (1.50 to 1.73, respectively). There was a interaction between fat inclusion and enzymes on the feed:gain ratios at 18 d of age. Based on the results of these studies fat inclusion levels in the diet appears to have an effect on enzyme efficacy.

Key Words: fat, enzymes, OptiCal

152 Fat digestibility in enzymatically treated soybean meal without and with choice white grease and vegetable oil. K. P. Goebel* and H. H. Stein, *University of Illinois*, *Urbana*.

An experiment was conducted to measure the digestibility of fat by weanling pigs fed enzymatically treated soybean meal and either soybean oil or choice white grease. Two sources of enzymatically treated soybean meals were used (HP-300 and HP-350). These meals are similar with the exception that an emulsifier, lecithin, is included in HP-350, but not in HP-300. The HP-300 meal contained 57.07% CP, 1.44% acid-hydrolyzed ether extract (AEE), and 2.30 trypsin inhibitor units (TIU) per mg, and HP-350 contained 53.60% CP, 3.73% AEE, and 1.50 TIU per mg. Two diets were formulated by mixing cornstarch, sugar, and each source of soybean meal. Two additional diets that were similar to the initial 2 diets with the exception that 6% choice white grease or 6% soybean oil was added to these diets were also formulated. Thirty-two weanling barrows (initial BW: 13.3 ± 0.8 kg) were randomly allotted to the 4 diets with 8 replicate pigs per diet in a 2 × 2 factorial design. Pigs were housed in metabolism cages. Pigs were fed experimental diets for 14 d with total collections of feces during the final 5 d. Feed intake and DM output were not different among treatments. The apparent total tract digestibility (ATTD) of DM and GE were not different among treatments regardless of soybean meal and fat source. The ATTD of AEE in HP-300 and HP-350 mixed with soybean oil was not differ-

ent (80.4 and 75.7%, respectively). The ATTD of AEE in HP-300 and HP-350 mixed with choice white grease was also not different (80.2% and 79.3%, respectively). Results indicated that the added lecithin in HP-350 did not increase fat digestibility in pigs fed diets supplemented with soybean oil or choice white grease.

Key Words: fat digestibility, lecithin, soybean meal

153 Effect of dietary DHA levels and different sources of oil (fat) on egg yolk DHA and ω-3 fatty acids levels. M. K. Manangi*, B. Wuelling, J. Hux, S. Carter, C. D. Knight, and M. Vazquez-Anon, *Novus International, Inc.*, *St. Charles, MO*.

A 5 wk experiment was conducted to evaluate the effect of different levels of DHA (docosahexaenoic acid) as DHA GOLD (a dried whole cell algae product, derived from *Schizochytrium* sp., contains a minimum of 18% DHA by weight) and sources of oil (fat) on egg yolk DHA and ω-3 fatty acids deposition. A total of 216 Hy-Line W-36 commercial laying hens, 40 wk old, were randomly assigned to 6 treatments with 36 cages/treatment and one hen/cage. The trial design was a 2 × 3 factorial with 2 levels (0 and 1%) of DHA GOLD and 3 sources (canola, flax and corn oil) of oil. Results indicate that DHA GOLD and oil sources had significant ($P < 0.05$) interaction on DHA, and total ω-3s fatty acids in eggs. Supplementation of DHA GOLD to diets with canola, flax and corn oil increased ($P < 0.05$) the DHA deposition from 19 to 163, 33 to 158 and 19 to 170 mg/egg, respectively. Supplementation of DHA GOLD to diets with canola oil and corn oil increased total ω-3s from 125 to 338 and 111 to 376 mg/egg, respectively. The DHA GOLD and flax oil combination did not affect ($P > 0.05$) total ω-3s. In summary, under present experimental conditions dietary supplementation of DHA GOLD increased egg DHA content that meets toward recommended daily allowance irrespective of tested oil sources. Total ω-3s in eggs increased in response to supplemental DHA GOLD for canola and corn oil diets but not for flax oil.

DHA GOLD is a registered trademark of Martek Biosciences Corporation, USA

Key Words: layer, DHA, ω-3s

154 Effect of different levels of flaxseed and DHA GOLD on egg yolk DHA deposition. M. K. Manangi*, B. Wuelling, J. Hux, S. Carter, C. D. Knight, and M. Vazquez-Anon, *Novus International, Inc.*, *St. Charles, MO*.

A 5 wk experiment was conducted to evaluate the effect of different levels of flaxseed, and DHA (docosahexaenoic acid) as DHA GOLD (a dried whole cell algae product, derived from *Schizochytrium* sp., contains a minimum of 18% DHA by weight) on egg yolk DHA. A total of 216 Hy-Line W-36 commercial laying hens, 24 wk old, were randomly assigned to 9 treatments with 24 individual cages per treatment and one hen per cage. The trial design was a 3 × 3 factorial with 3 levels (0, 0.5 and 1%) of DHA GOLD and 3 levels (0, 3 and 6%) of flaxseed. All diets were isolipidic and soybean oil was used to replace oil from flaxseed. Results indicated a significant ($P < 0.05$) interaction of DHA GOLD and flaxseed levels on DHA, total ω-3 fatty acids, and vitamin E levels. DHA and ω-3s content in egg increased linearly with the addition of DHA GOLD by itself or in the presence of flaxseed. Addition of 3% flaxseed improved DHA egg content from control but was less effective than DHA GOLD treatments. Further increase of flaxseed from 3 to 6% did not result in additional DHA deposition in egg, except when 0.5% DHA GOLD was present in the diet. The optimum DHA level of 173mg/egg was achieved by feeding hens' 1% DHAGOLD + 3% flaxseed compared with 35.9mg DHA/egg for hens fed the control diet ($P < 0.05$). The combination of 1% DHA GOLD and 3% flaxseed also resulted in significantly ($P < 0.05$) higher total ω-3s (389mg/egg) compared with hens fed diets supplemented with 0 or 0.5% DHA GOLD in combination with 0, 3 or 6% flaxseed. Supplementation of 1% DHA GOLD alone with no flaxseed resulted in a deposition of 141mg of DHA/egg whereas 6% flaxseed with no DHA GOLD resulted in 52mg of DHA/egg. Eggs from hens fed 1% DHA GOLD showed an increase of 373% vitamin E compared with eggs from non-DHA GOLD supplemented hens. In summary, DHA GOLD supplementation was more effective at enriching eggs with DHA than flaxseed by itself. Combination of 3% flaxseed with 1% DHA GOLD optimized the deposition of DHA in egg.

DHA GOLD is a registered trademark of Martek Biosciences Corporation, USA

Key Words: layer, DHA, ω-3s

155 The interaction of dietary fatty acids on the egg yolk fatty acid composition. R. Poureslami*[1,4], K. Raes[2], and E. Delezie[3], G. Huyghebaert[3], A. B. Batal[1], and S. De Smet[4], [1]*University of Georgia*, *Athens,* [2]*University College West-Flanders*, *Kortrijk, Belgium*, [3]*Institute for Agricultural and Fisheries Research*, *Melle, Belgium*, [4]*Ghent University*, *Melle, Belgium*.

Two experiments were conducted to investigate the interaction of dietary fatty acids (FA) on the egg yolk FA composition. In Exp I, 288 ISA-brown laying hens (45–50 wk of age) were divided into 32 dietary treatments in 3 replicates. Diets were prepared mixing a type of fish oil (FO) with 4 vegetable oils in different proportions resulting in a wide range of diet FA composition. Two levels of fat were introduced to the diets (3 and 6%). In Exp II, 63 hens were assigned to each of 7 dietary groups. A mixture of 2 levels and 3 types (differing in 20:5n-3/22:6n-3 ratio) of FO in combination with 2 vegetable oils were applied. Stepwise multiple regression and ANOVA were used to analyze the data in Exp I and II respectively. In Exp I, dietary saturated (SFA), monounsaturated (MUFA), polyunsaturated (PUFA) FA and the interaction between them affected SFA and MUFA proportions in the egg. The egg 18:2n-6 proportion was mainly explained by the dietary provision of 18:2n-6 (Partial R^2 55%) followed by the inverse impact of dietary MUFA. The 20:4n-6 composition in the egg was inversely related to the dietary n-3 long chain (LC) PUFA (Partial R^2 50%), more than to the dietary level of the precursor 18:2n-6. The linear effect of dietary 18:3n-3 was very determinant for the egg 18:3n-3 proportion (Partial R^2 93%) while, it had a negligible impact on the n-3 LC PUFA composition in the egg (Partial R^2 7%). About 77% of the variation in the egg yolk 22:6n-3 composition was explained by 22:6n-3 proportion in the diet. In Exp II, the level of FO (2 v. 1%) was more effective than its type on the n-3 LC PUFA composition in the egg. In conclusion, interactions between dietary FA affect SFA and MUFA composition in the egg while, direct dietary provision is the most crucial factor in achieving high deposition of n-3 FA in the egg yolk.

Key Words: fatty acids, interaction effect, egg yolk

156 The effect of omega-3 fatty acid rich algae biomass supplementation on production and egg and plasma components from 61 to 69 weeks of age. H. M. Yakout*[1], C. L. Novak[2], and Z. Wen[3], [1]*Alexandria University*, *Alexandria, Egypt*, [2]*Land O'Lakes Purina Feed*, *Kansas City, MO,* [3]*Virginia Tech*, *Blacksburg*.

Commercial White Lohmann LSL-Classic hens (n: 192) were randomly assigned to one of 4 dietary treatment groups to test the use and response of omega-3 fatty acid containing algal biomass supplementation on egg production parameters and egg components. Biomass was supplemented to a corn-soybean meal based diet at a rate of 0, 2, 4 or 8% establishing treatments 1, 2, 3 and 4, respectively. All diets were iso-caloric and iso-nitrogenous and were fed ad libitum from 61 to 69 wks of age. Cage was considered the experimental unit (4 hens/ cage) with each treatment replicated 12 times. Overall, Trt had no affect on feed consumption which averaged 117.6 g/ h/ d. Egg production ranged from 89.8 to 91.7% for all treatments ($P \geq 0.05$) with the highest producing hens consuming diet 1 and lowest consuming diet 4. Additionally, no significant differences were observed among trt for feed efficiency which averaged 0.517 g. egg mass /g. feed. Trt 1 had numerically higher egg weights (68.1 g.) compared with biomass supplemented trt with an average of 66.53 g/ egg. Trt 1 had numerically the greatest egg mass (62.4 g.) and dietary treatments had no significant effects on wet egg components. Trt 2 had numerically the best specific gravity value (1.087). Overall, increasing dietary biomass resulted in elevated yolk color ($P \leq 0.001$) with the darkest noted in eggs from hens consuming trt 4 (7.2; using a Roche Color fan), while trt 1 was the lightest (6.5). Yolk and plasma total lipids, and yolk phospholipids were similar among treatments, while plasma phospholipids were reduced ($P \leq 0.06$) in hens consuming trt 3 (524.7 mg/dL) as compared with hens fed trt 1 (736.0 mg/dL). Yolk DHA content was significantly increased with all dietary biomass levels up to 8% (2.64%) as compared with the control (0.31%). Based on the information from this trial, supplementing a corn-soybean meal based diet with biomass up to 8% during late first cycle lay resulted in minimal affects on production parameters. Additionally, yolk color and DHA content was increased while plasma phospholipids were reduced by feeding 4 or 8% biomass.

Key Words: biomass, plasma phospholipids, laying hens

Nonruminant Nutrition Symposium: Nutrigenomics

157 Practical uses of nutrigenomics and gene expression patterns to develop and evaluate nutritional strategies. K. A. Dawson*, *Alltech Center for Animal Nutrigenomics and Applied Animal Nutrition*, *Nicholasville, KY*.

In addition to providing information on the regulation of physiological activities; applications of nutrigenomic and transcriptomic techniques are providing new tools for evaluating the value and effectiveness of nutritional strategies in domestic livestock. Detailed studies of gene expression patterns associated with different forms and levels of selenium in animal diets have begun to elucidate the critical hidden effects of specific mineral forms in several species. While it is clear that diets which use selenium incorporated into growing yeast (selenium yeast) can significantly and uniquely influence the expression of genes associated with recognized antioxidant systems, such materials also have other significant effects on genes and metabolic pathways that influence basic cellular repair mechanisms, the production of stress proteins, energy production systems, immunological systems, neurological function and reproductive systems. Tissue specific gene expression patterns determined with standardized microarrays clearly indicate major differences in various dietary forms of selenium and can be used to differentiate the effects of selenium yeast from those associated with sodium selenite. Such genomics tools have allowed for an understanding of the effects of specific nutrients in unprecedented detail and have opened new frontiers in nutrition and dietary manipulations. Gene expression patterns also provide useful tools for initially comparing dietary treatments and can be used to rapidly screen for key nutritional effects and to evaluate supplementation strategies. Using these comparison techniques, it has been possible to compare alternative antioxidant systems that can partially replace traditional dietary ingredients like vitamin E in animal feed. In chickens, the value of comparing the effects of diets using gene expression patterns and marker genes has been validated by examining more traditional methods for determining antioxidant status in the serum and by examining meat quality. In the future, Nutrigenomics approaches will undoubtedly improve the efficiency of techniques for evaluating dietary formulations and provide basic biochemical information that will lead to a new understanding of basic nutritional principles.

158 Early life nutritional conditioning with dietary phosphorus. C. M. Ashwell*[1] and R. Angel[2], [1]*Department of Poultry Science, North Carolina State University*, *Raleigh*, [2]*Department of Animal and Avian Sciences, University of Maryland*, *College Park*.

The recent technologies that have led to the new field of functional genomics are providing a clearer understanding of how organisms interact with their environment and in particular their diet. We are beginning to learn how the diet may have long-term influence on performance and health. A form of epigenetic regulation has been recently described called fetal "programming." We have observed similar apparent programming by dietary manipulation in the perinatal period of the chicken. When birds are challenged with a diet low in phosphorus (P) for 90 h immediately post-hatch they obtain the ability to better utilize P later in life. This increased utilization of P (1.24-fold, $P < 0.001$) from the diet can partially be explained by an enduring increase (2.4-fold, $P < 0.05$) in the expression of the intestine-specific Na/P cotransporter (NaPcoT) IIb gene during programming as well as later in life when fed P restricted diets. The resulting data provide the first evidence for neonatal programming of gene expression in an oviparous species. Studies are ongoing to determine if the mechanism of persistent responses of gene expression to stimuli are epigenetic in nature. If epigenetic regulation is involved in dietary conditioning the opportunities for nutrition to impact both the animal and its offspring are almost limitless.

159 Using nutrigenomics to elucidate interrelationships in trace mineral metabolism. S. L. Hansen*[1], J. W. Spears[2], and R. S. Fry[2], [1]*Iowa State University*, *Ames*, [2]*North Carolina State University*, *Raleigh*.

Nutrigenomics is the study of dietary influence on gene expression. This presentation will focus on the area of trace mineral metabolism and the information that can be gained through the use of nutrigenomics. Numerous interactions between certain trace minerals may occur as minerals compete for intestinal absorption and transport throughout the body. Because of these interactions it has become apparent that it is no longer appropriate to examine the metabolism of a single mineral without consideration for the mineral "ionome" as a whole. Nutrigenomics presents a new way of looking at an old problem; while we have known for many years about the antagonistic relationship between minerals such as iron, manganese, and copper, it is only in recent years that specific gene products have been identified as potential points of interaction between these elements. For example, in 2 experiments where weaned pigs were fed varying levels of dietary iron, a strong negative relationship between dietary iron and tissue manganese concentration was observed. Using quantitative-PCR it was found that intestinal expression of divalent metal transporter 1 (dmt1) was depressed in pigs fed high dietary iron. Elucidating points of interaction, such as dmt1, which is a transporter for both iron and manganese, allows nutritionists to more accurately formulate diets. Utilizing nutrigenomics in the field of mineral metabolism has many potential benefits, including redefining mineral requirements of animals in the face of a new generation of plant and animal genetics, and diminishing environmental impacts by decreasing excessive oral supplementation of minerals. In summary, nutrigenomics provides biological targets at which to aim studies of animal trace mineral metabolism, which should increase our knowledge of mineral interactions and lead to more accurate dietary mineral recommendations.

Key Words: interactions, minerals, nutrigenomics

160 A functional genomics view of selenium in energy metabolism, obesity, and diabetes. X. G. Lei*, *Cornell University*, *Ithaca, NY*.

The trace element Se and Se-dependent glutathione peroxidase-1 (GPX1) have been considered to protect against diabetes. Intriguingly, we found a spontaneous development of type 2 diabetes-like phenotypes in GPX1 overexpressing mice at 6 mo of age. Later, other laboratories demonstrated similar deleterious effects of overexpression of other antioxidant proteins on sensitizing mice to diabetes. Most striking, 8 major human studies have recently shown hyperglycemic, hypolipidemic, and pro-diabetic effects of Se supplement. Because pigs are an excellent model for human nutrition, we have conducted a series of experiments to elucidate functional genomics of porcine selenoproteins in glucose and lipid metabolism. We first identified all 25 porcine selenoproteins using *in silico* cloning followed by PCR. We then determined the effects of dietary Se deficiency and excess on gene expression of all 25 selenoproteins in various tissues of pigs using quantitative real-time Q-PCR. Recently, we induced obesity in pigs by feeding them with a high-fat diet and determined effects of obesity on gene expression of the 25 selenoproteins. Our results indicate that gene expression of

13 selenoproteins was altered by dietary Se deficiency or excess non-unilaterally. The induced-obesity enhanced or decreased gene expression of 17 selenoproteins in various tissues of pigs. Microarray data have been generated from the dietary Se and fat experiments to establish systems biology related to body energy metabolism, selenogenome, and porcine genome. Our findings will reveal novel metabolic roles of Se in energy metabolism, obesity, and diabetes.

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Key Words: energy metabolism, gene expression, genomics

161 Alternative protocols to presynchronize estrous cycles in dairy cattle before a timed AI program. J. S. Stevenson*, *Kansas State University*, *Manhattan*.

Our objective was to test potential presynchronization protocols applied before a timed AI (TAI) protocol to improve the percentage of cows having a functional CL, high concentrations of progesterone, and successful ovulation after both GnRH injections. At calving, cows were assigned randomly to receive either of 5 presynchronization treatments. Three Presynch protocols were tested in which 2 injections of $PGF_{2\alpha}$ (PGF) were administered 14 d apart, with either 14 d (PRE14; n = 122), 12 d (PRE12; n = 123), or 10 d (PRE10; n = 151) intervening before initiating a TAI protocol. Two treatments were a progesterone (P4) insert (CIDR) for 7 d plus PGF at insert removal. Insert removal occurred either 10 d (CIDR10; n = 157) or 3 d (CIDR3; n = 117) before initiating a TAI protocol. The TAI protocol was a standard Cosynch protocol (GnRH 7 d before and 72 h after PGF with TAI at 72 h after PGF). Cosynch was the control (n = 157) with cows starting this protocol at random stages of the estrous cycle. From a subset of cows (49 to 51 cows per treatment), blood samples were collected at d −28, −14, 0 (onset of TAI protocol), 7, 9, 14, and 21 d. Ovarian scans occurred on d 0, 7, 9, and 14. Diameter of follicles and CL were measured at each exam and ovulation response to both GnRH injections was determined at d 7 and 14. Ovulatory incidence after the first and second GnRH injections varied but did not differ among treatments. Concentrations of P4 were greater ($P \leq 0.05$) before the first GnRH injection in all treatments compared with CIDR3. Before the second GnRH injection, P4 was greater ($P \leq 0.05$) in the CIDR3 treatment than in all other treatments. Luteal regression and synchronization rate (successful luteolysis and ovulation after second GnRH injection) did not differ among treatments. Pregnancy rate per AI (PR/AI) at 60 d post timed AI was less ($P \leq 0.05$) in CIDR3 cows compared with all other treatments. It was concluded that none of the Presynch treatments improved key responses (ovulation, luteolysis, and synchronization rate) known to improve PR/AI compared with a standard Cosynch protocol without presynchronization.

Table 1. Key responses of treated cows during the timed AI ovulation synchronization protocol

Treatment	n	First GnRH Ovulation, %	P4 ng/mL	2nd GnRH Ovulation, %	P4 ng/mL	Luteal regression, %	Synch rate, %	n	60-d PR/AI
PRE14	50	62.0	3.9[a]	86.0	1.0[a]	93.9	86.0	122	28.7
PRE12	51	60.8	3.7[a]	88.2	0.5[c]	100	88.2	123	33.6
PRE10	49	67.3	2.4[b]	79.6	0.7[ac]	95.7	79.6	151	30.5
CIDR10	51	64.7	3.0[ab]	86.3	0.6[ac]	100	86.3	157	30.3
CIDR3	51	47.1	0.9[c]	90.2	1.5[b]	83.0	86.3	117	13.9
Cosynch	50	62.0	3.7[a]	78.0	0.9[ac]	93.0	76.0	157	30.6

[a-c] Means differ ($P \leq 0.05$).

Key Words: ovulation, luteolysis, timed AI

162 Effects of presynchronizations with GnRH/$PGF_{2\alpha}$ vs. progesterone before Ovsynch in noncyclic dairy cows. G. Yilmazbas-Mecitoglu*[1], A. Keskin[1], A. Gumen[1], E. Karakaya[1], R. Darici[2], and H. Okut[3], [1]*University of Uludag*, *Bursa, Turkey*, [2]*Tarfas Co.*, *Bursa, Turkey*, [3]*University of Yuzuncu Yil*, *Van, Turkey*.

The aim of this study was to compare efficiency of GnRH/PGF2α vs. progesterone (P4) presynchronizations (Presynch) on overall Ovsynch (OVS) outcome in noncyclic dairy cows. Ultrasonographic examinations were done with 7 d interval to determine cyclicity. Noncyclic cows (n = 157; no CL in each ovary at both examinations) were randomly divided into 3 groups. In GP group (n = 61), PGF2α was administrated 7 d after GnRH injection and OVS was started 11 d after PGF2α administration (GnRH-7d-PGF2α-11d-OVS). In PR group (n = 54), cows were treated for 7 d with an intravaginal P4 implant (PRID; without oestradiol capsule) then 11 d after removing the implant OVS was started (7d PRID-11d-OVS). Control group (n = 42) did not receive any presynch protocol and OVS was started at the same time with other groups. Spontaneous recovery in control and presynch rates in GP and PR groups (cows became cyclic at the beginning OVS) were found to be different ($P < 0.004$) between control (47.6%; 20/42) and presynch groups (72.1%; 44/61 in GP and 77.8%; 42/54 in PR groups). Response to first GnRH of OVS did not differ among groups (73.8%; 31/42 in control, 73.8%; 45/61 in GP and 70.4%; 38/54 in PR groups). Interestingly, response to first GnRH of OVS was higher ($P < 0.0007$) in cows that did not respond to presynch than cows responded in GP and PR groups (96.5%; 28/29 and 47.8%; 55/86). Synchronization rates were similar among groups (78.6%; 33/42 in control, 88.5%; 54/61 in GP and 85.2%; 56/54 in PR). Conception rate (31 d) did not differ among groups (42.9%; 18/42 in control, 47.5%; 29/61 in GP and 46.3%; 25/54 in PR). Embryonic loss (between 31 and 62 d) did not differ among groups (4 cows in control, 1 cow in GP and 1 cow in PR). However, conception rate (31 d) was greater ($P < 0.001$) in cows that responded to presynch than those that did not respond in GP and PR groups (55.8%; 48/86 and 20.7%; 6/29). Although conception rate did not differ among groups, cows that responded to presynch had higher conception rate than cows that did not respond.

Key Words: Ovsynch, presynchronization, noncyclic dairy cows

163 Comparison of estrus and ovulation synchronization protocols: effects on ovarian follicular dynamics, corpus luteum growth, and circulating steroid concentrations in lactating dairy cows. M. M. Herlihy*[1,2], M. A. Crowe[2], M. G. Diskin[3], and S. T. Butler[1], [1]*Teagasc Moorepark DPRC*, *Cork, Ireland*, [2]*University College Dublin*, *Ireland*, [3]*Teagasc Athenry APRC*, *Galway, Ireland*.

This study compared estrus and ovulation synchronization protocols at first service in lactating dairy cows (n = 61) > 42 d postpartum. At 10 d before AI animals were randomly assigned to: 1) d −10 GnRH (10 μg i.m. Buserelin) and CIDR insert (1.38 g P4); d −3 $PGF_{2\alpha}$ (25 mg i.m. dinoprost); d −2 CIDR out and AI at observed estrus (CIDR_OBS); 2) same as CIDR_OBS, but GnRH 36h after CIDR out and TAI (timed AI) 18h later (CIDR_TAI) or 3) same as CIDR_TAI, but no CIDR (OVSYNCH). Transrectal ultrasound was used to assess follicle size before ovulation and on d8 and d15 after AI to measure the corpus luteum (CL). Blood samples were collected to determine concentrations of estradiol (d −3, d −2, d −1, d0) and progesterone (d −2, d −1, d0, d1, d4, d6, d8, d11, d15). P4 concentrations immediately before CIDR removal were greater ($P < 0.001$) for CIDR_OBS and CIDR_TAI compared with OVSYNCH (1.78, 1.59 and 0.62 ng/mL; CIDR_OBS, CIDR_TAI and OVSYNCH, respectively). At the time of the second GnRH, E2 was higher ($P < 0.06$) for CIDR_OBS and CIDR_TAI compared with OVSYNCH (2.78, 2.57 and 1.69 pg/mL). E2 concentrations at the time of expected AI were higher ($P < 0.001$) for CIDR_OBS compared with CIDR_TAI and OVSYNCH (1.59, 0.36 and 0.33 pg/ml). Diameter of the DF before ovulation was greater ($P < 0.05$) for CIDR_OBS compared with OVSYNCH (18.3 vs. 16.1 mm).

An interaction ($P < 0.05$) was observed for P4 concentrations, where P4 tended to be lower in CIDR_OBS on d4 and 6, but greater on d15 compared with CIDR_TAI and OVSYNCH. CL diameter and volume was not affected by treatment on d8, but both CL volume (9991, 7808, and 8186 mm^3; $P = 0.1$) and diameter (27.0, 23.9, and 24.0; $P = 0.08$) on d15 tended to be affected by treatment (CIDR_OBS, CIDR_TAI and OVSYNCH, respectively). Both P4 supplementation and GnRH on the day before TAI impact ovulatory follicle size, E2 concentrations, and postovulatory P4 profiles.

Key Words: Ovsynch, CIDR, dairy cow

164 Effects of reducing interval from GnRH to $PGF_{2\alpha}$ in Ovsynch protocol on pregnancy rate in cyclic lactating dairy cows. A. Gumen*[1], G. Yilmazbas-Mecitoglu[1], A. Keskin[1], E. Karakaya[1], Y. Celik[2], and H. Okut[3], [1]*University of Uludag*, *Bursa, Turkey*, [2]*TARFAS Co.*, *Bursa, Turkey*, [3]*University of Yuzuncu Yil*, *Van, Turkey*.

Ovsynch protocol was designed to synchronize ovulation, thereby allowing timed artificial insemination (TAI) of all cows without detection of estrus and Ovsynch has been proven to be an acceptable alternative to estrus detection programs in large dairy farms. The aims of this study were 1) to ovulate one day younger follicle by decreasing interval between first GnRH to PGF2α of Ovsynch 2) to compare pregnancy rates in Ovsynch vs. Modified Ovsynch (interval between first GnRH to PGF2α decreased to 6 d) in cycling lactating dairy cows. The day of first GnRH of Ovsynch was designated d 0. The ovaries of cows were examined by ultrasonography twice, one week apart, to determine cyclic cows (had Corpus Luteum on either ovary) from −7 to 0 d. Cyclic cows (n = 859) were divided into 2 groups: OVS group (n = 421) received the Ovsynch protocol (GnRH-7d-PGF2α-56h-GnRH-18h-AI) and cows in MOV group (n = 438) had a Modified Ovsynch (MOV) protocol (GnRH-6d-PGF2α-56h-GnRH-18h-AI). Ultrasonography were performed at the time of first GnRH and PGF2α administration to detect first ovulatory response, at the time of AI to determine maximal follicle size and 7 d after AI to determine second ovulatory response. Pregnancy diagnosis was performed 30 and 60 d post insemination by ultrasonography. Response to first GnRH of Ovsynch was similar between OVS (54.2%, 228/421) and MOV (55.3%, 242/438) groups. Synchronization rate (ovulatory response to second GnRH of Ovsynch) was higher ($P < 0.004$) in MOV (90.4%, 396/438) than OVS (83.8%, 353/421). Pregnancy rate was similar in OVS (42.5%, 179/421) and MOV cows (37.9%, 166/438). Follicle size at the time of AI was greater ($P < 0.0001$) in OVS (16.01 ± 0.1 mm) than MOV (15.3 ± 0.1 mm). Thus, Modified Ovsynch protocol not only increased synchronization rate but also decreased follicle size. Unexpectedly, this protocol did not improve pregnancy rate in cycling dairy cows.

Key Words: synchronization, Ovsynch, dairy cows

165 Presynchronization with hCG 7 d before initiation of Resynch improves fertility similar to a double–Ovsynch Resynch protocol in lactating dairy cows. J. O. Giordano*, J. N. Guenther, M. S. Ares, M. C. Wiltbank, and P. M. Fricke, *University of Wisconsin*, *Madison*.

Our objective was to compare a Double-Ovsynch protocol for resynchronization of ovulation (Resynch) to a novel Resynch protocol that reduces the interbreeding interval (IBI) to 35 d. Lactating Holstein cows on a commercial dairy received a Resynch protocol using GnRH and cloprostenol (PGF) as follows: (d 0, 200 μg GnRH; d 7, 750 μg PGF; 56 h, 100 μg GnRH; 16 h, TAI). Cows were blocked by parity and were randomly assigned to one of 3 treatments to receive: 1) Resynch–25 (C), Resynch protocol initiated 25 d after a prior TAI (n = 418, IBI = 35 d). 2) HGPG, hCG (2000 IU Chorulon on Day 18 after TAI) 7 d before Resynch–25 (n = 450, IBI = 35d); 3) Double–Ovsynch (DO), a modified Ovsynch protocol (d 0, 100 μg GnRH; d 7, 500 μg PGF; d 10, 100 μg GnRH) which was initiated 22 d after a prior TAI followed 7d later by Resynch–39 (DO, n = 405, IBI = 49 d). Pregnancy was diagnosed 29 d after Resynch TAI using ultrasound and 53 d after Resynch TAI using palpation to determine pregnancies per AI (P/AI). Based on logistical regression analysis, P/AI 29 d after TAI was not affected ($P = 0.42$) by parity, and HGPG and DO cows had more ($P < 0.01$) P/AI than C cows [HGPG = 37.3% (168/282; DO = 35.8% (145/260); C = 28.0% (117/301]. When analyzed separately, P/AI did not differ ($P = 0.64$) between HGPG and DO cows. Pregnancy loss from 29 to 53 d after TAI was not affected ($P = 0.88$) by lactation and did not differ ($P = 0.34$) among treatments [HGPG = 11.0% (18/145); DO = 6.3% (9/135); OV = 8.6% (10/106)]. At 53 d after TAI, HGPG and DO cows continued to have more ($P = 0.02$) P/AI than C cows [HGPG = 32.6% (145/300); DO = 33.4% (135/269); OV = 25.4% (106/311)], and P/AI did not differ ($P = 0.80$) for HGPG and DO cows. We conclude that the HGPG Resynch protocol increased fertility of resynchronized cows similar to that of a Double-Ovsynch Resynch protocol while reducing the interbreeding interval by 14 d.
Supported by Hatch project WIS01171.

Key Words: Double-Ovsynch, hCG, resynchronization

166 Comparison of responses to Ovsynch for Holstein–Friesian and Swedish–Red cows. A Keskin*[1], G Yilmazbas-Mecitoglu[1], A Gumen[1], E Karakaya[1], Y Celik[2], H Okut[3], and M. C. Wiltbank[4], [1]*University of Uludag*, *Gorukle, Bursa, Turkey*, [2]*TARFAS Co*, *Karacabey, Bursa, Turkey*, [3]*University of Yuzuncu Yil*, *Van, Turkey*, [4]*University of Wisconcin-Madison*, *Madison*.

The Ovsynch protocol was designed to synchronize ovulation, thereby allowing timed artificial insemination (TAI) of all cows without detection of estrus; however, the effectiveness of Ovsynch in different breeds of dairy cows has not been previously compared. The aim of this study was to compare the response to Ovsynch in cycling lactating dairy cows of 2 different breeds (Holstein–Friesian [HF] vs. Swedish–Red [SR]). A total of 495 cyclic cows (n = 347 HF, n = 148 SR) were housed together and treated with Ovsynch (GnRH–7d–PGF2α–56h–GnRH–18h–TAI). Cows were not presynchronized before the Ovsynch. Milk production was different ($P < 0.001$) between breeds (40.3 ± 0.5 in HF and 34.9 ± 0.7 in SR). Ovulatory responses, synchronization rate, maximal follicle size at the time of AI, and percentage pregnant per AI (%P/AI at 31 and 62 d after AI) were compared between breeds. Ultrasonography was performed during Ovsynch at first GnRH, PGF2α, at time of AI, and 7 d after AI. Ovulatory response and synchronization rate were similar in HF vs. SR cows (60.2% vs. 62.1%; 88.4% vs. 88.5%, respectively). Cows that ovulated to the first GnRH of Ovsynch had reduced ($P = 0.02$) follicle size at time of AI (15.9 ± 0.12 vs. 16.4 ± 0.16 mm). Maximal follicle size at time of AI was greater ($P < 0.004$) for HF (16.4 ± 2.2 mm) than SR (15.5 ± 2.3 mm) cows. The %P/AI tended to be greater for SR than HF cows at the 31 d pregnancy diagnosis (58.1% vs. 51.1%; $P = 0.16$) and was greater in SR than HF cows at the 62 d pregnancy diagnosis (56.1% vs. 46.1%; $P = 0.04$). Embryonic loss was greater ($P = 0.04$) in HF (10.1%) than SR (3.4%) cows between 31 and 62 d of pregnancy. Hot season significantly decreased %P/AI in HF cows ($P < 0.001$), but not in SR cows. Thus, although the GnRH treatments of Ovsynch were equally effective in SR and HF cows, there was better fertility following Ovsynch in SR than HF cows, probably due to the decrease in fertility during the hot season in HF but not SR cows.

Key Words: Ovsynch, breed, reproduction

167 Manipulation of protein feed levels during Ovsynch TAI and early embryonic development to improve fertility in lactating dairy cows. M. B. Gordon* and R. Rajamahendran, *University of British Columbia*, *Vancouver, BC, Canada*.

This study compared the effects of feeding 2 levels of crude protein (CP, 16% vs. 18.5%) on fertility and milk production in lactating dairy cows subjected to a timed insemination. To achieve its milk yield potential the modern dairy cow is dependent on a high intake of dietary nitrogen. However, excessive protein intake, particularly rumen degradable protein is associated with reductions in fertility, plasma progesterone concentrations, and exacerbation of negative energy balance. Although Ovsynch timed artificial insemination (TAI) program allows for the control of ovarian follicular and corpus luteum development without the need for estrus detection, pregnancy rates are still far from the satisfactory rates achieved over 30 years ago. Lactating Holstein dairy cows (n = 180) were synchronized for first service breeding using Ovsynch TAI (2 treatments of GnRH, 9 d apart with a treatment of PGF2α 48 h before the second GnRH treatment, and TAI 16–18 h later). Cows were blocked for similar parity and DIM. Group 1 (control) was fed a diet consisting of 18.5% CP (High). Group 2 was fed a diet consisting of 16% CP (Low), which began 7 d before initiation of Ovsynch and continued until pregnancy diagnosis at 32 d. Groups were housed together with access to feed via Insentec electronic feed intake bins. Pregnancy per AI was 24.4% and 34.1% ($P = 0.08$) for High and Low groups, respectively. Parity had an affect on pregnancy per AI. A lower average milk production during the 49 d of treatment was observed in multiparous cows in the Low group (47.8 ± 1.05 kg) compared with the High group (50.2 ± 1.03 kg, $P = 0.11$). However, no differences in milk production were observed in the 3 weeks preceding and following treatment. Lower milk urea nitrogen was observed on d 7 and d28 in the low group ($P = 0.02$). No differences in progesterone concentrations were observed between treatments. In summary, feeding a diet with a slightly lower protein content increased pregnancy to TAI, with minimal effects on milk production.

Key Words: Ovsynch, fertility, crude protein

168 Reproductive tract differences in repeat-breeder cows. R. A. Cushman*, J. R. Miles, and S. E. Echternkamp, *U.S. Meat Animal Research Center*, *Clay Center, NE*.

The objective of the study was to evaluate the reproductive tracts of repeat-breeder cows that failed to calve in 2 consecutive years compared with cows that calved regularly. The hypothesis was that repeat-breeder cows would have smaller reproductive tracts and fewer antral follicles. Beef cows ranging from 3 to 13 years of age were classified as repeat-breeder (n = 37) or control (n = 34) cows. Cows were examined twice daily for behavioral estrus and artificially inseminated 12 h after observed estrus. Three to 8 d after estrus, cows were slaughtered, reproductive tracts were recovered and transported to the laboratory. All visible antral follicles were counted, ovaries were measured and weighed, and the diameter of the endometrium was measured in a subset of cows (n = 44) at the thickest point on the horn ipsilateral to the corpus luteum. The uterus was flushed and embryos were collected. Granulosa cells from small antral follicles (<5 mm) were pooled and frozen for real-time RT-PCR analysis. Reproductive traits were analyzed using the GLM or GLIMMIX procedure of SAS with group as the independent variable and day and age as co-variates. Repeat-breeder cows had smaller ovaries ($P \leq 0.006$) when corrected for day ($P > 0.13$) and age ($P > 0.17$), and fewer follicles ($P = 0.02$) when corrected for day ($P = 0.0009$) and age ($P = 0.42$). There was no difference in endometrial diameter ($P = 0.46$), or granulosa cell anti-Mullerian hormone ($P = 0.87$) or Pentraxin 3 ($P = 0.63$) mRNA levels between repeat-breeder and control cows when corrected for day ($P > 0.0.16$) and age ($P > 0.44$), but embryo recovery rate tended to be greater in control cows ($P = 0.06$). Regression analysis identified a positive relationship of antral follicle count to endometrial diameter ($P = 0.009$) and ovarian size ($P < 0.0001$). Fewer ovarian antral follicles in repeat-breeder cows may contribute to reduced fertility. The positive relationship between antral follicle count and endometrial diameter suggests that the number of ovarian follicles may influence proliferation of the endometrium in the early luteal phase of the cow.

Key Words: cow, reproductive tract, fertility

169 The effect of supplementation with conjugated linoleic acid on the reproductive performance of lactating dairy cows. I. A. Hutchinson*1,2, P. Lonergan[2], A. C. O. Evans[2], R. J. Dewhurst[3], and S. T. Butler[1], [1]*Teagasc*, *Moorepark DPRC, Cork, Ireland*, [2]*University College Dublin*, *Dublin, Ireland*, [3]*Teagasc*, *Grange, Meath, Ireland*.

Spring-calving dairy cows (n = 389) on a single pasture-based commercial dairy farm were randomly assigned to one of 2 dietary treatments (lipid encapsulated conjugated linoleic acid (Lutrell, BASF, Germany; CLA, n = 192) or No supplement (Control, n = 197)). The CLA cows received 50 g/day of a lipid supplement containing 5 g of both trans-10, cis-12 and cis-9, trans-11 CLA from 0 to 60 d in milk. Milk samples were collected 3 times per week, and each sample was analyzed for progesterone using a competitive ELISA test to determine interval to first ovulation. Milk yield and composition were measured fortnightly. Breeding commenced on a fixed calendar mating start date (Apr 8 2009), and continued for 16 weeks. Trans-rectal ultrasonography was carried out at 30–36 d and 60–66 d post AI to diagnose pregnancy. Milk yield, milk composition, and interval to first ovulation data were analyzed using mixed model analysis. All other reproductive data was analyzed using Chi-squared analysis. A reduction in milk fat concentration (36.9 vs. 30.7 g/kg; $P < 0.001$) and yield (0.91 vs. 0.84 kg/day; $P = 0.031$) was observed in CLA cows during supplementation. Milk yield was increased during CLA supplementation (24.7 vs. 27.2; $P = 0.003$). There was no effect of CLA on interval to first ovulation postpartum (40.2 vs. 44.4 d, CLA and control, respectively), conception rate to first service (35.1 vs. 37.0%), embryo mortality (14.3% vs. 21.4%) or 6-week in-calf rate (43.6% vs. 37.0%, all $P > 0.1$). In conclusion, supplementing dairy cows with CLA reduced milk fat synthesis but did not improve measures of reproductive performance, perhaps indicating energy availability was not the most limiting factor influencing herd fertility in this study.

Key Words: CLA, reproduction, dairy cows

170 The impact on pregnancy rates in dairy cattle artificially inseminated with semen prepared by number of progressivley motile sperm. L. Rabinovitch*[1], U. Shalit[1], M. Deutsch[1], Y. Zeron[2], and P. Chenoweth[3], [1]*Medical Electronic Systems*, *Caesarea, Israel*, [2]*Sion A.I. Company*, *Shikmim, Israel*, [3]*Charles Sturt University*, *Wagga Wagga, New South Wales, Australia*.

The trial objective was to evaluate the pregnancy rates of dairy cattle inseminated with varying amounts of progressively motile sperm, post thaw (PMPT). In phase 1, straws were prepared to contain specific numbers of progressively motile sperm, post thaw. In phase 2, cows were inseminated and pregnancy rates were analyzed. All semen testing and dosing was performed at an operating AI stud facility (SION A.I. Company) using an SQA-Vb, automated sperm quality analyzer for bulls (Medical Electronic Systems). Forty ejaculates collected from four bulls were split into four groups and 2000 straws per group were targeted

to contain: Group A, B and C; 1.5, 3.5 and 7.0 million PMPT sperm/straw respectively. The target for group D (Control) was 15.0 million total sperm per straw per the AI stud routine. Two hundred twenty-eight straws from groups A, B and C were quality control tested based on mean (+/− SE) values for PMPT sperm and demonstrated: (A) 1.5 (+/− 0.05); (B) 3.0 (+/− 0.09) and (C) 6.2 (+/− 0.18) million. Seventy-six straws from Group D (Control) established a mean (+/− SE) value of 13.6 (+/− 0.15) million. In total, 6,494 cows in over 500 farms were blindly inseminated between January and April 2009. At approximately 42 days post-insemination, pregnancy rates (per cow per cycle) were determined per rectal palpation by group as follows: (A) 34.2%; (B) 39.3%; (C) 43.2%; (D) 38.6%. The relative difference in pregnancy rates for groups A, B and C versus the control (D) were: −11.4%, 1.8% and 11.9%, respectively. Pregnancy rates in groups A, B and C correlated to the number of progressively motile sperm (r = 0.96). It is concluded that the number of progressively motile sperm per AI dose significantly impacts subsequent bovine pregnancy rates. Further, it is possible to accurately produce AI straws based on the number of PMPT sperm. Use of these findings could help improve bovine AI reproductive performance while allowing more effective utilization of superior bulls.

Key Words: bovine semen, SQA-Vb, bull AI

171 Effect of flunixin meglumine on prostaglandin metabolites and progesterone in lactating dairy cows. A. Ahmadzadeh*[1], S. Read[1], K. G. Carnahan[1], and J. C. Dalton[2], [1]*University of Idaho*, *Moscow*, [2]*University of Idaho*, *Caldwell R&E*.

Strategies to inhibit or reduce secretion of $PGF_{2\alpha}$ during early embryonic development may reduce embryonic loss and increase reproductive performance of dairy cattle. The objective was to examine the effect of flunixin meglumine (FM), a non-steroidal, anti-inflammatory drug, on $PGF_{2\alpha}$ secretion and luteal function by characterizing plasma prostaglandin metabolites (PGFM) and progesterone (P4) concentrations in lactating dairy cows during the luteal phase of the estrous cycle. Starting on d −35, estrous cycles of cows were synchronized using Presynch-Ovsynch. On d −9 (12 d after the second $PGF_{2\alpha}$ injection), and after detection of a corpus luteum (CL), Ovsynch was initiated. Ultrasonography was performed on d 0, 3, 7 and 15 to confirm ovulation and presence of a CL. Cows were not inseminated. On d 15 cows were assigned randomly to 2 groups: 1) FM group (n = 9) received 2.0 mg per kg BW (i.m.) of FM, 2) Control group received saline (n = 8). Jugular blood samples were collected at 30 and 0 min before treatment and at 30 and 60 min and each h thereafter for 6 h. Blood samples were also collected daily from d 15 to d 22. Mean P4 concentrations on the day of treatment (d 15) were not different between groups (6.3 vs. 7.2 ± 0.5 ng/mL). Plasma PGFM concentrations were not different between groups before treatment. Flunixin meglumine caused a transient decrease ($P < 0.05$) in plasma PGFM concentrations (58 ± 8.5 pg/mL) within 60 min after administration and concentrations remained low throughout the sampling period. Plasma PGFM remained unchanged in saline-treated cows (150 ± 9.2 pg/mL). Mean P4 concentrations decreased ($P < 0.05$) during 7 d after treatment; however, the rate of P4 decline over time tended ($P = 0.09$) to be greater for Control compared with FM. The results suggest that FM decreased plasma PGFM, suggesting FM negatively affects $PFG_{2\alpha}$ secretion in lactating dairy cows during the luteal phase of the estrous cycle. Moreover, FM may enhance luteal function by decreasing $PFG_{2\alpha}$.

Key Words: flunixin meglumine, prostaglandin $F_{2\alpha}$, dairy cows

172 Development of a mechanistic metabolic model of regulation of reproductive processes in dairy cattle. P. Celi[2], I. Lean[2], H. Raadsma[2], A. Rabiee[2], and J. P. McNamara*[1], [1]*Washington State University*, *Pullman,* [2]*University of Sydney*, *Camden, NSW, Australia*.

The objective was to construct and begin evaluation of a deterministic, mechanistic, dynamic model of nutritional and genetic control of reproductive processes in the dairy cow. The objective of this conceptual research model is to describe control of reproductive processes in dairy cattle at the metabolic level; and to be suitable for evaluation of data, concepts and hypotheses regarding underlying genetic, nutritional and physiological control of reproduction. We began with an existing model of metabolism in the cow, published and validated (Molly, UC Davis), which describes utilization of glucose, amino acids and fatty acids by muscle, adipose, visceral and mammary tissues at an aggregated metabolic pathway level. Elements of genetic background, response to nutritional environment and metabolic hormones are explicitly embodied in equation forms and parameter values. Next, a model of reproductive processes was developed that included flux of follicle stimulating hormone, luteinizing hormone, estrogen and progesterone in cycling and pregnant animals; as well as development of the calf to term. The models are integrated into one system to link genetic elements (for example, genetic merit for milk); nutrient use and reproductive processes, with an integration interval of one day. Based on published data, equations describe production of estrogen and LH, breakdown of estrogen and progesterone by the liver (mass action related to rate of metabolism); growth of the follicles as a function of glucose, IGFI and growth hormone (Michaelis-Menten); conception and growth of a single calf to term as a function of progesterone, glucose, amino acids and total energy (Michaelis-Menten). Degradation of steroids is related to metabolic rate through both intake of nutrients and output of milk components and to continuation of pregnancy. The model behavior for these variables (pattern and direction of response) is consistent with literature values from studies not used in the development. This research model should be useful to frame specific hypotheses on control of reproductive processes by genetic and nutritional driven mechanisms.

Key Words: reproduction, nutrition, research model

173 Effect of dietary supplementation of mannan-oligosaccharides and *Lactobacillus*-based probiotics on indigenous intestinal bacterial ecology and intestinal microarchitecture of broilers reared under heat stress. M. U. Sohail*, I. Ahmad, H. Rehman, K. Ashraf, S. Yousaf, S. Ashraf, and H. Zaneb, *University of Veterinary and Animal Sciences*, *Lahore, Punjab, Pakistan, 54000.*

The present study aims at evaluating the effects of dietary supplementation of prebiotics or probiotics alone or in combination on growth performance, relative-weight of viscera, mucosal microarchitecture and some selected intestinal microbiota in broilers reared under hot humid conditions. Day-old broilers (n = 250) were randomly divided into 5 groups. Birds in the control group were reared under standard management conditions and fed a corn-based basal diet without any dietary supplementation. The birds exposed to cyclic-heat stress (35°C and 75%RH, 8hr/d, 1000–1800 h from d22 to 42), were fed a basal diet (HS group) alone or supplemented with 0.5% mannan-oligosaccharides (MOS), or 0.1% *Lactobacillus*-based probiotics (LP) or combination of both (symbiotic). On d 42, 15 birds from each group were killed to determine relative-weights of visceral organs, mucosal morphometry and numeration of jejunum and cecal *Clostridium perfringens*, coliform and *E. coli*. The data were analyzed using ANOVA. Results revealed that heat stress decreased ($P < 0.01$) body weight gain, feed conversion ratio (FCR) and relative weights of organs compared with the control group. Dietary supplementations increased the FCR ($P < 0.05$), relative weights of spleen ($P < 0.01$), small intestine ($P < 0.01$) and cecum ($P < 0.01$) compared with HS group. However, supplemented diets did not affect the relative weights of bursa of Fabricius ($P = 0.07$) liver, pancreas, gizzard and heart. Heat stress increased the cecal population of coliform, ($P < 0.05$) *Clostridium perfringens* ($P < 0.01$) and *E. coli* ($P < 0.05$) compared with control group without affecting the jejunal ($P = 0.61$) bacterial count. Supplementation of MOS alone or probiotics reduced ($P < 0.05$) the cecal count of *Clostridium perfringens*. The villus height was more ($P < 0.05$) in supplemented groups compared with the HS group. In conclusion, supplementation of prebiotics and probiotics is a good tool for maintaining production performance of broilers during hot humid months.

Key Words: broiler, heat stress, prebiotics, probiotics

174 Effects of turning frequency during incubation on broiler embryonic development. Y. M. Lin*[1], J. T. Brake[1], S. Yahav[2], and O Elibol[3], [1]*North Carolina State University, Department of Poultry Science, Scott Hall*, *Raleigh,* [2]*Institute of Animal Science, ARO, The Volcani Center*, *Bet-Dagan, Israel 50250*, [3]*Department of Animal Science, Faculty of Agriculture, University of Ankara*, *Ankara, Turkey*.

The effects of turning broiler hatching eggs 24 (24X) or 96 (96X) times daily to E15 was studied. Eggs were obtained from Ross 344 male x Ross 708 female broiler breeders at 36 wk of age. Freshly laid eggs were weighed and selected to provide equal egg weights in each turning treatment before storage for 1 d at 16 C and 60% RH followed by preheating at 24 C for 12h prior to setting. Each of 180 individually weighed eggs per turning treatment constituted a replicate. The 24X treatment was turned 24 times daily to E18, while the second group was turned 96X from E0 to E15 followed by 24X to E18 before transfer to hatching baskets in individual pedigree bags. Incubators were operated at 53% RH at all times and an air temperature of 37.5 C until E12, 37.3 C from E13 to E 18, and 36.9 C thereafter in Natureform NMC-1000 incubators. At E15 of incubation, 30 fertile eggs were necropsied to determine embryo length, and weights of the egg, embryo, yolk sac, and embryonic fluids. Chick BW and length were measured on all chicks at E20.5. A T-test was used to compare means and variances. Embryo length at E15 was greater ($P < 0.05$) in the 96X treatment but with a greater variance ($P < 0.05$) as well as a greater variance ($P < 0.05$) in relative yolk sac weight and embryo weight. However, at hatching (E20.5) chick weight relative to initial egg weight and chick length was greater ($P < 0.05$) in the 24X treatment but there was greater variance ($P<0.05$) in the relative chick weight. These data indicated that more frequent turning to E15 resulted in a faster growing but less uniform embryo at E15. However, after the 96X turning frequency was discontinued at E15 the 96X treatment regained its uniformity as embryo growth relative to the 24X treatment apparently slowed to E20.5. These data suggest that embryo growth and development is affected by turning frequency

Key Words: broilers, incubation, turning

175 Effects of arginine, vitamin E and mannanoligosaccharides after coccidiosis vaccination and challenge in broiler chickens. D. J. Chan-Diaz*[1,2], D. Caldwell[1], S. Pohl[1], G. Casco[1], A. Pro[2], S. Fitz-Coy[3], and C. A. Ruiz-Feria[1], [1]*Texas A&M University*, *College Station*, [2]*Colegio de Postgraduados*, *Montecillos, Mexico*, [3]*Intervet/Schering-Plough Animal Health*, *Millsboro, DE*.

Arginine (ARG), vitamin E (VE) and mannanoligosaccharides (MOS) have immunomodulatory effects. One d old broiler chicks (n = 200) were housed in wire cages and assigned to one of 8 treatments in a 2 × 4 factorial experiment: vaccinated (VA; Coccivac-B, 1X dose / chick at d 1) or non-vaccinated (NV) and fed a control diet (CTL, 3100 kcal / kg of EM, 22% CP, 1.4% ARG, and 40 IU of VE / kg of feed) or CTL plus ARG and VE (AVE; 0.3% and 40 IU, respectively); CTL plus MOS (MOS, 0.2%), or CTL plus ARG, VE and MOS (AEM, same levels). At 24 d, all birds were orally challenged with 2×10^5 oocysts from a mixed field-strain *Eimeria* inoculum (*E. acervulina*, *E. maxima* and *E. tenella*). The BW was recorded weekly; intestinal lesion score (LS) and immune organ weight (bursa of Fabricius, spleen, and thymus) were measured at d 30 (9 birds / treatment); oocyst shedding (OS; oocysts / g of feces) was measured from d 29 to d 31. Data were analyzed (ANOVA) and means separated using the Tukey procedure ($P < 0.05$). At wk 4, VA birds were heavier than NV birds, but the effect of diet was not significant. The spleen and bursa were not affected by treatment, but birds in the group VA-MOS had the highest thymus weight. Birds in the VA-MOS and NV-CTL group had the highest LS (1.56 ± 0.2), whereas birds in the VA-CTL group the lowest LS (0.67 ± 0.2) in the upper intestine (duodenum). The OS was not affected by treatment at d 29 or 31, but at d 30 VA birds had less oocysts in feces (556,342.5 ± 140,756.2) than NV birds (1,021,775.0 ± 140,756.2). Thus, MOS supplementation increased LS but also increased the thymus weight. Vaccinated birds were heavier and had lower OS than NV birds irrespective of diet. The beneficial effects of ARG and VE were not noticeable, perhaps because birds were kept in cages and oocyst cycling was prevented.

Key Words: arginine, vitamin E, coccidiosis

176 The effect of double interspiking on fertility, stress, and hormone levels in broiler breeder males in heat-stressed environments. K. M. Chung*, M. O. Smith, and H. G. Kattesh, *University of Tennessee*, *Knoxville*.

The male management technique of double interspiking is sometimes used to counteract fertility decline experienced by broiler breeders. The objective of this experiment was to investigate the effects of this practice on flock fertility, testosterone concentrations, and stress responses of broiler breeder males undergoing double interspiking in heat stressed environments. In a completely randomized design study, 2 hundred and 88 pullets and 36 roosters (Ross 708) were assigned to 3 groups at 21 weeks of age. All groups were housed on plastic slatted floor pens and experienced a simulated heat stress environment in which room temperature cycled from 23.8 to 30°C. Double interspiking was carried out among 2 groups at 42 and 52 weeks of age. Beginning when birds were 32 weeks of age, eggs were set every 2 weeks, candled at d 12, and percent fertility calculated. Testosterone and corticosterone levels were measured by RIAs at specific time points, and heterophils (H) and lymphocytes (L) were counted to calculate H:L ratios. All data were analyzed using the mixed model ANOVA (ANOVA) procedure of SAS 9.1 (SAS Institute, Cary, NC, USA), and least squares means used to determine significance. Introduction of new males resulted in a fertility increase ($P < 0.01$) of 21.8% between control birds and spiked birds after the first interspike and a sustainment of fertility levels after the second interspike. Testosterone concentration declined ($P < 0.0001$) from 1.95 ng/mL to 0.11 ng/mL as the birds aged. The male management practice of double interspiking shows promise in increasing fertility levels in a broiler breeder flock.

Key Words: broiler breeder, double interspiking, heat stress

177 Effects of breeder feeding and trace mineral source on leg health and bone traits of broiler progeny. P. E. Eusebio-Balcazar*[1], E. O. Oviedo-Rondón[1], A. Mitchell[2], J. Brake[1], M. J. Wineland[1], V. Moraes[1,3], and N. Leandro[1,4], [1]*North Carolina State University*, *Raleigh,* [2]*USDA-ARS, BARC*, *Beltsville, MD*, [3]*Universidade Estadual Paulista, UNESP*, *Jaboticabal, SP, Brasil*, [4]*Universidade Federal de Goiás*, *Goiania, GO, Brasil*.

This study evaluated the effects of breeder feeding practices and trace mineral (TM) sources for breeders on leg health and bone traits of broiler progeny at 49 d. Cobb 500 breeders were fed either corn (C) or wheat (W) based diets during rearing and production using either sigmoid late fast (LF) or sigmoid late slow (LS) feed allocation programs until peak egg production. At 23 wk, 69 females representing the BW distribution of each pen were placed in a 2/3 slat layer house where feeder space remained the same (S) or increased (M). From 56 to 62 wk of age, breeders were fed corn-soybean diets with 5% DDGS and either inorganic (ITM) or an organic (OTM) source (Mintrex P) to replace 30% of Cu, Zn, and Mn. Total levels of the TM evaluated were 25, 125, and 125 ppm, respectively. Eggs produced at 62 wk of age were incubated. Progeny were placed in 64 floor pens with 15 males and 15 females/pen and 4 replicates per breeder treatment. Broiler gait scores (GS) and prevalence of leg problems were evaluated at 11 and 47 d. Bone mineral density (BMD) and mineral content (BMC) were determined with DEXA. Data were analyzed as a 2 × 2 × 2 × 2 factorial design considering main factors of diet type, feeding program, feeder space and TM source. For GS data, the log odds of probabilities were modeled within factorial effects to obtain the likelihood of observing each leg problem using GLIMMIX. Results indicated that broilers coming from breeders fed diets with 30% OTM were more likely to have better walking ability than broilers from breeders fed ITM in both GS evaluations. Broilers from breeders fed ITM and having M feeder space in production were more likely to have valgus deformations than the same group fed OTM. Wheat diets fed to breeders and broilers caused lower BMD and BMC in broilers at 49d. OTM fed to breeders caused thicker shanks in broilers. Shank BMD and BMC was higher in broilers from breeders fed OTM compared with those breeders fed only ITM in the LS and S groups only. It appeared that 30% OTM in breeder diets may help to reduce some leg health issues observed in broiler progeny influenced by breeder feeding practices.

Key Words: breeder nutrition, trace minerals, leg problems

178 Dietary vitamin E supplementation and shelf life of ground broiler chicken meat during refrigerated storage. B. Saenmahayak*, M. Singh, J. B. Hess, W. A. Dozier III, and S. F. Bilgili, *Auburn University*, *Auburn, AL*.

This study was conducted to determine the microbial spoilage and oxidative stability of ground raw and cooked breast and thigh meat from broiler chickens fed graded levels of vitamin E during refrigerated storage. A total of 480 female broilers were assigned to 4 dietary vitamin E treatments (IU/kg of feed): 30 (basal level), 60, 120 and 240. Each of the 4 dietary treatments was fed in a 3 stage feeding program to 12 replicate pens of 10 birds and reared to 49 d of age. Upon processing, one-half of the replicate pens from each dietary treatment were used for raw and the other half for cooked meat treatments. Boneless-skinless breast and thigh meat (5 birds per pen) was ground, pooled by pen, formed into patties, vacuum packaged (oxygen impermeable) either raw or cooked (internal temperature of 80°C), and held under 2°C. Samples were analyzed for microbial spoilage (aerobic plate counts; APC, lactic acid bacteria; LAB, and yeast and molds; YAM) and lipid oxidation (TBARS) following 1, 3, 6, 12 d of refrigerated storage. Microbial numbers increased with storage time in both raw breast and thigh meat ($P < 0.05$), with APC counts on thigh meat reaching 7 $\log_{10}$ CFU/g after 12 d of storage. Cooking reduced microbial counts and slowed the rate of microbial growth in breast and thigh meat during refrigerated storage. Vitamin E supplementation affected microbial counts only for raw (APC on 6 d) and cooked (APC and LAB on 6 and 12 d, and YAM on 12 d) for thigh meat, with levels of 240 IU/kg significantly impeding microbial growth as compared with basal levels. Lipid oxidation increased during refrigerated storage on both raw and cooked ground meat (breast < thigh meat). Dietary vitamin E supplementation at levels > 120 IU/kg significantly reduced the rate of lipid oxidation in cooked ground breast and thigh meat as compared with the basal level. In this study, microbial and oxidative changes that occur during refrigerated storage of ground cooked broiler meat appeared to correlate and were positively influenced by dietary vitamin E supplementation.

Key Words: vitamin E, shelf-life, lipid oxidation

179 Impact of feeding time and photoperiod on egg production patterns in broiler breeder females. D. C. Paul*, M. J. Zuidhof, Ali Pishnamazi, and R. A. Renema, *University of Alberta*, *Edmonton, Alberta, Canada*.

The purpose of this study was to determine the effects of feeding time, dietary energy and photoperiod on egg production patterns in broiler breeder females. A total of 192 Ross 708 broiler breeder females were housed in 6 light- and temperature-controlled environmental chambers and each chamber containing 32 individual cages. The experiment was a 4 × 2 × 2 factorial of design, with 4 feeding time treatments (morning, noon, afternoon, or split feeding with 50% of the daily feed allotment split between morning and afternoon); 2 dietary metabolizable energy levels (high, 2900 or low, 2700 kcal/kg); and 2 photoperiods (24L:0D or 16L:8D). Standard breeder BW targets were achieved using daily feed restriction throughout the study period. Individual body weight was measured once per week. SAS Proc mixed was used to analyze the data.

Split feeding had increased egg weight compare to other feeding time ($P = 0.1$). Moreover, the split feeding, high energy (2900 kcal/kg) and photoperiod (16L:8D) interaction had the highest egg weight. Hens were energy efficient with split (two times) feeding system than one time and shorter photoperiod. However, the main effects of dietary energy and photoperiod had no significant effect on egg weight and egg production. Efficiency of broiler breeder female can be improved ensuring split feeding, dietary high energy and photoperiod (16L:8D).

Key Words: feeding time, photoperiod, egg production

180 Dietary camelina meal for broiler chickens: 1. Growth performance at 0, 5, and 10% inclusion rates. R. M. Hulet*, P. H. Patterson, A. Y. Pekel, and T. L. Cravener, *The Pennsylvania State University*, *University Park*.

Camelina sativa is an oilseed plant from the Brassicaceae family. It has recently been grown in N. America for biodiesel production with the residual meal utilized as a dietary protein supplement with a significant complement of omega-3 fatty acids. An experiment was conducted to examine the effect of dietary camelina meal (CM) supplementation on broiler live performance. A total of 864 Ross × Cobb-500 straight run chicks were allocated to control (Con), 5% or 10% CM diet treatments with 8 replicated pens per treatment from 1 to 35d. Data were analyzed using a 3-way ANOVA design with significance determined at the $P \leq 0.05$ level. The CM utilized in this study contained 33.6% CP, 15.0% Fat and 4.22% total omega-3 fatty acids. Birds were given water and feed ad libitum. Birds and feed were weighed at 0, 14, 28, and 35 d of age. Body weight, feed intake and conversion were calculated at each period. Cumulative feed intake was not significantly different between dietary treatments. However, body weight at both 28 and 35 days, respectively, was significantly less for broilers fed the 10% CM diet (1.38, 2.52 kg) when compared to the broilers fed 5% CM (1.48, 2.20 kg) and Con (1.46, 2.17 kg) diet. Mean body weight was similar between the broilers on the Con and 5% CM dietary treatments at both 28 and 35 d. Therefore, feed conversion for the 0 to 35 day period was significantly greater for the 10% CM fed broilers (1.783) over the 5% CM (1.702) and Con (1.698) fed broilers. Mortality was not significantly different at any period or cumulatively with an overall average of 5.44% for the experiment. Based on this study, broiler growth performance equal to a Con diet can be achieved by feeding diets with an inclusion rate of at least 5% CM.

Key Words: *Camelina sativa*, broiler chickens, biofuel

181 Evaluation of a poultry house for the presence of *Salmonella* and fungi at different sites through the broiler production continuum. J. A. Byrd*, C. L. Sheffield, and T. C. Crippen, *USDA-ARS-Food and Feed Safety Research Unit*, *College Station, TX*.

Companies continue to produce safe and wholesome products while facing increased regulatory pressure to control foodborne pathogens in poultry. Although many risk factors that contribute to *Salmonella* concentrations have been identified, precise identification of the most effective sites for intervention have not been established. The present observational study evaluates a new poultry house with different environmental parameters on *Salmonella* and fungal incidence at different points of production. One broiler house with 4 consecutive flocks was studied. Preharvest sample points included tray pads (2/sample point), litter (12/sample point), water (3/sample point), feed (3/sample point) and birds (20/sample point) sampled at d 0, 18, 32, 46, and 62. All samples were evaluated for *Salmonella* and fungi. Prior to placemen on the farm, *Salmonella* and fungi was detected in all water, feed, hatchery (traypads), and in 18% of the litter samples. Water samples were 100% positive for *Salmonella* at Days 1 and 18 in Flocks 1–3. Similarly, *Salmonella* was detected in high levels (60–100%) in Flocks 1 and 3 on Days 1 and 18. However, ceca samples evaluated for *Salmonella* were found under 5% on all days except for Flock 3 which had Salmonella 95% (Day 1) and 25% (Day 18). Fungal samples tend to decrease as the broilers get closer to market. The relationship between *Salmonella* and fungi will be evaluated. The data demonstrates the importance of pathogen-free environmental conditions even on new farm. Data from this study may help poultry professionals understand how environmental factors including fungi may affect foodborne pathogens in poultry and the difficulty that may be encountered in making risk management decisions.

Key Words: environmental, *Salmonella*, fungi

182 Effect of abrupt versus gradual changes to daylength on productivity of broilers. K. Schwean-Lardner* and H. L. Classen, *University of Saskatchewan*, *Saskatoon, SK, Canada*.

With the objective of determining the impact of an abrupt change in day length and light intensity on productivity and welfare of broilers, 3 lighting programs were tested using Ross x Ross 308 broilers (2,160 male and 2,565 female). Birds were housed within 10 sex-separate pens in each of 9 rooms at 30 kg/m^2. The lighting schemes tested were: 1. Control (C) - 23Light (L) (20 lx (l)):1Dark (D) (0 l) from d 0–38, 2. Abrupt (A) - 23L (20 l):1D (0 l) to d 10, then an abrupt change to 14L (1 l):10D (0 l) to d 38, 3. Gradual (G) d 0 - 23L (20 l):1D (0 l); d 1 - 21L (20l):1 dusk:1D: (0l):1 dawn; followed by gradual changes in day length and intensity until d 10 - 13.5L (6l): 1 dusk: 8.5D (0l) 1 dawn. Data were analyzed with a nested design of Proc GLM, and when significant, Duncan's Multiple Range test for mean separation. Specific comparisons between abrupt and gradual data were analyzed using A Priori contrasts. At 14 and 21 d of age, birds raised under the A and G program were lighter than those raised under the C program, and contrasts show G birds were heavier than A. Daily feed consumption, measured from d 7 to d 13, showed a significant drop in intake when the abrupt lighting change took place, while no decline was noted in the gradual change. Birds on C ate the most until 21 d and overall. G birds ate more than A from 7 to 14 d and 14–21 d, but less from 21 to 38 d. Overall, birds on these 2 programs ate similar amounts. Gain to feed ratios were poorest for C birds, and were better for G vs A birds until 14 d and thereafter the ratios were similar. Mortality or uniformity did not vary with lighting program. Birds raised on C had a higher percentage of carcass based on live weight than A, higher breast yield than A or G, and a higher percentage of wings than G birds. In conclusion, abrupt changes to a lighting program cause an immediate and dramatic decline in feed intake and feed conversion efficiency that are not noted when the changes are made gradually.

Key Words: broiler, daylength

183 Influence of long-bright, increasing-dim, and split-dark-bright lighting programs and strain on broiler performance. R. J. Lien*, J. B. Hess, and S. F. Bilgili, *Auburn University*, *Auburn, AL*.

Broilers were provided lighting programs either historically used to maximize growth, or meeting US National Chicken Council or European Union guidelines, to determine their influence on performance. Forty males of tray pack (TP) or breast yield (BY) strains were placed by strain in each of 2 1.5 by 3.7 m pens in 12 light controlled rooms. Four rooms were provided a long-bright photoperiod treatment (LB) (23L:1D and 2 footcandles [FC]). Four rooms were provided increasing-dim treatment

(ID) (1–7 d, 23L:1D; 8–14 d, 12L:12D; 15–21 d, 14L:10D; 22–28 d, 17L:7D; 29–35 d, 20L:4D; 36–47 d, 23L:1; 1 FC to 7 d and 0.25 FC thereafter). Four rooms were provided a split dark period and bright intensity treatment (SDB) (16L:4D:2L:2D and 2 FC). Ten birds per pen were processed at 47 d to determine parts weights and yields. Data were analyzed by GLM of SAS at a significance of $P < 0.05$ for live and $P < 0.10$ for processing variables. Feed consumption and BW were reduced in ID relative to LB and SDB at 15 and 21 d (all Ps < 0.0001). BW were greater ($P = 0.036$) in ID and SDB than LB at 47 d. Feed conversion was improved ($P = 0.006$) at 15 d in ID relative to LB and SDB, but otherwise unaffected ($P > 0.05$). Weight and consumption were usually more ($P < 0.05$) in TP than BY, and TP feed conversion was better at 15 ($P = 0.011$) and 22 d ($P = 0.023$). Mortality was greater ($P = 0.003$) in TP than BY. Carcass yields were unaffected by treatment ($P = 0.75$) or strain ($P = 0.87$). Wing ($P = 0.038$) and drum ($P = 0.028$) weights were greater in ID than LB and SDB. Total breast ($P = 0.08$) and fillet ($P = 0.086$) yields were greater in LB than ID, with SDB intermediate. Tender yields were greater ($P = 0.059$) in LB than SDB, with ID intermediate. Wing yields were greater ($P = 0.029$) in LB and ID than SDB. All parts were heavier ($P < 0.10$) in TP than BY and there were no strain effects ($P > 0.10$) on parts yields. Fat pad weights ($P = 0.033$) and yields ($P = 0.002$) were greater in BY than TP. These results confirm our previous observations that broiler lighting can influence performance to a greater extent than strain, particularly with respect to breast yield.

Key Words: broiler, lighting, production

184 Free-choice feeding of free-range meat chickens. A. C. Fanatico*[1], V. B. Brewer[2], C. M. Owens[2], and A. M. Donoghue[1], [1]*USDA Agricultural Research Service, Poultry Production and Product Safety Research*, *Fayetteville, AR,* [2]*University of Arkansas Department of Poultry Science*, *Fayetteville*.

Specialty poultry production is growing, including free-range, organic, and small flocks. Feed is a high cost, particularly for organic producers and small-scale producers. Free-choice feeding, where feed ingredients are provided in separate containers, may offer cost savings, including the use of on-farm ingredients, reduction in feed transportation, and milling costs. A study was conducted to determine the impact of free-choice feeding on performance in free-range meat chickens. Pens of slow-growing chickens (20 birds per pen) were randomly assigned to one of 2 treatments: fully formulated diet (FF; control) or free-choice (FC) diet. There were 5 replications of these treatments. Birds were raised in floor pens in a naturally ventilated house; popholes provided access to grassy yards during the day. During the starter period (wk 0–3), formulated feed was provided to both treatments. During the grower period (wk 4–6), FC treatment also received formulated feed along with free-choice ingredients for training, and during the finisher period (wk 7–12), FC only received free-choice ingredients. Birds were commercially processed at 83 d. The formulated diet was a commercial product with an average of 20.75% crude protein (1.04% total sulfur amino acids); while the free-choice diet chosen by birds at 11 weeks was 13.2% crude protein (0.70% total sulfur amino acids). Final live weights were analyzed by *t*-test (SAS 9.2) and did not differ between treatments ($P > 0.05$); however, ready-to-cook yields and breast yields were higher in the birds from the FF treatment ($P < 0.05$). These higher yields are most likely due to amino acid supplements in the formulated feed. The diet chosen by FC birds at end of finisher period was less expensive than the formulated diet ($0.07/kg vs. $0.08/kg). These data indicate that while free-choice feeding of free-range chickens resulted in a 1.4% lower breast yield than formulated feeding, FC feed cost was lower. The USDA National Organic Program is planning to ban synthetic methionine, and when that occurs, there may be no difference in yield among birds from formulated and free-choice diets.

Key Words: dietary self selection, poultry, free-range

185 Omega-3 PUFA and lutein enrichment: Different feeding strategies and effect on storage stability. S. Nain* and R. A. Renema, *University of Alberta*, *Edmonton, AB, Canada*.

Enrichment diets high in ground flax may cause irritation to the gut, which may affect absorption of omega-3 polyunsaturated fatty acids (ω-3 PUFA) from flax as well as other dietary enrichment ingredients. This study assessed the egg enrichment with ω-3 PUFA and Lutein when provided alone in the diet, in combination, or when fed in alternate day patterns. A total of 144 individually caged Lohman White Leghorn layers (56 wk) were fed 1 of 6 diets balanced for energy and protein for 60d as follows: Control (C) = Standard hen ration; Lutein (L) = 500 ppm lutein; Flax (F) = 10% flaxseed; Lutein/Flax mix (LF); Alternating L and F diets every day (Alt1) or second day (Alt2). Egg traits were determined and yolks collected at 0d, 14d, 28d and 56d. Eggs from 57d were stored at 4 C for 30d for assessment of oxidative stability through TBARS analysis. Data were analyzed using proc Mixed of SAS. Hen diet did not affect egg production, egg weight, albumin height or shell thickness. Although, absolute yolk weight was higher in birds on C diet as compare to other diets, but % yolk weights were similar. Total ω-3 PUFA in LF and F eggs averaged 13.9 mg/g yolk compared to 11.6 mg/g yolk in Alt1 and Alt 2 eggs and 8.8 mg/g in L and C diets. Lutein followed a similar enrichment pattern, with birds fed L or LF having the highest egg content (25.7 µg/g yolk). While L and LF eggs had 3-fold more lutein than C or F eggs (8.4 µg/g), those from alternate day fed hens had 2-fold more lutein. Including both flax and lutein in the hen ration did not reduce egg lutein enrichment. Inclusion of lutein generated the lowest TBARS values (0.60 mg/MDA in L and LF) compared to diets without lutein (0.75 mg/MDA in C and F), demonstrating a potential antioxidant role in the egg. Yolk lutein concentration was positively correlated to canthaxanthin (r= 0.65, P=<.0001) and β-carotene (r= 0.40, P<.0001). Egg storage did not affect yolk lutein and β-carotene amount, whereas canthaxanthin was reduced. Lutein enrichment improves the overall carotenoid profile and also enhances stability during storage of egg, and was not negatively affected by ω-3 PUFA enrichment using flaxseed.

Key Words: lutein, ω-3 PUFA, TBARS

186 Effect of egg storage conditions on gene expression during turkey embryonic development. J. A. Hamidu*[1], M. Li[1], G. M. Fasenko[2], and L. L. Guan[1], [1]*University of Alberta*, *Edmonton, Alberta, Canada*, [2]*University of New Mexico*, *Albuquerque*.

Different conditions of avian egg storage before incubation are known to cause variation in embryonic mortality in poultry species. We hypothesized that genes regulating apoptosis (*Blc-2, Bcl-xL, Bax, Bak* and *Bok*) or early embryo development (*Btg1*) could be differentially expressed under different storage conditions which may play a role to control turkey embryonic development. In this study, eggs from Hybrid turkey flocks were stored for 4 d and 14 d under standard storage conditions Total RNA was extracted from pooled embryo samples (n = 5 per treatment) after incubating the eggs for 6 d at 37.5°C and 56% RH. The expression levels of *Blc-2, Bcl-xL, Bax, Bak, Bok* and *Btg1* genes were compared using quantitative real time PCR analysis. The data was analyzed by PROC MIXED model procedure of SAS at $P \leq 0.05$. LSmean differences between egg storage treatments were separated by PDIFF. The results showed that the genes associated with pro-apoptotic processes were differentially expressed in 14 d vs. 4 d egg storage treatment: *Bax* and *Bok* were upregulated ((*Bax*, 1.71 fold, $P = 0.0428$; *Bok*, 1.39 fold, $P = 0.007$) while *Bak* was downregulated but not significant (0.37 fold, $P = 0.0628$). Moreover, the genes associated with anti-apoptotic events were upregulated (*Bcl-2*, 1.34 fold, $P = 0.3026$; *Bcl-xL*, 1.23 fold, $P = 0.0003$). However, the expression of *Bcl-2* was not statistically different between treatments. These genes were identified to be involved in different KEGG pathways of apoptosis: mitochondrial pathway or p53 pathway. The *Btg1* gene, was also downregulated following egg storage for 14 d compared with 4 d (0.54 fold, $P = 0.0150$). Our findings demonstrate increased expression of apoptosis events and decreased response to growth and development at the molecular level following egg storage for 14 d. This study shows that the probability to control some of the effects of egg storage commercially is promising if apoptosis can be controlled.

Key Words: egg storage, RNA, gene expression

187 Body weight change, breast muscle, and reproductive tract development in broiler breeder hens and their effects on fertility and egg production. N. Leksrisompong*, J. T. Brake, and E. O. Oviedo-Rondon, *North Carolina State University, Department of Poultry Science, Scott Hall*, *Raleigh*.

A study was conducted to determine the effects of the relationship among changes in BW gain, breast muscle, and reproductive tract development in broiler breeder females. Pullets were reared in 16 litter floor pens from hatching to 22 wk of age. Females that represented the BW distribution of each pen were selected and moved at 22 wk to 128 individual cages. Individual BW was taken at 22, 25, 26, 33, 48, and 53 wk of age. BW change between each period was determined. Breast muscle weight was estimated in vivo with real-time ultrasound (RTU) at 25, 26, 48, and 53 wk. A multiple linear regression equation that included BW, area of breast muscle (BM) taken by RTU and strain was estimated. Fertility was measured at 31 and 48 wk. Total egg production per hen was recorded. At 53 wk, all hens were necropsied to determine weights of BM, ovary, and oviduct segments. Results indicated that RTU can be used to estimate BM weight (r2 = 0.91) in broiler breeders. It was found that BW change between 22 to 26 wk was positively correlated with BM weight (r = 0.70), but negatively correlated with total egg production (r = 0.37). Breast muscle at any age was negatively correlated with infundibulum (r = 0.25) and with total egg production (r = 0.26). Breast muscle was also negatively correlated with fertility when evaluated at 31 wk, but not at 48 wk. Changes in BW in time periods other than 22 to 26 wk were not correlated with total egg production or fertility. It would appear that, in the presence of excess feed between 22 and 26 wk, hens developed their breast muscle at the expense of their infundibulum, and this may affect fertility, and total egg production.

Key Words: real-time ultrasound, broiler breeder, oviduct

188 Effects of temperature on egg size and quality. A. G. C. DesLauriers*, M. J. Zuidhof, R. A. Renema, D. Paul, and A. Pishnamazi, *University of Alberta*, *Edmonton, Alberta, Canada*.

Environmental temperature has a large impact on broiler breeder maintenance requirements. Energy for maintenance accounts for up to 3/4 of total energy intake. Therefore incremental changes in maintenance requirements may substantially influence energy available for other processes such as growth or egg production. Thus temperature is important for egg production, egg size and chick size. An experiment was conducted to determine the effect of temperature on egg size and

quality. A total of 192 individually caged broiler breeders were exposed to differing environmental temperature treatments (15, 19, 23, and 27°C). The treatments were randomly assigned to 6 individual environmental chambers for 2 week periods, with 15 replicates of each temperature treatment over a 20 week trial period. All eggs were collected, weighed and graded daily. Temperatures were recorded using automated data loggers positioned at bird head height, on a 30 min interval and were averaged for the 24 hour period prior to oviposition. Data were analyzed as a 2 way ANOVA using the mixed procedure of SAS. Significant differences were reported at $P < 0.05$. Egg size increased from an average of 57.5 ± 0.24 g in the 15°C treatment with each increasing temperature trial up to 23°C (60.0 ± 0.24 g); a further temperature increase to 27°C resulted in a drop in egg size (58.0 ± 0.24 g), presumably due to heat stress. Temperature was found to have a significant effect on production of grade A eggs with the highest percent of grade A's in the 19°C and 23°C treatment. The 27°C treatment had the lowest percentage of grade A eggs and the highest incidence of soft shelled eggs. Shelless eggs were also highest in the 27°C treatment (0.708 ± 0.123%) although not significantly different from the 19°C treatment. The 15°C treatment had the lowest incidence of misshapen shells (0.302 ± 0.252%). Overall the data suggested that maintenance energy requirements increased with decreasing environmental temperatures and at the highest environmental temperature tested, there was indirect evidence of metabolic stress (reduced egg size and quality).

Key Words: temperature, egg size, egg quality

189 The impact of distillers dried grains plus solubles (DDGS) diets on hen performance, egg quality, and manure nutrients. P. H. Patterson, A. Y. Pekel, A. Adrizal, H. K. Burley*, T. L. Cravener, E. F. Wheeler, and P. A. Topper, *The Pennsylvania State University*, *University Park*.

Diets including 10% DDGS with (D+P) or without (D) the probiotic Provalen (500g/1000kg) were compared with a corn-soybean based control diet (CON) in a commercial hen house. Three groups of 39,800 Lohmann LSL-Lite hens were fed isocaloric, amino acid balanced research diets from 20 to 65 wk of age with 2 of 6 rows of stacked cages with manure belts assigned randomly per diet. Replicated monthly data, including hen body wt (BW), egg production (EP) and weight (EW), albumen height (AH), Haugh units (HU), yolk color (YC), and shell strength (SS) and thickness (ST), was collected from 558 hens in a section of each cage row. Feed/water intake, BW, EP, case weight, mortality, feed cost (FC), and egg income (EI) was also tallied weekly by the egg company for each diet. Monthly samples of fresh manure were taken off the manure belts (6/treatment) and from the manure storage building (2/treatment) and analyzed for moisture and agronomic nutrients. Statistical analysis was done with SAS version 9.1 using Tukey's mean comparisons with $P \leq 0.05$ deemed significant. Diet did not significantly impact BW, EW, HU, SS, or ST ($P > 0.05$); however, CON hens had lower EP, AH, and YC than D and D+P hens ($P \leq 0.05$). Manure moisture, total nitrogen (N), ammonium-N (NH_4-N), organic-N, and total potash (K_2O) did not differ significantly by diet, although manure total phosphorus (P_2O_5) was higher for CON samples ($P < 0.05$). Stored manure samples from CON had greater moisture and less NH_4-N than samples from D and D+P hens ($P < 0.10$). Weekly company data summarized for the entire study showed that EP averaged 85.8, 85.2, 85.7% and total eggs per hen housed at 65 wk of age were 271, 270 and 271 for CON, D, and D+P diets, respectively. Mean feed intake and feed conversion were 100.0, 100.0, and 104.3 g/hen/d and 1.91, 1.95, 1.95 kg feed/dozen eggs for the CON, D, and D+P diets, respectively. Weekly EI from selling eggs to the breaker market averaged $12,851, $12,801, and $12,864, weekly FC averaged $6,705, $6,599, and $6,671, and, therefore, weekly EI minus FC (e.g., farm revenue) averaged $6,146, $6,215, and $6,209 for CON, D, and D+P diets, respectively.

Key Words: distillers grains, hen performance, manure

190 Breeder hen age affects chick early innate immune function. M. L. Johnson* and D. R. Korver, *University of Alberta*, *Edmonton, Canada*.

Newly hatched broiler chicks do not possess a well-developed acquired immune system, therefore they rely to a large extent on innate immunity. As hens age, chick quality is usually considered to increase, however this is typically assessed on physical parameters such as chick weight and body length, rather than on disease resistance. The objective of this study was to examine the effects of broiler breeder hen age on innate immune function in young broilers. Hens were fed a commercial-type diet and fertile eggs were collected and incubated weekly at 3 hen ages: Early (30–33), Mid (44–47) and Late (57–59) wk of hen age. Hen body weight, settable egg production, hatchability, chick body weight at hatch were assessed. Whole blood was collected from chicks at 1 and 4 d of age to assess the ability of chick lymphocytes to kill *Escherichia coli* in vitro. Data were analyzed as a mixed model ANOVA in SAS. Differences were considered significant at $P \leq 0.05$. Hen body weight increased by 12% and settable egg production decreased by 38% from Early to Late production. Hatchability during the Late period was 11 and 9% lower than the Early and Mid periods, respectively. Hen fertility decreased from Mid to Late production. Chick body weight at hatch increased by 21% between the Early and Late production periods. At the Early hen age, the bactericidal activity of chick immune cells increased by 27% between 1 and 4 days of age; there were no chick age-related differences in bactericidal activity at either Mid or Late hen ages. At d 1, chick immune cell bactericidal activity at the Early hen age was 4.6- and 16.1-fold greater than at the Mid and Late breeder age, respectively; at d 4, bactericidal activity at the Early hen age were 3.4- and 4.8-fold greater than at the Mid and Late hen ages, respectively. At the Mid and Late hen ages, chick immune cell bactericidal activities were not different from each other at either chick age. As hens age, chick hatch weight increases, but chick innate immune cell bactericidal activity is greatest when hens are at the early stages of the production cycle.

Key Words: broiler breeder age, innate immunity, chick quality

191 Sperm production and testicular development of broiler breeder males reared on shortened growth cycles. J. R. Moyle*, S. M. Whipple, D. E. Yohoo, and R. K. Bramwell, *University of Arkansas*, *Fayetteville*.

Feed restriction is an important tool used in the rearing of broiler breeds to control growth and maintain body weight. Feed restriction during the growing phase is typically 60–80% less than what birds would eat ad libitum, resulting in a perceived animal welfare issue. Because males are typically more severely feed restricted than females, this is perceived to be especially stressful to the growing cockerels. During this time the reproductive systems of the males are going through formative stages and improper management can have lifelong effects on their reproductive performance. Therefore, the objective of this study was to raise males under feed management programs that would require less sever feed restriction while still rearing replacement breeder males to the recommended target body weight of 3.060kg at 12, 15, 18, 21 and 24 wks of age, respectively. Males were placed at 3 wk intervals so that all males were light stimulated at the same time but at different ages with the same body weight. There were a total of 5 treatment groups based

on the age of the male at the time of light simulation. All males were reared in the same light controlled house at the University of Arkansas Research Farm. Males were light stimulated and testes development, semen analysis, fertility and mating activity were recorded for each group of males. To measure semen production, males were housed in individual cages, with 24 males from each treatment tested. All data were analyzed using ANOVA and means were considered significantly different when P values were less than 0.05. Results found that males lit at 18 wks of age had the highest semen volume (0.46mL) followed by males lit at 24 (0.31mL), 15 (0.29mL), 21(0.27mL) and 12 wks (0.27mL), respectively. Sperm count per ejaculate was highest for the males lit at 18 wks of age followed by males lit at 21, 24, 15, and 12 wks, respectively. Males that were 21 wks or older at the time of lighting responded quicker to light stimulation than did younger males.

Key Words: broiler breeder, sperm production, lighting

192 Germination of *Bacillus subtilis* C-3102 in the gut of conventional and germ-free chicken. T. Hamaoka*[1], N. Otomo[1], B. Y. Lee[1], Y. Tadano[2], T. Marubashi[2], J. Marshall[3], and A. Van Kessel[3], [1]*Calpis U.S.A., Inc.*, *Mt.Prospect, IL*, [2]*Calpis co. Ltd.*, *Tokyo, Japan*, [3]*University of Saskatchewan*, *Saskatchewan, Canada*.

Bacillus subtilis C-3102(BSC) is utilized in a probiotic product Calsporin (Calpis Co. Ltd., Japan) and made available worldwide. Shifts in intestinal microbial colonization patterns are observed when there is an improvement in production performance by BSC. To determine the mechanism of action of BSC, we have conducted 2 trials to investigate the germination of BSC spores in gastrointestinal tract of conventional and ex-germfree monoassociated chickens. Ten 28-d old conventional broilers (Cobb) were assigned to individual cages. A corn-soybean based diet was fed with 3.0×10^5 CFU/g of BSC spores. At the age of 55-d, 10 birds were killed to collect gut contents from crop, gizzard, jejunum, ileum, cecum and feces. Samples were diluted and plated directly to enumerate spores plus vegetative cells (total count). Remaing sample was heat treated (60°C for 30min) and plated again to enumerate spores. The total count (log CFU/g) of BSC at each gut location ranged from 4.85 to 5.47 and was not different. Spore ratio was 61% and 95% of total count in gizzard and cecum, respectively, suggesting germination of spores at these locations. Germ-free chickens (Ross308) were reared in HEPA-filtered sterilized isolators by methods developed at the University of Saskatchewan. Chicks were fed *ad libitum* a gamma irradiated corn-soybean diet supplemented with $3x10^5$ CFU/g of BSC spores. At 14-d of age, 10 birds were killed and intestinal contents were collected for enumeration of BSC as above. The total count (log CFU/g) increased ($P < 0.05$) from 5.78 in crop to 7.16 in cecum. The spore ratio ranged from 59.2% to 82% of total count and is consistent with the conventional birds which showed lower ratio in gizzard (68.5%) and cecum (59.2%). We conclude that BSC spores germinate in the chicken gastrointestinal tract, primarily in gizzard and cecum.

Key Words: *Bacillus subtilis*C-3102, Calsporin, germ-free

193 Examining the sitter duck condition. K. Murdoch[1], K. Seward[1], J. Riley[1], D. T. Ort[2], and M. J. Wineland*[2], [1]*Maple Leaf Farms*, *Milford, IN,* [2]*North Carolina State University*, *Raleigh*.

The sitter duck condition observed in the duck industry can cause downgrading at the plant. During the loading and unloading process of driving the ducks onto and off the truck some ducks would sit and not continue walking the ramp during the process resulting in the following ducks stepping over and on the sitter ducks causing scratches which results in downgrading of the carcasses. Observations were made pertaining to level on truck transport, duration of transport. Ducklings were evaluated at unloading at the plant for 2 trials. Thirteen blood parameters were measured using an i-Stat Analyzer in both trials. Additionally in the second trial CK and LDH were determined. Parameters were evaluated by condition of sitter or normal and by sex of bird in trial 1. In trial 2, sitter and normal ducklings were evaluated on 6 farms, and on 2 of these farms the initially sampled ducklings were evaluated 24 h later after being held in the holding pen with feed and water. Data was analyzed in a factorial design using GLM Procedure of SAS. Sitter ducks were more prevalent when transported on the upper levels of the transport truck where they were required to walk a steeper incline at loading and unloading. In the first trial sitter ducks demonstrated significantly elevated pCO2, Na^+ (30.97 versus 29.41) and (141.27 versus 138.45) respectively and significantly lower K+ (4.10 versus 4.23). In the second trial Na^+, glucose and ionized Ca was significantly elevated. Approaching significance was K+ where it was lower in the sitter than the normal duckling. CK and LDH was significantly greater in the sitter ducks than the normal ducklings (3913 versus 2506 and 861 versus 444 respectively). Ducklings which were evaluated at unloading and then again 24 h later in the holding pen demonstrated a reduction in the sitter duckling to levels comparable to the normal duckling. Evidence suggests that the sitter condition is related to exertion and ramp slope during unloading. Additionally tissue damage is indicated by the elevated CK and LDH as well as the elevated plasma Na^+ and decreased K+ levels.

Key Words: duckling, immobility, blood parameters

194 The effects of body weight on production and overall fertility and duration of fertility in broiler breeder hens. R. K. Bramwell*, D. E. Yoho, J. R. Moyle, and S. M. Whipple, *Department of Poultry Science, University of Arkansas*, *Fayetteville*.

Evaluating fertility problems in commercial broiler breeder flocks has traditional been targeted at the management and well being of the male. However, previous research has shown variation in the ability of individual broiler breeder hens within a flock to become fertilized. This variability is consistent with specific hens throughout their reproductive life and may or may not be related to age or body weight. This study was designed to evaluate the physiological capacity of broiler breeder hens to become fertilized under conditions of age and body weight. Two hundred pullets from each of 4 broiler breeder hen strains of were obtained from a commercial hatchery and reared into production according to industry standards. At 21 wks of age, birds were light stimulated and separated into one of 2 groups; either at or below target weight (C), or heavy or above target weight (H) and housed in individual cages. H birds were maintained at +300 g as compared with the C group until 60 wks of age. At 30 wks of age, hens were artificially inseminated with 100 million spermatozoa in a 0.05cc volume from a pooled semen sample. Inseminations continued at 5 wk intervals until 60 wks of age. All eggs were collected daily to determine fertility by day and week post-insemination. Values were analyzed by breeder hen strain and body weight group for 3 wks following each single insemination with all fertility values calculated from the single insemination until fertility ceased. Data were analyzed using JMP statistical software using ANOVA with means compared using the LSD method with significance determined when $P < 0.05$. Results from this trial indicate that the C groups had higher weekly egg production values as compared with the corresponding H groups. While fertility varied by age, the C group had consistently better fertility (48.5% and 40.0% life of flock fertility) and average duration of fertility (16.70 and 14.71 d) as compared with the H groups, respectively. Results indicate that body weight has a significantly

detrimental effect on fertility values and duration of fertility in most breeder hen strains regardless of age.

Key Words: broiler breeder, fertility, reproduction

195 Comparing the physiological capacity for fertility in caged broiler breeder hens from four commercial strains. R. K. Bramwell*, J. R. Moyle, S. M. Whipple, and D. E. Yoho, *Department of Poultry Science, University of Arkansas*, *Fayetteville*.

Maintaining fertility in commercial broiler breeder flocks, along with egg production, is one of the critical factors and goals of the breeder manager. However, previous research has shown genetic variability of broiler breeder hen strains to all reproductive characteristics. This variability may be consistent with hen strains, particularly yield type strains, but can often be altered with management programs. This study was designed to evaluate the physiological capacity of different strains of broiler breeder hens to become fertilized using artificial insemination, therefore eliminating natural mating and male libido effects. Two hundred pullets from each strain of broiler breeders were obtained from a commercial hatchery and reared into production according to industry standards. At 21 wks of age, birds were light stimulated and 100 hens per strain were separated into blocks of 10 individually caged hens with 10 replicate blocks per strain. Additional hens were housed in floor pens and were used to replace caged hens that had died or ceased egg production during the trial. At 30 wks of age all caged hens were artificially inseminated with 100 million sperm in a 0.05cc volume from a pooled semen sample. Inseminations continued at 5 wk intervals until 60 wks of age. All eggs were recorded and collected daily to determine fertility by day post-insemination. Values were analyzed by hen strain until the cessation of sperm activity was determined. Data were analyzed using JMP statistical software using ANOVA with means compared using the LSD method with significance determined when $P < 0.05$. Results indicate that while each hen strain varied in overall fertility following the single inseminations (from 42.7 to 46.1%), age had little effect on these hens (low of 38.4 and a high of 49.8%). There was no difference in overall duration of fertility for any of the hen strains with all strains averaging a duration of fertility between 15.6 and 15.8 d post- insemination. Results indicate that when hens are caged and natural mating factors are eliminated, fertility values are very similar for the 4 hen strains included in this study.

Key Words: broiler breeder, fertility, reproduction

196 Modeling energy utilization of broiler breeder hens is affected by environmental temperature and dietary energy. A. Pishnamazi*, M. J. Zuidhof, R. A. Renema, and D. Paul, *University of Alberta*, *Edmonton, Alberta, Canada*.

The accurate prediction of energy requirement affects the effectiveness of feed allocation decisions. This analysis was conducted to identify a model to estimate partial coefficients of ME partitioning of broiler breeder (BB) hens. A total of 288 hens (Ross 708) were individually caged in 1 of 6 environmentally controlled chambers at 21 wk. Ten, 2-wk temperature treatments were imposed from 21 to 41 wk, with 4 randomly rotating temperature treatments (15, 19, 23, and 27 C). Birds in each chamber were fed either a High Energy (HE, 2900 kcal/kg) or a Low Energy (LE, 2700 kcal/kg) diet. An energy utilization model was used to account for average daily ME intake twice/wk and calculate maintenance energy requirements (MEm). This model used a metabolic BW coefficient of 0.67. The nonlinear mixed model employed a normally distributed term associated with hen metabolic BW, and exponential terms of average daily gain (ADG), egg mass (EM) and temperature. The MEm at 21 C was 159.38 kcal/kg0.67, with a temperature adjustment of −0.2995 kcal/C. The ME requirement for gain was 0.4013 kcal/g, with a temperature adjustment of −0.0234 and EM was 0.6183 kcal/g. According to this model, a broiler breeder hen weighing 3.0 kg, gaining 15g/d and producing 60g egg/d require 382, 376, or 369 kcal/d at 15, 21, and 28 C, respectively. This translates to 136.4, 134.3, or 131.8 g/d of 2,800 kcal ME/kg feed, respectively. Birds fed HE had a higher ADG coefficient than birds on the LE diet. However, both MEm and EM coefficients did not differ. The greatest impact of temperature is on MEm, whereas dietary energy affected growth.

Key Words: energy requirements, broiler breeders, environmental temperature

198 Use of dried distillers grains throughout a beef production system: I. Stocker phase. E. K. Buttrey*[1,2], F. T. McCollum III[1], J. C. MacDonald[2,3], and K. H. Jenkins[3], [1]*Texas AgriLife Extension Service*, *Amarillo*, [2]*West Texas A&M University*, *Canyon*, [3]*Texas AgriLife Research*, *Amarillo*.

During the winters of 2008 and 2009, a study was conducted at the Texas AgriLife Research facilities in Bushland, Texas, to evaluate dried distillers grains as a supplement to wheat pasture. Each yr, 60 preconditioned Hereford steers (initial BW = 198 kg ± 3) were revaccinated against viral and Clostridial pathogens and implanted with 36 mg of zeranol. Steers were stratified by BW and randomly assigned to one of 15 2.2-ha wheat pastures (4 steers/pasture). Treatments were assigned within 5 blocks of 3 pastures. Treatments were: 1) Control (CON)- no supplement, 2) dry rolled corn (DRC), and 3) dried distillers grains (DDG). DRC and DDG were fed at 0.5% BW (DM) daily, pro-rated and delivered 6 d/wk. Full BW was measured and supplement amounts were adjusted every 28d. All steers had ad libitum access to water and a monensin-containing mineral supplement throughout grazing. Forage mass was measured by clipping at initiation and termination of grazing. Across yr, steers grazed an average of 128 d. Initial forage mass was not different among treatments ($P = 0.49$; Table 1). However, treatment affected final forage mass. At the end of grazing, DRC pastures had more ($P = 0.02$) residual forage mass than CON and DDG was intermediate. Gain was greater for DDG steers than CON and DRC ($P < 0.01$). Final forage mass suggests DRC depressed forage intake, while DDG had less influence on intake while increasing weight gain.

Table 1. Effect of stocker treatment on forage mass and steer performance

Item	CON	DRC	DDG	SE
Initial forage, kg DM/ha	2515	2750	2696	202
Final forage, kg DM/ha[a,1]	640	969	848	134
Gain, kg/d[b]	1.29	1.31	1.40	0.03
Adjusted gain, kg/d[b,2]	1.30	1.29	1.40	0.03

[a]Treatment effect, $P = 0.07$; pairwise CON < DRC, $P = 0.03$.
[b]Treatment effect, $P = 0.003$; pairwise DDG > CON, DDG > DRC, $P < 0.01$.
[1]Initial forage mass used as covariate.
[2]Final forage mass used as covariate.

Key Words: dried distillers grains, supplement, wheat pasture

197 Use of dried distillers grains throughout a beef production system: II. Finishing phase. E. K. Buttrey*[1,2], F. T. McCollum III[1], J. C. MacDonald[2,3], and K. H. Jenkins[3], [1]*Texas AgriLife Extension Service*, *Amarillo*, *West Texas A&M University*, *Canyon*, [3]*Texas AgriLife Research*, *Amarillo*.

To evaluate the effects of feeding dried distillers grains throughout a beef production system, a 2-yr study was conducted using a 3 × 2 factorial arrangement of treatments. Factors were wheat pasture supplement (no supplement, dry-rolled corn, and dried distillers grains; CON, DRC, and DDG, respectively) and finishing diet (steam-flaked corn based diet containing 0 or 35% DDG, SFC and 35DDG, respectively). Each yr, 60 preconditioned Hereford steers (initial BW = 198 kg ± 3) were stratified by BW and randomly assigned to one of 15 2.2-ha wheat pastures (4 steers/pasture). Supplements were assigned within 5 blocks of 3 pastures. Supplements were fed at 0.5% BW daily, pro-rated and delivered 6 d/wk. Following the grazing period, pastures within supplement treatment were randomly assigned to SFC or 35DDG. Steers were fed once daily ad libitum and pens of steers were harvested when estimated fat thickness reached 1.27 cm. A 3-way interaction between supplement, finishing diet, and yr was detected for HCW ($P = 0.08$) and carcass-adjusted total system weight gain ($P = 0.04$). Wheat pasture ADG was greater for DDG steers compared with CON and DRC steers ($P < 0.01$; 1.40, 1.30, and 1.29 kg/d for DDG, CON and DRC, respectively). With the exception of carcass-adjusted G:F for which DRC was greater than CON and DDG was intermediate ($P = 0.03$; 0.161 vs. 0.150, DRC and CON, respectively, 0.154 DDG), finishing performance and carcass traits were not affected by wheat pasture supplement ($P \geq 0.12$). Initial and final BW, DMI, and ADG were similar for SFC and 35DDG steers ($P \geq 0.20$). Steers receiving SFC had greater carcass-adjusted G:F ($P < 0.01$, 0.160 vs. 0.149), dressing percent ($P = 0.01$, 63.6 vs. 62.8), and twelfth rib fat thickness ($P < 0.01$, 1.27 vs. 1.12 cm) than 35DDG steers. The use of dried distillers grains as a supplement to wheat pasture results in greater ADG on wheat. However dried distillers grains included in steam-flaked corn based finishing diets appears to reduce G:F and dressing percent.

Key Words: dried distillers grains, stocker, finishing

199 Comparison of wheat or corn dried distillers grains with solubles on rumen fermentation and nutrient digestibility in feedlot heifers. L. J. Walter*[1], T. A. McAllister[2], W. Yang[2], K. Beauchemin[2], and J. J. McKinnon[1], [1]*University of Saskatchewan*, *Saskatoon, SK, Canada,* [2]*Agriculture and Agri-Food Canada Research Centre*, *Lethbridge, AB, Canada.*

A 5 × 5 Latin square design trial was conducted to evaluate rumen fermentation and apparent nutrient digestibility in 5 rumen cannulated heifers (420 ± 6 kg) fed diets supplemented with wheat (WDDGS) or corn (CDDGS) dried distillers grains with solubles. The composition of the control diet was 88.7% rolled barley grain, 5.5% supplement and 5.8% barley silage (DM basis). Treatments included replacement of barley grain at 20 or 40% of the diet DM with WDDGS or CDDGS. Contrasts included CDDGS vs. WDDGS; Control vs. CDDGS or WDDGS; 40% WDDGS vs. 40% CDDGS. Rumen pH, duration and area under pH curve thresholds of 5.8, 5.5 and 5.2 were not affected ($P > 0.05$) by treatment. WDDGS increased ($P \leq 0.05$) rumen NH_3-N levels relative to the control and CDDGS treatments, but decreased ($P = 0.04$) propionate relative to the control. Both DDGS sources increased ($P \leq 0.03$) rumen butyrate concentration and the digestibility ($P \leq 0.04$) of NDF, ADF and ADIN. WDDGS decreased ($P \leq 0.02$) DM and GE digestibility while CDDGS increased ($P \leq 0.001$) CP digestibility. With the exception of ADF ($P = 0.78$), feeding 40% WDDGS reduced ($P \leq 0.02$) nutrient digestibility relative to 40% CDDGS. Inclusion of WDDGS and CDDGS increased ($P < 0.001$) N and P intakes as well as excretion, with WDDGS having the greatest ($P < 0.001$) effect. Fecal N and P excretion was increased ($P < 0.001$) for WDDGS, but not for CDDGS ($P = 0.56$ and 0.27). Both DDGS sources resulted in higher ($P < 0.001$) urinary N and P output. Replacement of barley grain with up to 40% WDDGS or CDDGS did not mitigate rumen fermentation conditions associated with acidosis. CDDGS had the largest beneficial influence on apparent nutrient digestibility, while both DDGS sources altered the amount and route of N and P excretion.

Key Words: corn DDGS, wheat DDGS, nutrient digestibility heifers

200 Effects of wet distillers grains plus solubles concentration in steam-flaked corn-based finishing diets on nutrient digestibility. M. K. Luebbe*[1], K. H. Jenkins[1], J. Patterson[1], E. K. Buttrey[2], and J. C. MacDonald[1,3], [1]*Texas AgriLife Research*, *Amarillo*, [2]*Texas AgriLife Extension*, *Amarillo*, [3]*West Texas A&M University*, *Canyon*.

Six ruminally and duodenally cannulated crossbred steers (BW = 481 ± 18 kg) were used to determine effects of corn and sorghum based (<15% sorghum) wet distillers grains plus solubles (WDG) on nutrient digestibility. Seven periods consisted of 17 d of adaptation and 4 d collection of feces, duodenal and ruminal samples. Steers were fed twice daily in equal proportions. Fecal and duodenal samples were collected 3 times daily with sampling time advancing 1 h to represent every hour between feeding. Ruminal fluid samples were collected in the same manner with the addition of samples collected before feeding and 8 h post-feeding each d during the 4 d collection period. Wet distillers grains (0, 15, 30, 45, and 60% dietary inclusion; 0WDG, 15WDG, 30WDG, 45WDG, and 60WDG, respectively) replaced cottonseed meal, supplemental fat (yellow grease), urea, and steam-flaked corn (SFC). Additionally, a dry-rolled corn control diet (DRC) was included. Dietary fat was set at a minimum of 6.5% and alfalfa hay was included at 10% of diet DM. Contrasts included DRC vs. SFC, and linear and quadratic effects of WDG level. Average ruminal pH was not different ($P = 0.99$). Change in ruminal pH was lowest ($P < 0.01$) for the DRC treatment. Dry matter and OM intake were not different ($P > 0.15$) among WDG level. Intake of NDF linearly increased ($P < 0.01$) with WDG level. Starch intake responded quadratically ($P = 0.06$) with WDG level. Total tract DM, OM, and NDF digestibility decreased linearly ($P < 0.01$) with WDG level. Total tract starch digestibility responded quadratically ($P < 0.01$) with WDG level (98.1, 99.0, 98.6, 98.2, and 97.4%; 0WDG, 15WDG, 30WDG, 45WDG, 60WDG, respectively). Dry-matter, OM, and starch intake was not different ($P > 0.80$) for DRC and SFC whereas intake of NDF was greater ($P = 0.04$) for DRC compared with SFC. Total tract DM and OM digestibility was not different ($P > 0.45$) for DRC and SFC. Total tract starch and NDF digestibility were greater ($P < 0.01$) for SFC compared with DRC. Level of WDG concentration and corn processing method impacts nutrient intake and digestibility.

Key Words: wet distillers grains, digestibility, corn processing

201 Effects of wet distillers grains plus solubles concentration in steam-flaked corn-based finishing diets on performance and carcass characteristics of beef steers. M. K. Luebbe*[1], T. C. Davis[1], K. H. Jenkins[1], F. T. McCollum III[2], N. A. Cole[3], and J. C. MacDonald[1,4], [1]*Texas AgriLife Research*, *Amarillo*, [2]*Texas AgriLife Extension*, *Amarillo*, [3]*USDA-ARS*, *Bushland, TX*, [4]*West Texas A&M University*, *Canyon*.

Six hundred crossbred steers (365 ± 35 kg) were used in a randomized complete block design to determine effects of a corn and sorghum based (<15% sorghum) wet distillers grains plus solubles (WDG) on animal performance and carcass characteristics in steam-flaked corn (SFC) diets. Forty-eight pens were utilized resulting in 8 replications per treatment. Wet distiller′s grains (0, 15, 30, 45, and 60% dietary inclusion; 0WDG, 15WDG, 30WDG, 45WDG, and 60WDG, respectively) replaced cottonseed meal, supplemental fat (yellow grease), urea, and SFC. Additionally, a dry-rolled corn control diet (DRC) was included. Dietary fat was set at a minimum of 6.5% with supplemental fat from yellow grease. Alfalfa hay was included at 10% of diet DM. Contrasts included DRC vs. SFC, and linear and quadratic effects of WDG concentration. Final BW, ADG, G:F, HCW, and fat depth were greater ($P \leq 0.05$) for SFC than DRC. Dry-matter intake tended ($P = 0.06$) to be greater for DRC than SFC. Marbling score, dressing percent, and LM area were not different ($P > 0.40$) for DRC and SFC. Final BW, ADG, HCW, fat depth, and marbling score decreased linearly ($P < 0.01$) with WGDS inclusion level. Gain efficiency and DMI responded quadratically ($P < 0.01$) across WDG inclusion levels. Dressing percent tended to decrease linearly ($P = 0.07$) with WDG level and LM area was not different ($P = 0.31$) across WDG inclusion levels. Feeding SFC improved animal performance and carcass characteristics compared with DRC. The relative energy content of WDG in SFC-based diets appears to dilute the energy density of the diets and negatively impacts animal performance.

Table 1. Distillers grains and animal performance

Item	0WDG	15WDG	30WDG	45WDG	60WDG	DRC	SEM
Final BW, kg[a]	616	614	600	597	581	601	7
DMI, kg	11.3	11.5	11.5	11.4	10.5	11.7	0.2
ADG, kg[a]	2.05	2.02	1.91	1.89	1.75	1.92	0.05
G:F, g/kg[a]	182	176	166	166	167	163	3

[a]Calculated from HCW divided by a common dressing percentage of 63%.

Key Words: wet distillers grains, corn processing, finishing diets

202 Supplementing modified wet distillers grains with solubles to long yearling steers grazing native range. K. M. Rolfe*, W. A. Griffin, T. J. Klopfenstein, and G. E. Erickson, *University of Nebraska, Lincoln*.

A 2-yr study was designed to evaluate the effects of supplementing modified wet distillers grains with solubles (MDGS) to long yearling steers while grazing native range (warm season grass). Steers (n = 240; BW = 229 ± 16 kg) were backgrounded on cornstalk residue from late fall to mid-spring (144 d). While grazing cornstalks calves were supplemented 2.27 kg/steer daily of Sweet Bran. Following backgrounding steers were allowed to graze smooth bromegrass pastures for 21 d. After grazing smooth brome calves were weighed, stratified by BW, assigned randomly to summer grazing treatments, and relocated to graze Sandhills range. Summer grazing treatments included: grazing native range with no supplementation (CON); and grazing native range with MDGS supplementation at a level of 0.6% BW (SUPP). Modified wet distillers grains with solubles was fed daily on the ground. Steers were allowed to graze Sandhills range for the remainder of the summer grazing period (137 d) before entering the feedlot in early fall. Upon time of harvest cattle were serially slaughtered in 2 groups within each summer grazing treatment. At the time of summer treatment assignment, BW was not different between SUPP and CON steers ($P = 0.36$). However at feedlot entry, SUPP steers were 47 kg heavier ($P < 0.01$) than CON steers. Therefore, SUPP steers had 0.31 kg greater ($P < 0.01$) ADG than CON steers. Because SUPP steers were heavier than CON steers at feedlot entry, 24 fewer days on feed in the feedlot ($P < 0.01$) were required to achieve the same final BW ($P = 0.85$). Feedlot ADG and DMI were not different between SUPP and CON steers ($P > 0.47$). Similarly, HCW, LM area, and BF did not differ between the 2 summer grazing treatments ($P > 0.19$). These data show that MDGS can be fed on the ground, increase gains during summer grazing, and decrease days on feed in the feedlot.

Key Words: modified wet distiller grains, supplementation, yearling steer

203 Influence of feeding dried distillers grains plus solubles in potato byproduct-based finishing diets. J. I. Szasz*[1,4], D. S. Secrist[2], K. K. Karges[3], C. W. Hunt[1], K. A. Johnson[4], and T. N. Bodine[5], [1]*Univer-*

sity of Idaho, *Moscow,* [2]*Agri Beef Co.*, *Moses Lake, WA*, [3]*Poet Nutrition*, *Sioux Falls, SD*, [4]*Washington State University*, *Pullman,* [5]*Performix Nutrition Systems*, *Nampa, ID*.

One hundred 44 crossbred yearling beef steers (mean BW = 372 kg) were used in a randomized complete block study to evaluate the influence of dried distillers grain plus solubles (DDGS; 10, 20, 30, or 40%, DM basis) fed in place of dry-rolled corn in finishing diets containing wet potato byproduct. Pen served as the experimental unit. Steers were fed twice daily in equal proportions using a bunk management approach that minimized accumulation of refused diet. Final BW ($P = 0.05$), DMI ($P = 0.05$), ADG ($P = 0.07$), and HCW ($P = 0.02$) increased quadratically with DDGS level, reaching maximum (636, 11.7, 2.17, and 405 kg, for final BW, DMI, ADG, and HCW, respectively) at the 20% DDGS level. Dry feed conversion (DMI/ADG) increased ($P = 0.04$) linearly from 5.31 to 5.53 for 10 and 40% DDGS, respectively, and performance-based diet NEg tended ($P = 0.11$) to decrease linearly from 1.444 to 1.382 Mcal/kg for 10 and 40% DDGS, respectively. Similar responses were noted for carcass-adjusted performance, with the exception that dry feed conversion was not different between dietary treatments. Dressing percentage and percentage of cattle grading USDA Choice or Prime were similar between dietary treatments; although, marbling score increased ($P = 0.07$) quadratically with DDGS, reaching maximum (508) at the 20% DDGS level. Liver abscess incidence and other measures of performance were similar across dietary treatments. DDGS fed in place of dry-rolled corn improved ADG when fed up to 20% of the diet DM, yet negative effects on feed conversion were realized with increasing DDGS level. These results parallel findings from published trials where ADG was improved between 20 and 30% DDGS, but are in conflict with research demonstrating optimized feed conversion near 20% DDGS in the finishing diet. Future research should identify possibilities for this discrepancy as well as evaluate graded levels of DDGS in potato byproduct-based finishing diets containing more aggressively processed grain (e.g., high-moisture, steam-flaked).

Key Words: feedlot, distillers grains, finishing cattle

204 Effect of feeding modified distillers grains and wet corn gluten feed compared to forage on ruminal pH, intake and digestibility when adapting cattle to finishing diets. M. G. Dib*[1], G. E. Erickson[1], T. J. Klopfenstein[1], J. O. Sarturi[1], R. Lindquist[2], K. M. Rolfe[1], C. D. Buckner[1], and V. R. Bremer[1], [1]*University of Nebraska*, *Lincoln,* [2]*Archer Daniels Midland*, *Columbus, NE*.

A 39-d grain adaptation metabolism study was conducted comparing a combination of modified distillers grains plus solubles and wet corn gluten feed (BYP) fed at decreasing levels (87.5% to 35%) to a traditional grain adaptation (CON) with decreasing forage (45% to 7.5%). In both adaptation schemes, dry-rolled corn increased (up to 57.5%). Measurements included DMI, ruminal pH, ruminal H2S, and DM digestibility (DMD) for the first adaptation diet and the finishing diet. Six yearling steers (BW = 405 ± 20 kg) were assigned randomly to 1 of 2 treatments in a CRD with 3 steers per treatment (BYP and CON). Cattle were fed ad libitum once daily. Five adaptation diets were used to increase corn with diets fed 9, 7, 7, 7, and 9 d, respectively. The last 9-d period consisted of a common finishing diet containing the combination of gluten feed and distillers grains (30% of diet DM). Intake and pH (wireless pH probes) measurements were collected every minute during the entire study. Ruminal gas samples were collected 8 h post feeding on the last 2 d of each period, and H2S concentrations were analyzed. Data were analyzed using the GLIMMIX procedure of SAS. During adaptation, DMI expressed as % of BW tended ($P = 0.09$) to be greater for steers fed CON compared with BYP during the first period, but was not different in subsequent adaptation diets ($P > 0.20$). Average pH was lower ($P < 0.01$) for BYP on adaptation 1 and 2 compared with CON (5.76 vs. 6.18; 5.75 vs. 6.07, respectively). No difference ($P > 0.44$) was observed between treatments in ruminal pH for adaptation 3 and 4. Average pH was lower ($P < 0.01$) for CON on the last period when both treatments were being fed the same diet (5.61 vs. 5.80). Both adaptation methods resulted in safe ruminal pH (>5.6) and H2S concentrations (<36 µmol/L gas). No difference ($P > 0.15$) was observed for DMD between treatments. Results suggest that decreasing inclusion of a combination of distillers grains and gluten feed was as effective as the traditional method using forage for adapting feedlot cattle to high-concentrate diets.

Key Words: byproducts, grain adaptation, metabolism

205 Effects of wet distillers grain and a direct-fed microbial on finishing performance and carcass characteristics of beef steers fed a sorghum-based finishing diet. J. R. Jaeger*[1], J. W. Waggoner[1], K. C. Olson[2], J. W. Bolte[1], and S. R. Goodall[3], [1]*Western Kansas Agricultural Research Centers, Kansas State University*, *Hays*, [2]*Kansas State University*, *Manhattan*, [3]*Nova Microbial Technologies*, *Omaha, NE*.

Angus x calves (n = 406; initial BW = 441 ± 31 kg) were stratified by BW and ultrasonically measured longissimus muscle characteristics and assigned randomly to 1 of 4 ration treatments (4 pen replicates per treatment). Ration treatments were: 1) soybean meal protein supplement (CON); 2) control plus direct-fed microbial (CON+DFM); 3) wet distiller′s grain plus solubles (WDGS; 15% of diet DM); and 4) WDGS plus direct-fed microbial (WDGS+DFM). Steers were fed for 106 d before harvest. Longissimus muscle characteristics were measured ultrasonically on d 0 and 70 of the feeding period. Increase in backfat thickness was greater ($P < 0.01$) for steers receiving WDGS compared those receiving the control diet during the first 70 d on feed. In addition, increase in longissimus muscle depth was greater ($P < 0.01$) for cattle receiving DFM compared those receiving no microbial treatment. Change in marbling score was similar ($P = 0.44$) among treatments. Steer ADG during the entire feeding period was greater ($P < 0.01$) for WDGS than for CON (1.66 and 1.43 ± 0.02 kg/d, respectively). Likewise, harvest BW was greater ($P < 0.01$) for steers receiving WDGS compared with steers receiving the control diet. Carcass weight was greater in steers fed WDGS+DFM compared with WDGS, but was lower in steers fed CON+DFM compared with CON (WDGS × DFM; $P = 0.01$). Dressing percent and LM area were similar ($P > 0.30$) between treatments. USDA yield grade ($P = 0.41$) and quality grade ($P = 0.45$) were also similar among treatments with 69.0% of steers grading choice or better. Under the conditions of our study, these data were interpreted to suggest that sorghum-based feeding diets containing WDGS and a direct-fed microbial may improve finishing performance and carcass merit compared with diets containing no distiller′s grains. Further research is needed to elucidate optimal use conditions of direct-fed microbials in sorghum-based finishing diets.

Key Words: beef cattle, distillers grains, direct-fed microbial

206 Feeding *Lactobacillus acidophilus* combined with *Propionibacterium freudenreichii* to determine performance and carcass characteristics in feedlot heifers fed with or without wet distillers grains plus solubles. B. K. Wilson*[1], B. P. Holland[1], T. G. Nagaraja[2], and C. R. Krehbiel[1], [1]*Oklahoma State University*, *Stillwater,* [2]*Kansas State University*, *Manhattan*.

Increasing corn prices related to increased ethanol production have had a significant impact on the cost of gain for cattle producers who rely on

corn-based diets, and the inclusion of wet distiller's grains plus solubles (WDGS) in feedlot diets has become a common practice in many regions of the US In addition, direct-fed microbials (DFM) have been shown to improve ADG and feed efficiency, alter ruminal fermentation, and decrease fecal shedding of harmful pathogens in feedlot cattle. The objective of this experiment was to evaluate the effects of *Lactobacillus acidophilus* (LA) combined with *Propionibacterium freudenreichii* (PF) on performance and carcass characteristics in feedlot heifers fed with or without WDGS. Crossbred heifers (n = 288; initial BW = 295 ± 28 kg) were assigned to 1 of 4 treatments in a randomized complete block design with a 2 × 2 factorial arrangement of treatments. Across the feeding period, heifers fed 30% WDGS tended ($P = 0.09$) to have greater ADG and had greater carcass-adjusted ADG ($P = 0.05$) compared with heifers fed dry-rolled corn. Dry matter intake was not affected ($P = 0.65$) by diet, although carcass adjusted F:G tended ($P = 0.08$) to be improved for heifers fed WDGS. Heifers fed 30% WDGS tended ($P \leq 0.10$) to have greater fat thickness at the 12th rib, lower marbling scores, and higher yield grades. The inclusion of LA combined with PF in the diet had no effect ($P > 0.10$) on performance or carcass merit in the present experiment. Feeding 30% WDGS to feedlot heifers improved animal performance. Similar results can be anticipated when a DFM is included in the diet.

Key Words: beef cattle, direct-fed microbials, wet distillers grains plus solubles

207 Growth performance of finishing steers fed dry or wet distillers grains plus solubles differing in sulfur content. J. O. Sarturi*, G. E. Erickson, T. J. Klopfenstein, J. T. Vasconcelos, W. A. Griffin, and J. R. Benton, *University of Nebraska*, *Lincoln*.

A finishing study was conducted to determine the effect of dietary sulfur on beef cattle finishing diets formulated with wet or dry distillers grains with soluble (DGS). Sulfur concentration in DGS was either 0.82 or 1.16% and similar between wet or dry DGS. Steers (n = 120, BW = 345 ± 34kg) were assigned to 1 of 13 treatments in a RCBD (9 steers/diet, except 12 steers for control) and fed for 151 d. Cattle were fed ad libitum once daily using Calan individual bunks. Treatments were designed with 3 DGS inclusion (20, 30, and 40%), fed either wet or dry that consisted of low or high sulfur concentration in DGS as a 3 × 2 × 2 factorial. A corn control diet was included resulting in a 3 × 2 × 2 +1 treatment design. All diets contained 15% corn silage, 5% supplement and a blend (60:40) of high-moisture and dry-rolled corn. Initial BW was based on weighing 3 d following a limit-feeding period of 5 d at 2% of BW. Final BW, ADG, and G:F were based on HCW using a 62% dressing percentage. Data were analyzed using the GLIMMIX procedures of SAS as a 3 × 2 × 2 factorial. Orthogonal contrasts were used for comparing DGS to the control diet. Intake linearly increased ($P = 0.02$) when dry 0.82% S DGS was included in the diet, but DMI was not affected when wet 0.82% S DGS was fed. When wet and dry 1.16% S DGS was added, DMI decreased linearly ($P < 0.01$) and quadratically ($P < 0.01$), respectively. Gain decreased linearly ($P = 0.02$) as wet DGS that was 1.16% S increased in the diet. Other diets did not result in a similar pattern. Steers fed wet DGS had improved G:F with similar ADG. A quadratic response ($P < 0.05$) was observed for G:F when wet DGS increased in the diet, with the greatest values at 20 and 30%, regardless of sulfur content. A linear ($P < 0.05$) decrease was observed for HCW and fat thickness as wet and dry 1.16% S DGS increased in the diet, while no changes were observed for wet and dry 0.82% S DGS diets. High sulfur DGS reduces DMI, ADG, and G:F when fed at high levels in beef cattle finishing diets, but depends on whether fed wet or dry.

Key Words: distillers grains plus solubles, feedlot cattle, sulfur

208 Comparing dry, wet, or modified distillers grains plus solubles on feedlot cattle performance. B. L. Nuttelman*, W. A. Griffin, J. R. Benton, G. E. Erickson, and T. J. Klopfenstein, *University of Nebraska, Lincoln*.

A finishing experiment was conducted to compare dry, wet, and modified (partially dried) distillers grains plus solubles. Crossbred, yearling steers (n = 440; initial BW = 353 ± 20 kg) were utilized in a RCBD with steers stratified within block, and assigned randomly to one of 55 pens (8 steers/pen). Pens were assigned randomly to one of 10 treatments as a 3x3+1 factorial. Diets contained 3 inclusions (20, 30, or 40%) of 3 different types: wet distillers grains plus soluble (WDGS, 34.8% DM), modified distillers grains plus soluble (MDGS, 50.6% DM), or dried distillers grains plus soluble (DDGS, 91.4% DM). The 0% inclusion, corn control was repeated within replication (10 replications) whereas all other treatments had 5 replications. Basal ingredients consisted of high-moisture and dry-rolled corn fed at a 60:40 ratio (DM basis), 15% corn silage, and 5% dry supplement (DM basis). No interactions between type and inclusion were observed ($P > 0.16$) for any variables. No difference was observed in ADG ($P = 0.30$) between WDGS, MDGS, or DDGS. Steers fed WDGS had 0.73 and 1.04 kg/d less ($P < 0.01$) DMI than MDGS and DDGS, respectively. Steers fed WDGS (0.165) had greater G:F ($P < 0.01$) compared with steers fed MDGS or DDGS (0.158 or 0.150, respectively). Cattle fed MDGS tended ($P = 0.06$) to have greater G:F than steers consuming DDGS. Type had no impact ($P > 0.15$) on carcass traits. A linear increase ($P = 0.01$) in DMI, quadratic response ($P = 0.04$) in ADG, and a linear increase ($P < 0.01$) in G:F were observed as distillers grains increased from 0 to 40%. Generally, ADG and G:F increased from 0 to 20% inclusion and little change from 20 to 40% inclusion. Increased levels of distillers grains increased HCW quadratically ($P = 0.05$) and increased fat depth ($P < 0.01$). Based on G:F, the feeding value of WDGS was 35.4 and 17.8% greater than DDGS and MDGS, respectively. Feeding value of WDGS, MDGS, and DDGS were 45.7, 26.5, and 9.3% greater than corn-based diets when included at 20, 30, or 40% of the diet DM, respectively.

Key Words: dried distillers grains plus solubles, finishing cattle, wet distillers grains plus solubles

209 Dietary saturated fatty acid source and parity influence lactational performance of early lactation Holstein dairy cows. M. Hollmann* and D. K. Beede, *Michigan State University*, *East Lansing*.

Dietary coconut oil (CO), a source of saturated, predominantly medium-chain fatty acids (FA), reduced enteric methane emission, but also reduced DMI and milk yield in our earlier studies. Here, we examined lactational performance of early lactation cows fed 2 sources of saturated FA, differing in predominant chain lengths. Dietary treatments were: no added fat (CTRL); 2.7% of DM as saturated long-chain FA (Energy Booster 100; EB) or 2.7% CO; or, a 2.7% mixture of equal parts EB and CO (INT). Primiparous (PP; n = 31) and multiparous (MP; n = 36) Holstein cows 10 to 14 d postpartum were fed one of 4 treatments for 16 wk in a randomized complete block design. CTRL diet contained corn and alfalfa silages (53% of DM), dry ground corn, soybean meal, plus mineral and vitamin supplement; it was formulated to contain 26.5% NDF (83% from forages), 17.6% CP, 29.6% starch, and 3.6% fat. Milk yield and DMI were recorded daily, and blood was collected weekly. Main effects of diet, parity, time (repeated measures), and relevant interactions were tested by least-squares ANOVA. Reported values differed ($P < 0.05$). Overall, cows fed CTRL had the greatest DMI. Fat source with greater chain length increased DMI linearly for MP cows (CO: 22.7; INT: 24.7; EB: 27.0 kg/d), and quadratically for PP cows (18.5; 21.0; 20.3 kg/d). Similar interactions of treatment by parity were observed for yields of solids-corrected milk and milk components. CO reduced milk fat (3.1%) and lactose (4.73%) concentrations compared with EB (3.8% and 4.92%), pooled across time and parity. Plasma glucose concentration did not differ among fat treatments and CTRL across the 16 wk. Fat source interacted with parity; INT had the lowest glucose concentration for PP, but highest for MP. During wk 1 to 4 of study, MP had lower plasma glucose than PP (52 vs. 58 mg/dL), which coincided with greater plasma BHBA (7.0 vs. 4.8 mg/dL) and NEFA (710 vs. 380 μeq/L) concentrations in MP. Body condition loss through wk 4 was greater for CO and CTRL than for INT and EB. Overall, dietary CO reduced DMI compared with EB leading to a greater FA mobilization in early lactation.

Key Words: dairy cow, fatty acid, metabolism

210 Adaptations in the transcriptome of adipose tissue in transition dairy cattle. S. Rocco[1], G. Duncan[1], J. Loor[2], J. Vierck[1], and J. P. McNamara*[1], [1]*Washington State University*, *Pullman,* [2]*University of Illinois*, *Urbana*.

Metabolic adaptations in adipose tissue are a critical part of establishment and maintenance of lactation. Our objective was to determine changes in the transcriptome of adipose tissue during the transition period. A total of 48 cows were grouped by their sire PTAM: High Genetic (PTAM = 870 kg), or Low Genetic (PTAM = 378); and half of each group was fed either to requirements (NE) or to 90% of energy requirements (LE), other components fed to requirements. Feed intake from 21 to 1 d prepartum was 13.6 (NE) and 12.7 kg (LE) DMI/d for (SE = 1.5): from 1 to 56 DIM it was 21.2 and 17.4 kg/d (SE = 1.4). Milk production was 36.1 and 33.3 kg/d for HG and LG cows from 27 to 56 DIM ($P < 0.05$). Adipose tissue biopsies at −21, −7, 7, 28 and 56 d around parturition extracted from a subset of these animals and the transcriptome was determined using the Affymetrix Bovine Gene Array on a subset of 21 animals and a total of 28 arrays. Analysis was done using standard array statistical techniques and pathway analysis. Further analysis and pathway analysis were conducted on genes that changed at least 2-fold with a *P*-value of 0.05) Genes that code for enzymes in the anabolic pathways (lipid uptake and synthesis) were consistently decreased to only 20 to 50% of prepartum, including thyroid hormone receptor spot 14, lipoprotein lipase, ATP-citrate lyase, acetyl-CoA carboxlyase and other genes in that pathway. Genes that code for enzymes involved in lipolysis (hormone sensitive lipase, β-2 adrenergic receptors, perilipin) were either unchanged or only moderately increased. Genes involved in synthesis of cellular components and cell cycle control (PPAR gamma, ADFP, ribosomal proteins) were highly expressed and slightly elevated in early lactation. Additional canonical pathways including cell morphology, intercellular signaling, connective tissue synthesis, and disease states all showed changes during the early lactation period. These data can be used to help understand the myriad of changes as cows rapidly lose body fat and can be integrated into systems models for dairy cattle metabolism and health.

Key Words: adipose, transcriptome, lactation

211 Use of omega-3 fatty acid rich algae and their oil as a feed supplement for dairy cattle. J. A. Stamey*[1], D. M. Shepherd[1], M. J. de Veth[2], and B. A. Corl[1], [1]*Virginia Polytechnic Institute and State University*, *Blacksburg,* [2]*Balchem Corp.*, *New Hampton, NY*.

Fish oil is used as a ration additive to provide omega-3 (n-3) fatty acids to dairy cows. Fish do not synthesize n-3 fatty acids; they must consume microscopic algae or other algae-consuming fish. New technology allows for the production of algal biomass for use as a ration supplement for dairy cattle. Lipid encapsulation of the algal biomass allows n-3 fatty acids to remain inert in the rumen, avoid biohydrogenation, and be available for absorption and utilization. Our objective was to examine use of algal biomass as a source for n-3 fatty acids. Four late-lactation Holsteins were assigned to a 4 × 4 Latin Square design. Their rations were supplemented with 1X or 0.5X rumen protected (RP) algal biomass supplement, 1X RP algal oil supplement, or no supplement. Supplements were lipid encapsulated (Balchem Corp., New Hampton, NY). The 1X supplements provided 29 g/d docosahexaenoic acid (DHA) and 0.5X provided half of this amount. Treatments were analyzed by orthogonal contrasts. Supplementing dairy rations with rumen protected algal supplements did not affect feed intake, milk yield, or milk composition ($P > 0.05$). Milk fat yield was 1.0, 1.1, 1.0, and 1.0 ± 0.07 kg/d for cows fed control, 0.5X RP algae, 1X RP algae, and 1X RP oil, respectively. Short- and medium-chain fatty acid yields were not influenced by supplements ($P > 0.05$). Both 0.5X and 1X RP algae supplements increased ($P < 0.01$) daily milk fat yield of DHA (0.5 and 0.6 ± 0.10 g/d, respectively) compared with 1X RP oil (0.3 ± 0.10 g/d), but all supplements were greater ($P < 0.01$) than control (0.1 ± 0.10 g/d). Yield of trans-18:1 fatty acids in milk fat was also increased by supplementation, suggesting supplements may have influenced rumen microflora. Trans-11 18:1 yield (13, 20, 27, and 15 ± 3.0 g/d for control, 0.5X RP algae, 1X RP algae, and 1X RP oil, respectively) was greater for supplements than control ($P = 0.05$). Rumen protected algal biomass provided better DHA yield than algal oil.

Key Words: micro-algae, n-3 fatty acid, rumen protection

212 Additive effects of propionate, trans10,cis12-CLA and acetate on milk fat production and composition in dairy cows. G. Maxin*[1], H. Rulquin[1], J. L. Peyraud[1], and F. Glasser[2], [1]*INRA-Agrocampus ouest*, *Rennes, France*, [2]*INRA*, *Theix, Saint-Genes-Champanelle, France*.

Several nutrients affect dairy cow mammary lipogenesis and thus milk fat production and composition. The individual effects of these nutrients have been long studied by digestive infusions, but it is still not known whether they are additive or interactive. The present study aims to investigate the effects on milk fat secretion of 3 of these nutrients: propionate (C3), acetate (C2) and trans10,cis12-CLA, supplied alone or together to dairy cows. Six Holstein cows were used in a 6 × 6 Latin square design with 14-d periods. The treatments were: control; C2 (ruminal infusion of 1500 g/d of C2); C3 (ruminal infusion of 800 g/d of C3); CLA (duodenal infusion of 1.60 g/d of trans10,cis12-CLA); C2+C3 (ruminal infusion of 400 g/d C3 + 750 g/d C2); and CLA+C3 (ruminal infusion of 800 g/d C3 + duodenal infusion of 1.60 g/d trans10,cis12-CLA). Milk yield and composition were measured at each milking and milk fatty acids (FA) at the end of each period. Compared with control, C3 and CLA decreased milk fat content and yield by 9% and 15% on average ($P < 0.05$). C2 tended to increase milk fat content ($P = 0.08$), but did not alter milk fat yield. CLA decreased the yields of all milk FA, except trans10,cis12-CLA, which increased. C3 decreased the yields of all even-chain FA ($P < 0.05$) and increased the yields and percentages of the odd-chain FA (C5 to C17, $P < 0.05$). C2 did not modify the secretion of the FA, except C16, which sharply increased ($P < 0.01$). The interactions between C3 and C2, and C3 and CLA on all the variables measured were never significant ($P > 0.15$), whatever the nutrient individual effects. When the 2 nutrients had the same individual effects, their effects added up when infused together (e.g., CLA+C3 on milk fat content); when they had opposite effects, there was compensation (e.g., C2+C3 on milk fat content). Under our experimental conditions, C2 and C3, and C3 and trans10,cis12-CLA had thus additive effects on mammary lipogenesis.

Key Words: dairy cows, milk fat, nutrients

213 Regulation of adipose tissue metabolism by coordinated changes in gene transcription during the transition period. S. Rocco*, G. Duncan, J. Kay, R. Bose, J. Vierck, and J. McNamara, *Washington State University*, *Pullman*.

Metabolic adaptations in adipose tissue are a critical part of establishment and maintenance of lactation. Adipose tissue not only stores and releases energy but also secretes a metabolic regulators and cytokines. Previous work determined that several enzymes and pathways adapt in a coordinated fashion to support establishment and success of lactation. Our objective was to identify specific changes in gene transcription that relate to adaptations in lipogenesis and lipolysis in the adipose tissue of transition dairy cattle. A total of 48 cows were grouped by their sire PTAM: High Genetic (PTAM = 870 kg), or Low Genetic (PTAM = 378); and half of each group was fed either to requirements (NE) or to 90% of energy requirements (LE), other components fed to requirements. Feed intake from 21 to 1 d prepartum was 13.6 (NE) and 12.7 kg (LE) DMI/d for (SE = 1.5): from 1 to 56 DIM it was 21.2 and 17.4 kg/d (SE = 1.4). Milk production was 36.1 and 33. Three kg/d for HG and LG cows from 27 to 56 DIM ($P < 0.05$). Adipose tissue biopsies at −21, −7, 7, 28 and 56 days around parturition were used to measure lipolysis, lipogenesis and gene expression by RT-PCR or gene array chips. Rates of lipogenesis were lower during lactation and lower in LE cows while lipolysis rates were higher for both conditions ($P < 0.05$). The mRNA expression of the beta-2 adrenergic receptor, hormone sensitive lipase and the co-lipase, perilipin, was several-fold higher ($P < 0.05$) in animals on restricted energy. The mRNA for caveolin-1 and caveolin-2 decreased 20 to 40% ($P < 0.05$) in lactation consistent with the increase in lipolysis and HSL activity. The gene expression array showed coordinated decreases in genes regulation lipogenesis (TRPSP14, −26%; AcCoCarb, −76%; LPL, −57%; ATP-Citrate Lyase, −22% (<0.05) as examples) and no change or moderate increases in those controlling lipolysis. Lactation is supported by coordinated change in gene expression and metabolic rates in adipose over varied dietary and genetic situations.

Key Words: lactation, adipose, regulation

214 Effects of dietary protein concentration and coconut oil supplementation on nitrogen utilization and production in dairy cows. C. Lee*, A. N. Hristov, K. S. Hyler, T. W. Cassidy, and M. Long, *Pennsylvania State University*, *PA*.

The objective of this experiment was to investigate the effect of dietary protein concentration and coconut oil (CO) on N utilization in lactating dairy cows. The experiment was conducted for 10 wks with 36 cows (132 ± 7.0 DIM; 13 primiparous and 23 multiparous) including 6 cannulated cows. Following a 2–wk covariate period, cows were blocked based on DIM and milk yield (average: 38.4 ± 1.2 kg/d) and assigned to the following treatments: 16% CP (DM basis, HighCP, control), 14% CP (LowCP) and 14% CP diet supplemented with 600 g/cow/d coconut oil (LowCPCO). The HighCP and LowCP diets contained 2.5% (DM basis) Megalac. Samples (ruminal fermentation, nutrients digestibility, N losses, and milk production) were collected at wks 5, 6, 7 and 8 of the trial. Compared with LowCP and HighCP, LowCPCO decreased DMI (21.5 vs. 23.7 and 24.7 kg/d; $P < 0.003$), milk yield (34.7 vs. 36.5 and 39.7 kg/d, $P = 0.01$) and milk fat content (3.1 vs. 3.6 and 3.7%; $P = 0.001$) and yield (1.1 vs. 1.3 and 1.4 kg/d; $P < 0.001$, respectively). Milk protein content and yield were not affected by diet. Compared with HighCP, the LowCP diet decreased milk yield (39.7 vs. 36.5; $P = 0.04$). Apparent digestibilities of DM, OM, NDF, ADF and N were greater ($P = 0.03$ to < 0.001) for HighCP compared with LowCP and LowCPCO. Ruminal ammonia ($P = 0.03$), blood urea–N ($P < 0.001$) and milk urea–N ($P < 0.001$) were increased by HighCP compared with LowCP and LowCPCO. Urinary N excretion was greater ($P < 0.001$) for HighCP compared with LowCP and LowCPCO. Cows fed the LowCPCO diet had lower ($P = 0.001$) fecal N excretion compared with the other diets and the highest ($P < 0.001$) milk N efficiency (36%) followed by LowCP (32%) and HighCP (28%). In conclusion, the 14% CP diet decreased urinary N losses and increased feed N efficiency, but decreased milk yield. Coconut oil supplementation decreased feed intake and milk yield, but increased feed N utilization efficiency compared with the control and LowCP diets.

Key Words: dietary protein, coconut oil, dairy cow

215 The effect of feeding ruminally protected lysine (RPL) on production performance and plasma amino acid profile of early lactation dairy cattle. J. E. Nocek*[1] and I. Shinzato[2], [1]*Spruce Haven Farm and Research Center*, *Auburn, NY*, [2]*Ajinomoto Co., Inc.*, *Tokyo, Japan*.

Thirty-six lactating Holstein cows were used to examine the effects of ruminally protected lysine (RPL) supplementation and dosage on production performance and plasma amino acid profile of high-producing dairy cows. Multiparous cows were balanced across treatments based on their 4 week of lactation average milk production as follows: Control, 75, 150, 225 g/d of RPL. These treatments were designed to deliver 0, 12, 24 and 36 g/cow/d of supplemental intestinally available lysine, respectively. Cows started the experimental period on the fifth week post-calving and remained on treatment for 4 weeks. Prior to treatment administration, all cows received the control diet for one week, which contained 75% of forage from corn silage. Control diet was fed to all cows throughout the experimental period, however, in addition, cows

received 500 g/d of corn meal premix top dressed once daily to deliver 0, 75, 150 or 225 g/d of RPL. Blood samples were taken for each cow before daily feeding on d 0 and 28 of the study for amino acid analysis. Dry matter intake was not affected by RPL dose when expressed as a percentage of body weight. Mean milk yield was the highest ($P < 0.03$) for cows receiving 150g RPL than Control or 225g RPL, with 75g RPL not being different than others (47.7, 43.2, 42.7 and 44.6kg, respectively). FCM was higher ($P < 0.05$) for cows receiving 75g RPL compared with control. Fat % was higher ($P < 0.05$) for 75g and 225g RPL compared with Control and 150g RPL, whereas protein %, lactose, MUN, and SCC were not affected by RPL dose. Protein yields, however, were the highest ($P < 0.01$) for 150g RPL and the lowest for 225g RPL. At 28d, plasma lysine showed a numeric tendency to be the lowest for 150g and the highest for 225g RPL, with 225g RPL having a 17.6% increase ($P = 0.12$) from d 0 to 28. Under the conditions of this study, 75g or 150g RPL provided the most efficient and consistent response in production performance of early lactation dairy cows.

Key Words: ruminally protected lysine, milk production, plasma AA

216 Effect of Protein Edge on ruminal microbial protein production and performance of lactating dairy cows. S. E. Boucher*[1], H. M. Dann[1], K. W. Cotanch[1], C. S. Ballard[1], R. J. Grant[1], and K. Yagi[2], [1]*William H. Miner Agricultural Research Institute*, *Chazy, NY,* [2]*ZEN-NOH National Federation of Agricultural Co-operative Associations*, *Tokyo, Japan*.

Sixteen lactating Holstein cows (4 ruminally cannulated; mean ± SD) 95 ± 17 d in milk were used in a 4 × 4 replicated Latin square design with a 2 × 2 factorial arrangement of treatments to determine the effects of Protein Edge (PE; Agriformulations, Inc., Waddington, NY) supplementation of diets varying in rumen undegraded protein (RUP) content on ruminal microbial protein production, ruminal fermentation, and lactation performance. Protein Edge is a blend of bacterial and fungal fermentation extracts that was reported previously to increase microbial protein production in vitro. The RUP content of the diets was either 36 (LoRUP) or 40% (HiRUP) of crude protein (CPM v.3.0), and PE was added at 0.11% of dry matter (DM). Treatments were: 1) no PE, LoRUP, 2) PE, LoRUP, 3) no PE, HiRUP, and 4) PE, HiRUP. Experimental periods were 21 d with a 15-d adaptation. Microbial protein production was estimated via urinary excretion of purine derivatives. Data were analyzed using the MIXED procedure of SAS. There was no effect of PE or RUP level ($P > 0.10$) on ruminal pH (mean ± SE; 6.0 ± 0.2) or ruminal concentrations of NH_3-N (9.0 ± 0.8 mg/dL), total free AA (2.2 ± 0.22 m*M*), or total VFA (135.6 ± 3.6 m*M*). Protein Edge increased ruminal microbial protein production ($P < 0.01$) with the no PE and PE diets averaging 527 ± 20 and 557 ± 20 g of microbial N/d, respectively. Protein Edge tended ($P = 0.07$) to increase milk yield (MY; no PE = 51.5 ± 1.7 and PE = 52.3 ± 1.7 kg/d). However, there was no effect of PE or RUP level ($P > 0.10$) on DM intake (26.2 ± 0.4 kg/d), fat-corrected MY (49.4 ± 1.6 kg/d), milk component yields or content, feed efficiency (1.99 ± 0.06), or feed-N efficiency (0.34 ± 0.01). Other than a trend for a slight increase in MY, there were no effects of PE on lactation performance. However, PE may be a useful additive to increase metabolizable protein supply because PE increased ruminal microbial protein production.

Key Words: Protein Edge, microbial protein production, lactating cows

217 Use of plasma concentrations to estimate bioavailability of methionine in rumen-protected products fed to dairy cows. G. A. Broderick*[1], S. M. Reynal[2], R. A. Patton[3], W. Heimbeck[4], and P. Lodi[5], [1]*U.S. Dairy Forage Research Center*, *Madison, WI*, [2]*University of Wisconsin*, *Madison*, [3]*Nittany Dairy Nutrition, Inc.*, *Mifflinburg, PA*, [4]*Evonik Degussa GmbH*, *Hanau, Germany*, [5]*Universidad Nacional de Rosario, Argentina*, *Rosario, Argentina*.

Plasma AA level was used to estimate Met bioavailability in 2 sources of rumen-protected Met (RPM): Mepron (RPM1) and Smartamine M (RPM2). Eight cows consuming 22 kg DM/d, yielding 34 kg milk/d and fitted with ruminal cannulas were fed a basal TMR containing (DM basis) 14% alfalfa silage, 54% corn silage, 7% grass hay, 9% ground shelled corn, 13% soybean meal, 3% additives, 15.7% CP and 36% NDF. The TMR were fed at 6-h intervals in 4 equal portions each day. For the calibration phase, cows were blocked by DIM into 2 squares and randomly assigned to balanced 4 × 4 Latin squares with 3-d periods. Solutions of DL-Met were infused into the abomasa via tubes inserted through the ruminal cannulas and omasal orifice to provide 0, 8, 16 and 24 g Met/d. Amounts actually infused were measured daily. Blood samples were collected from alternate jugular veins every h over the last 6 h of the 3-d period. Blood plasma was deproteinized and stored at –20°C until analyzed. For the feeding phase, cows were re-randomized within square and assigned to 4 treatments: 0.24 g Met/d fed as 28.2 g/d of RPM1 or 31.6 g/d of RPM2, or 24 g DL-Met infused into the abomasum. Both RPM1 and RPM2 were fed 4x daily by hand mixing 1/4 the daily dose into the TMR. Design and blood sampling were the same as the calibration phase except periods were 7-d; abomasal Met infusion was for the last 72 h of each period. Plasma Met (PMet) concentrations were determined by ion-exchange chromatography with ninhydrin detection. Plasma Met concentration was regressed on Met infusion levels using Proc GLM in SAS to develop the response curve used to estimate Met bioavailability after correction for recovery of DL-Met infused during the feeding phase. The regression equation from the calibration phase was: Plasma Met (μM) = 0.498*Met infused (g/d) + 3.42 μ*M* ($P < 0.0001$; $r^2 = 0.533$). Rearranging and applying this equation yielded a mean recovery of infused Met of 95%. Mean (±SE) bioavailabilities, corrected to 100% recovery of infused Met, were 75 (±20)% for RPM1 and 88 (±23)% for RPM2. These bioavailabilities were not different ($P = 0.51$) within the precision of this study.

Key Words: methionine, rumen-protection, blood

218 Evaluation of a ruminally protected lysine product to increase milk protein production and plasma lysine concentration. S. E. Boucher*[1], H. M. Dann[1], K. W. Cotanch[1], C. S. Ballard[1], R. J. Grant[1], and I. Shinzato[2], [1]*W.H. Miner Agricultural Research Institute*, *Chazy, NY*, [2]*Ajinomoto Co., Inc.*, *Tokyo, Japan*.

Fifteen multiparous Holstein cows (mean ± SD) 122 ± 38 d in milk were used in a replicated 3 × 3 Latin square design to evaluate the efficacy of a ruminally protected Lys (RPL; Ajinomoto Co., Inc.) product to increase milk protein production and plasma Lys concentration. Experimental periods were 21 d with a 15-d adaptation. Dietary treatments were 1) control diet adequate in metabolizable protein (MP)-Lys, 2) diet deficient in MP-Lys, and 3) Lys deficient diet made adequate in MP-Lys with RPL. The RPL was assumed to contain 20% bio-available Lys and was added to the Lys deficient diet at 0.65% of dry matter (DM). The basal diets contained 50% forage and 50% concentrate. The MP-Lys contents of the Lys adequate, Lys deficient, and RPL diets were 6.5, 5.7, 6.7%, respectively, and the MP-Met content of the diets was 2.3% (CNCPS v.6.1; AMTS.Dairy, AMTS LLC, Cortland, NY). Cows were fed once and milked 3 times daily. Milk samples were collected from 3 consecutive milkings on d 18 and 19 of each period. Blood was collected on d 19 and 20 of each period at 2, 4, 6, and 8 h after feeding and compos-

ited by cow and period for AA analysis. Data were analyzed using the MIXED procedure of SAS. There was no effect of diet on DM intake (mean ± SE; 29.6 ± 0.76 kg/d), milk yield (49.9 ± 1.64 kg/d), milk fat % (3.71 ± 0.12%), milk fat yield (1.85 ± 0.07 kg/d), milk true protein (TP) % (3.19 ± 0.04%), or milk TP yield (1.59 ± 0.06 kg/d). There was an effect ($P < 0.001$) of diet on plasma Lys concentration (% of total plasma AA) with the Lys adequate diet resulting in the highest (4.27 ± 0.06%), the RPL diet was intermediate (3.74 ± 0.06%), and the Lys deficient diet was the lowest (3.52 ± 0.06%). Based on the plasma data, the Lys adequate diet and RPL increased MP-Lys supply compared with the Lys deficient diet. However, improved MP-Lys supply did not result in increased milk protein production in this experiment.

Key Words: ruminally protected lysine, milk protein, plasma lysine

219 Effect of rumen-protected lysine and methionine on lactating performance in lactating water buffalo. C. X. Zou*[1], Q. F. Tang[2], G. S. Qin[1], B. Z. Yang[1], S. L. Li[1], S. J. Wei[1], K. Liang[1], L. L. Li[1], X. W. Liang[1], and Z. S. Xia[2], [1]*Buffalo Research Institute*, *Nanning 530001, China*, [2]*College of Animal Science, Guangxi University*, *Nanning 530005, China*.

The present experiment was undertaken to determine the effects of RPLys (rumen protected lysine) and RPMet (rumen protected methionine) supplements on lactating performance in lactating water buffalo. Fifteen early lactation, healthy lactating water buffaloes were selected, according to species, last lactation milk yield, calving time and similar parity. Animals were randomly divided into 5 group, using 5 × 5 Latin square design with 5 periods and 5 treatments, i.e., the control group1 (basal diet CP = 16%), the control group2 (basal diet CP = 20%), treatment 1: basal diet CP = 16% plus RPLys 40g/d; treatment 2: basal diet CP = 16% plus RPMet 15g/d; treatment 3: basal diet CP = 16% plus RPLys30 g/d plus RPMet 6 g/d. The results showed: (1) Effect of RPLys and RPMet supplements on lactating performance in lactating water buffalo showed non-significantly difference ($P > 0.05$), but RPLys and RPMet supplements could improve lactating performance in lactating water buffalo and RPLys was the better. Compared with control group1 and control group2, RPLys supplements increased milk yield by 10% and 5.9%. (2) Effect of RPLys and RPMet supplements on dry matter intake (DM) in lactating water buffalo showed non-significantly difference ($P > 0.05$), but RPLys and RPMet supplements could reduce dry matter intake (DM) in lactating water buffalo. (3) RPLys and RPMet supplements can improve milk protein, milk total solid matter, non-fat milk solid content and lactose content in lactating water buffalo, compared with control group1, milk protein of RPLys, RPMet and RPLys+ RPMet supplements increased by 29%, 36.8% and 54.3% ($P < 0.05$), compared with control group2, Milk protein increased by 3.9%, 10.2% and 24.4% ($P < 0.05$). Only RPLys supplements could increase milk fat in lactating water buffalo, and only RPMet supplements could improve milk fat in lactating water buffalo. Therefore, RPLys and RPMet supplements could improve lactating performance in lactating water buffalo.

Key Words: RPLys, RPMet, lactating water buffalo

220 Effect of rumen protected γ-aminobutyric acid on performance and health status of early lactating dairy cows. D. M. Wang, Z. Liu, F. Yang, H. Y. Liu, C. Wang*, Y. M. Wang, and J. X. Liu, *Institute of Dairy Science, Zhejiang University*, *Hangzhou 310029, P. R. China*.

The objective of this study was to investigate the effects of rumen-protected γ-aminobutyric acid (GABA) addition on DMI, milk performance, and plasma metabolites in Chinese Holstein dairy cows. Forty-eight cows (days in milk = 60 ± 5; average milk yield = 37.3 ± 5.4 kg/d) were blocked based on days in milk, milk production, and parity and were randomly assigned to one of 4 treatments. Dietary treatments were 4 adding levels of GABA: 0 (control), 30, 60, and 90 g/day, respectively. The experimental period was 7 weeks. Milk yield and milk composition (fat, protein, and lactose) were recorded weekly, and serum parameters of antioxidant status, neuropeptide Y, and GABA were analyzed on wk 1, 4, and 7. The DMI of grass hay was significantly higher ($P < 0.05$) in the GABA-added cows than those on control. Milk yield increased ($P < 0.05$) in 30 g GABA-added cows, but leveled off in 90 g GABA-added animals. Milk protein yield was higher ($P < 0.05$) when 30 or 60 g of GABA was added but there was no difference ($P > 0.05$) between control and 90 g GABA-added animals. Milk fat content was not different among treatments ($P > 0.05$). Serum glutathione peroxidase increased for 60 g group ($P < 0.05$), and serum malondialdehyde reduced for all GABA-added group ($P > 0.05$) compared with the control. No statistical difference was observed in the neuropeptide Y between all the treatments ($P > 0.05$). In summary, addition of rumen-protected GABA at 30 g could increase feed intake, improve milk performance, and is beneficial to the dairy cow health.

Key Words: γ-aminobutyric acid, dry matter intake, milk performance

ADSA-SAD Undergraduate Competition: Dairy Foods

221 Chocolate milk as a sports recovery drink. H. L. Weeks*, D. R. Winston, and R. E. James, *Virginia Polytechnic Institute and State University*, *Blacksburg*.

Exercise depletes muscle tissue of energy and the body of fluids and nutrients. Athletes constantly seek the best recovery drink following exercise. However, which is best? Milk, nature's most nearly perfect food, must be included in the debate. Water replaces fluids lost during exercise, but lacks protein, vitamins, and other nutrients that chocolate milk offers. Sports drinks, like Gatorade and Powerade, replace fluid losses from sweat and are a source of electrolytes and energy such as glucose. However, excess sugar in sports drinks is not easily digested immediately after exercise. Fortunately, casein protein in milk is easily digested. Milk also contains vitamins A, B2, B12, D and E. Tryptophan in milk helps produce serotonin to reduce stress and relax muscles. Calcium strengthens bones and helps to build muscle, useful after exercise when muscles are depleted of energy. Reduced-fat chocolate milk is superior to plain milk after exercise because it includes other factors, such as caffeine and sugars. Caffeine decreases fatigue and sugar is a source of energy. Two similar studies conducted with 9 trained cyclists show that endurance athletes, like long distance runners and cyclists, were able do to exercise longer before feeling fatigued. Both studies analyzed cyclists who worked until exhaustion, received one of 3 beverages during a 4-h rest period, and cycled again until exhaustion. Three cyclists were assigned to each beverage. Both studies used a fluid replacement drink (Gatorade) and a carbohydrate replacement drink (Endurox R4). One study used low-fat chocolate milk and the other whole chocolate milk, containing 2% and 3.5% fat respectively. Cyclists consuming low-fat chocolate milk became fatigued at the same time as cyclists consuming Gatorade. However, cyclists drinking chocolate milk in the second study easily exceeded the cycling time for athletes drinking Gatorade by 9 min and Endurox R4 by 11 min. Consuming reduced-fat chocolate milk after exercise is the best way to replenish fluids, carbohydrates and protein. Chocolate milk restores muscle tissue in endurance athletes better than water, sports drinks or plain milk.

Key Words: sports recovery, chocolate milk

222 Dairy foods and the prevention of childhood obesity. J. E. Anderson* and C. C. Williams, *Louisiana State University*, *Baton Rouge*.

For the past decade, overweight and obesity have been on the rise, with the most significant increase occurring in children and adolescents. Overweight and obesity are defined as body mass indexes (BMI) of ≥25 and ≥30, respectively. BMI is calculated using the equation weight/height^2, and the equation differs slightly for children. Overweight and obesity have also been shown to increase the possibility of certain diseases and health problems. The National Health and Nutrition Examination Surveys (NHANES; 1976–1980 and 2003–2006) show that for children aged 2–5 years, prevalence increased from 5.0% to 12.4%; for those aged 6–11 years, prevalence increased from 6.5% to 17.0%; and for those aged 12–19 years, prevalence increased from 5.0% to 17.6%. As a result, the National Dairy Council has partnered with the National Football League to start the Fuel Up and Play 60 program. This program incorporates good nutrition and physical activity to help children develop better lifelong habits. Studies have shown that inadequate consumption of nutrient-rich foods, specifically low-fat and fat-free dairy foods, fruits, and vegetables and whole grains, can contribute to obesity in young adults. Three to 4 servings of dairy products per day not only promote healthy bone development but may also aid in weight loss. So, stocking the refrigerator with milk, yogurt, and cheese may make it easier to lose weight without forfeiting calories necessary for proper growth and development in children and adolescents.

Key Words: dairy foods, childhood obesity

223 Understanding the ropy milk test. R. A. Russell* and C. D. Thompson, *University of Kentucky*, *Lexington*.

Ropy milk is a stringy or slimy condition of milk that is caused by bacteria that contaminate milk after leaving the udder. It also represents a source of much debate and controversy within the dairy industry with regard to the appropriateness of the test. The 2 most common bacteria believed to cause ropiness are *Alcaligenes viscolactis* and *Enterobacter aerogenes*. These bacteria are able to contaminate the milk because of improperly cleaned or sanitized areas. The bacteria can originate from both the farm and the plant. Ropiness in milk became a problem before 1920 and was resolved, but the problem has risen again in recent years. A trend to larger dairy farms is reported as one possible reason for ropiness because it takes more care and precaution to keep facilities clean. Another potential reason ropiness has reappeared is because of transporting milk longer distances. Ropiness appears in the milk about 12 h after it is removed from the cow. It normally occurs in pasteurized milk but is sometimes not observed because it is consumed before sufficient bacterial growth has taken place. While the milk may be thicker than usual, flavor does not differ. Another reason it may not be detected is that many of the organisms that cause ropiness grow slowly at refrigerated temperatures. Testing of milk for ropiness can be done by incubating a small sample of the milk at temperatures of 15 to 22°C for 24 to 36 h. After the allotted time, to test for ropiness, a wooden stick can be inserted into the milk looking for a stringy condition. Instead of using the wooden stick, the milk could also be slowly poured from the vial looking for strands of rope or slime. Bacteria that cause ropy milk have been found in bedding, cooling tanks, barnyards, pastures, pipe lines, and milk cans. These bacteria may originate from farms or milk plants. Thus, the key to keeping ropy milk from becoming a problem is proper cleaning and sanitizing of facilities. Controversy around the ropy milk test centers on concerns that the repeatability of the test, using clean equipment, has been low.

Key Words: ropy milk, ropiness, milk quality

224 Conjugated linoleic acid in milk is related to the diet of lactating dairy cows. H. L. M. Tucker* and E. L. Karcher, *Department of Animal Science, Michigan State University*, *East Lansing*.

Conjugated linoleic acid (CLA) is a naturally occurring fatty acid in milk that has beneficial human health properties. Researchers are interested in increasing *cis-9, trans-11* CLA in milk. Implications to enhance *cis-9, trans-11* CLA in milk are to decrease the risk of heart disease, cancer, and diabetes in humans. Sources of CLA include mixed grains, vegetable oils, and animal products. However, concentrations of CLA are higher in dairy products and products made from other ruminant animals (Beaulieu, 1998). Manipulation of the diet of dairy cows may be one way to increase concentrations of CLA in milk. The addition of 0.5% fish oil and 2.5% oil from extruded soybeans to the diet of lactating dairy cows caused a 3.5-fold increase of *cis-9, trans-11* CLA in milk fat

(AbuGhazaleh et al., 2006). Management practices may also influence CLA concentrations. For example, pasture grazed cattle produce more CLA compared with grain fed cattle. Dairy cows grazing pasture and receiving no supplemental feed had a 500% increase of CLA in milk fat compared with cows fed typical lactating cow rations (Dhiman et al., 1999). The dairy industry can potentially market products with increased concentrations of CLA to human consumers. The products made from milk with increased CLA have similar properties when compared with non-enriched products. Butter from enriched milk has comparable spread ability and storage temperatures (Jones et al., 2005). The opportunity to enrich products with CLA without compromising on taste and texture represents an opportunity for a niche market. This market may increase revenue for the dairy industry by appealing to consumers who want healthier products and do not want to change their eating habits.

Key Words: conjugated linoleic acid, pasture

225 Using microfiltration to extend milk shelf life. E. W. Cloninger*, *Pennsylvania State University*, *University Park*.

The goal of the United States dairy industry is to sell a wholesome, nutritious product. To accomplish this goal, the industry must remain economically competitive. Shelf life stability can offer a competitive advantage. Pasteurization using the ultra-high-temperature (UHT) method achieves the desired extended shelf life but has the undesirable consequence of a cooked flavor. As a result, membrane processes such as microfiltration (MF) have led to new advancements in the dairy processing world by providing a lower temperature option that allows for minimal flavor changes while extending shelf life. MF is defined as the passage of products under relatively low pressure through a semi permeable membrane with pore size ranging from 0.2 to 5 μm. It is because of this small pore size that contaminants such as bacteria can be filtered out. According to a study conducted at Cornell University, MF was shown to significantly decrease total bacterial counts by 3.79 logs. The study also found that MF reduced the SCC in the milk permeate to undetectable levels. It also showed that microbial shelf life was extended to more than 92 d when MF was used in conjunction with HTST pasteurization. Although MF did decrease the bacterial population, the rate of proteolysis that contributes to off-flavors during refrigeration was not seen to be reduced. MF has already been commercially used by companies in Canada and the United Kingdom. These 2 companies promote the fresh taste, nutritional quality, and long-shelf life of their milk. Additional research will show more uses for MF in improving milk quality. In summary, combining MF with current technologies can maintain a nutritious, wholesome product while extending milk's shelf life.

Key Words: microfiltration, shelf life

226 Reducing milk price volatility through innovative programs at the local and global level. W. Robinson*, *Clemson University*, *Clemson, SC*

The sustainability of dairy marketing has been the primary question on the minds of dairy farmers across the globe. Record low milk prices have severely plagued the dairy industry especially during 2009. This trend of unstable marketing in the dairy industry has endangered the future of many dairy producers at an international level. Though decreased milk prices have exposed many dairy farmers to the possibility of bankruptcy, many innovative programs have been introduced to the industry to counteract these causes and therefore prolong the futures of many dairy producers. The programs created to ensure survivability of dairy marketing are comprised of both governmental and private innovations. Smaller scale, grass-roots, programs are typically constructed and operated by private producers and companies within the dairy industry. Some of the practices involved with these small scale programs focus on many aspects of niche marketing such as practicing methods of organic farming, producing products of specialized quality, processing and marketing products on-farm, as well as utilizing free-range grazing. The governmental innovations which have been discovered and are now practiced to fight the epidemic of unstable milk prices and include both single and united governmental plans which are used internationally. Single governmental plans include such programs as Cooperatives Working Together (CWT), Component Pricing, as well as the Hayvanciligi Destek program. Furthermore, the united plans regarding governmental innovations to reduce instability in milk prices include specialized marketing networks as the North American Free Trade Agreement as well as marketing techniques currently utilized by the European Union. Through active involvement in one or more of these programs dairy producers are learning how to overcome the epidemic of low priced milk and maintain their livelihood in the dairy industry. These practices also allow for a greater degree of security in milk prices and greater opportunity for the marketing of US dairy products in the future

Key Words: CWT, government programs, milk price

Teaching/Undergraduate and Graduate Education: Graduate and Undergraduate Teaching 1

227 The Missouri Pathways Partnership—Inroads in distance education. E. L. Walker*[1], S. P. Webb[1], J. D. Ulmer[2], and A. Evert[3], [1]*Missouri State University*, *Springfield,* [2]*Texas Tech University*, *Lubbock,* [3]*Redlands Community College*, *El Reno, OK*.

The Agriculture Pathways Partnership was developed in 2004 to offer place-bound students the opportunity to earn Bachelor's of Applied Science (B.A.S) degree from Missouri State University (MSU). The ultimate goal of the Partnership is to increase the number of 2–year college students earning B.A.S. degrees and as a result improve the trained workforce in the agriculture industry. Students earn a B.A.S. degree in Agriculture after completing up to 85 h at a community college and a minimum of 40 h of upper division hours, with a minimum of 30 upper division hours through MSU. Students taking courses through MSU have the option of taking courses offered via interactive television (ITV), internet, weekend, intersession, and internship experiences. Faculty, staff, and students from 5 Missouri and 2 Oklahoma locations participate in the program. An evaluation was conducted to determine the impact of the program on student learning, satisfaction, and suggestions for improvement. The mixed–methods evaluation design was used and included student surveys, focus groups, and personal phone interviews. According to student surveys, courses offered via ITV are perceived as comparable to the face-to-face courses. Over 73% of student participants agreed or strongly agreed that Pathways courses were successful, that they liked the course format, and felt they would continue to take other courses through Pathways. Eighty-five percent of the faculty participating in Pathways agreed or strongly agreed that the Pathways courses were as rigorous as traditionally taught courses. However, students reported problems in student support ranging from enrolling, gaining access to blackboard, and applying for graduation. Students have also reported lack of motivation when no instructor was present in the classroom. Other factors which are challenges to the Pathways Program include regional weather variation, non-matching site academic calendars, ITV technology, personal student conflicts, and state–wide differences in degree requirements and regulations.

Key Words: distance education, teaching, agriculture degree

228 The effect of supplemental online resources in distance education format on undergraduate animal science laboratory instruction. J. Q. Bing*, S. E. Pratt-Phillips, and C. E. Farin, *North Carolina State University*, *Raleigh*.

The objective of this study was to determine if using supplemental online resources (SOR) in a distance education (DE) format would be effective in enhancing student learning. Seventy-two students in an undergraduate animal science laboratory course completed a pre-test on anatomy as well as completed a pre-survey to determine their experience with, and attitudes toward, SOR. The SOR were made available for randomly selected laboratory lessons through online modules. Two laboratory practical exams were administered, one mid-semester and one at the end of the semester, and included questions from labs for which SOR was made available as well as labs that had no SOR. Questions from the pre-test were included in the exams and these responses generated the "post-test" scores. At the end of the semester, students completed a post-survey regarding their opinions of the usefulness of SOR. Student learning and performance was evaluated using an ANOVA model that included test scores, SOR availability and their interactions. Results are presented as mean ± SEM. Post-test scores (87 ± 2%) were higher ($P <$ 0.0001) than pre-test scores (34 ± 2%), indicative of student learning. On Lab Practical 1, students scored higher ($P < 0.0001$) on questions from SOR laboratories compared with non-SOR laboratories (77 ± 2% and 74 ± 2%, resp.). In contrast, on Lab Practical 2, students scored higher ($P < 0.0001$) on questions from non-SOR laboratories compared with SOR laboratories (86 ± 2% and 83 ± 2%, resp.). In the post-survey, 62 of 72 (86%) of students believed the SOR was at least somewhat useful for improving their grade; however, student perceptions of the value of SOR to impact their performance were not consistent with actual performance. Factors other than SOR may play a greater role in influencing student performance.

Key Words: anatomy, online, supplemental online resources

229 APPLAUSE—A tool for improving student presentations. M. M. Beck* and R. Johnson, *Clemson University*, *Clemson, SC*.

Increasingly, clear and effective communication skills are sought by professional schools, potential graduate mentors, and employers; as educators of both graduate and undergraduate students, we are remiss if we fail to impart techniques that enhance the ability of our students to communicate effectively. Many resources exist for developing PowerPoint presentations with effective use of color schemes and fonts. Fewer resources exist for students to use in developing effective presentation skills and such techniques are typically not a curricular focus. APPLAUSE is a conceptual framework for students to use in developing and giving effective oral presentations. Using the letters of the acronym as a guide, students have the following prompts: A – Audience analysis; P – Pause then grab; P – Pointer precision; L – Lively voice; A – Adjust in action; U – Use appropriate gestures; S – Simplicity; E – Expect questions. These simple but straightforward prompts are useful regardless of the context; most speakers at scientific meetings know their subject matter well and, with attention to these details, could turn mediocre or good presentations into great presentations. Paying particular attention to the 2 P's – the first at the beginning to better ensure audience connection and the second, precise use of the pointer – can have immediate and marked effects on the presentation; misuse of both are among the most common distractions to effectiveness. Student feedback from 6 classes of ~15 students each, primarily senior undergraduates, indicates that use of the APPLAUSE framework made a positive difference in the effectiveness of their presentations.

Key Words: student presentations, communication effectiveness

230 Student performance is enhanced by pedagogical shift to lecture podcasts. J. J. Parrish* and R. L. Monson, *University of Wisconsin*, *Madison*.

The study examines the effects in reproductive physiology of comparing traditional lecture to use of enhanced podcasts. The course was taught at the junior-senior level and consisted of 2, 50-min lectures and a 2-h wet lab, for each of 15 weeks in the fall semester. Baseline data from the traditional course was from 2006. In 2007, enhanced podcasts replaced traditional lectures, which allowed replaying the broadcast in iTunes software so that viewing was computer platform independent. No change was made to the laboratory over the course of the study. Due to a sabbatical leave of the instructor in 2007, all students were required to view the podcasts for the lecture material. In 2008 and 2009 students had the option of viewing the podcasts or attending live lecture. Scores on 3

lecture exams were recorded in years 2006 – 2009, with years hereafter referred to as year 1–4. There were 44, 61, 53 and 67 students completing the class in years 1 - 4 respectively. Exams consisted of multiple choice, true-false, and essay questions. However no change was made in the exams over the 4 years and while students could review exam results in class, no exams were returned to students during this period. There were significant effects of exam, year and exam by year interaction, $P < 0.05$. The lsmean percentage scores on exams over the course of the 4 years were 80.8, 83.1 and 82.2 for exams 1 – 3 respectively. While exams scores were different ($P < 0.05$) and there was some variation over the years ($P < 0.05$), differences were minor. When the lsmean percentage overall exam score for each year was examined, the scores were 78.8, 82.7, 83.9, and 82.9 for years 1 – 4 with year 1 different ($P < 0.05$) from years 2 - 4 but no difference was found between years 2 - 4 ($P > 0.05$). Attendance in live lectures was 98%, 0%, 15% and 1% in years 1 – 4 respectively. In year 2 no live lecture was offered. However, in years 3 and 4 a live lecture was offered but attendance was low. The results demonstrate that lectures given via an enhanced podcast improve exam performance and given the choice, students chose to take the podcast over the live lecture.

Key Words: podcast, learning assessment, reproductive physiology

ADSA Southern Section Symposium: Dairy Cattle Grazing in the Southern USA

231 Why dairy producers are choosing to graze (again) in southeastern United States. M. E. Sowerby*, *University of Florida*, *Gainesville*.

Grazing dairy cows between milkings was the norm, not the exception, in southeastern United States until herd sizes began out-growing available pasture and environmental rules forced cows to be confined to ensure soil nutrient loads were managed. Free stall barns and total mixed rations increased cow comfort, milk production and cost of production. The current trend to intensive rotational grazing of cows in the Southeast is an adapted version of the New Zealand model, with low requirements for machinery (tractor and bush hog, minimally) and buildings (milking center only). Southeastern dairy producers like their rotational grazing systems because of: 1) low labor needs, 2) less machinery and buildings to purchase or build and maintain, 3) greater cow longevity, 4) less herd health problems, 5) flexibility to add more feed (and consequently more production) when feed and milk prices are favorable, 6) more free time for owners, and 7) greater return on assets. Challenges noted by rotational graziers include: 1) optimizing grass growth and quality, 2) mud, 3) cow comfort in hot, cold and inclement weather, and 4) cash flow, especially with seasonal milk production. With lower start up costs, however, more new dairies are grazing dairies in the Southeast.

Key Words: rotational, grazing, dairy

232 Nutritional and management strategies for lactating dairy cows housed on pasture-based systems in the southeastern US. C. R. Staples*[1], L. E. Sollenberger[1], J. H. Fike[2], B. Macoon[3], and R. S. Fontaneli[4], [1]*University of Florida*, *Gainesville*, [2]*Virginia Tech University*, *Blacksburg*, [3]*Mississippi State University*, *Raymond*, [4]*Embrasa Brasileira de Pesquisa Agropecuaria*, *Brazil*.

Well-managed grazing systems for lactating dairy cows in southern climes offers several advantages including 1) year-around grazing, 2) forages of comparable or better quality than those mechanically harvested, and 3) substantially reduced farm costs (feed and overhead) compared with barn housing. During 2 summers of study, lactating Holstein cows (n = 106; 116 DIM) were assigned to treatments in 3 periods examining 2 forage species, 2 rotational stocking rates, and 2 supplementation rates. Bermudagrass (BG; *Cynodon* spp. Cv. 'Tifton 85') supported less milk (16.2 vs. 17.3 kg/d) per cow but more milk per ha (118 vs. 87 kg/d) than the legume *Arachis glabrata*. Lower production per cow grazing BG was likely due to lower quality of BG (58.8 vs. 71.2% IVOMD) and lower forage intake (7.6 vs. 11.3 kg/d). Greater production per land area was due to a greater mean pregraze herbage mass (7270 vs. 4650 kg of DM/ha), herbage allowance (1.9 vs. 1.5 kg of DM/kg of body weight), and optimal stocking rate (10 vs. 5 cows/ha) on BG pastures. Supplementing concentrate at 0.5 vs. 0.33 kg per kg of milk increased milk production by 2.1 kg/d, with the increased response being more efficient for cows grazing BG vs. legume (0.87 vs. 0.43 kg of milk per d) due to less substitution of forage with concentrate (0.18 vs. 0.51 kg per kg). In winter, concentrate-supplemented Holstein cows rotationally grazing rye-ryegrass (*Secale cereale* L. and *Lolium multiflorum* Lam.) pastures produced more milk (23.5 vs. 20.5 kg/d) at 2.5 vs. 5.0 cows/ha stocking rate. In a 276-d study, Holstein cows housed in cooled free stalls and fed a TMR produced more milk (29.8 kg/d) than concentrate-supplemented cows managed on pastures of rye plus ryegrass in winter and BG in summer (25.0 kg/d) or on rye-ryegrass plus clovers in winter and pearl millet (*Pennisetum glaucum*) in summer (25.2 kg/d).

Key Words: grazing, dairy, nutrition

233 Nutrient management considerations for grazing dairies. S. R. Hill*, *Department of Animal and Dairy Science*, *Mississippi State University, Mississippi State*.

Waste and nutrient management concerns have grown in recent years as people demand a safe food product, but also clean and environmentally friendly methods of producing food. Grass based or grazing dairies do not seem to fit the typical description of a Concentrated Animal Feeding Operation (CAFO). In a true grazing system, cows are not confined for more than 45 d of the year and, by definition alone, grazing dairies sustain forage growth for the majority of the year. According to the Clean Water Act, these are 2 requirements to be considered an Animal Feeding Operation and to be called a CAFO the farm must meet certain size requirements (>700–1000 head). However, State governments have the ability to restrict these regulations and in some areas farms as small as 70 to 100 cows could be considered a CAFO and be required to hold an NPDES permit. This means that despite not fitting the image of a CAFO, grass based grazing dairies must also make waste and nutrient management a top priority. A case study done in the Netherlands showed that using more homegrown feeds such as pasture and reducing inputs from purchased feeds and organic fertilizers decreased the total amounts of N and P surplus at the whole farm level. Certain practices common on grazing dairies (i.e., irrigation, rotational grazing, watering methods) may increase the potential for surface water contamination. Some grazing dairies also face issues not common to confinement dairies, such as protecting wetlands and conserving wildlife areas, where waste regulations are concerned. Some nutrient budgets for grazing animals have been established, but more research is needed to determine the effect grazing practices have on waste and nutrient management, at the whole farm level.

Key Words: nutrient management, grazing

234 Reproduction and genetic programs for seasonal pasture-based dairy production systems. S. P. Washburn*, *North Carolina State University*, *Raleigh*.

The objective is to discuss concepts and challenges associated with reproductive management in seasonal breeding and calving in pasture-based dairy production systems. Seasonal breeding and calving as part of a pasture-based dairy system is an attractive option for some dairy producers for reasons of lifestyle as well as for matching cattle nutritional requirements to forage quality and availability. In hotter climates, seasonal systems also allow producers to avoid breeding or calving at times of the year when heat stress would have a more negative impact. Herd fertility needs to be high enough to consistently achieve more than 80% of cows and heifers conceiving within breeding seasons of 8 to 12 weeks. Such success requires greater than 80% of cows to be cyclic at the start of breeding with conception rates at first insemination typically above 50%. This corresponds with 21-d pregnancy rates that exceed 40%, well above rates achieved in confinement systems. Breed differences in fertility are evident but improved fertility within breed can likely be achieved over time by placing more emphasis on daughter pregnancy rates in selecting sires to use. Use of crossbreeding is very common in

pasture-based dairy herds and data from crossbreeding studies have documented heterosis for reproduction among crossbred cows. Dairy producers with interests in seasonal breeding and calving may either choose to use a selection index that places more weighting on fertility or choose to avoid use of sires with negative fertility evaluations for their daughters. On commercial pasture-based dairy herds, the use of short periods of AI followed by use of bulls with natural service is common. As with any dairy production system, differing strategies will likely be optimal for producers with differing resources and goals. Although milk production per cow is often less, lower facility and equipment costs, lower feed costs, improved animal health, and the ability to expand the herd internally by improved reproductive efficiencies provide the opportunity for well-managed seasonal pasture-based dairy systems to be economically competitive.

Key Words: reproduction, seasonal, pasture-based

235 Comparisons of the economics and costs of producing milk on conventional versus grass-based "New Zealand style" dairies in Mississippi. C. W. Herndon*, *Mississippi State University*, *Mississippi State*.

Enterprise budgets were employed to estimate the costs of producing milk and income over various costs categories for conventional dairies and compared these costs to grass-based "New Zealand style" dairies in Mississippi. Conventional dairies in Mississippi utilize a corn silage, protein concentrate feed ration along with some pasture grazing to supplement nutrient requirements during limited period of the year. Grass-based dairies rely on intensively managed pasture grazing to provide the vast majority of dairy cow nutrient requirements while feeding very limited amounts of feed concentrate throughout the year. Economic analyses were conducted in 2009 which estimated the costs of producing milk on a dollar per kilogram (kg) basis on a 500-cow conventional dairy and a 1,200-cow grass-based dairy. Findings indicate for the 500-cow conventional dairy using a 10,435 kg rolling herd average that the cost of feed concentrates alone constituted almost 50% of total direct costs, or 15.4 cents per kg. Including corn silage, hay, and pasture management, these costs increased to 64% of total direct costs, or 20.1 cents per kg compared with total direct costs of 31.3 cents per kg. Comparing similar cost categories on a 1,200-cow grass based dairy with a 5,445 kg rolling herd average found that feed concentrates accounted for only 25% of total direct cost, or 6.6 cent per kg. When adding costs for hay, silage and pasture management, costs increased to 9.0 cents per kg, or 33% of the 27.1 cents per kg total direct cost. Total direct costs were not the same between the 2 types of Mississippi dairies because the grass-based dairy included salaries of $145,000 for a farm manager, herdsman, and additional staff. These costs clearly show when feed costs escalate, as has been the case since 2006, conventional dairies face greater risks of suffering economic losses which threaten the continued survival of this style of dairy operation. However, a grass-based dairy operation could survive when feed cost increase dramatically due to less reliance on feed concentrates for cow nutrient requirements.

Key Words: dairy cost of production, grass based dairy

ADSA-SAD Undergraduate Competition: Dairy Production

236 Precision feeding for improved sustainability efforts. V. J. Eubanks*, *Clemson University*, *Clemson, SC*.

With an increase in environmental awareness, sustainable agriculture has taken a forefront in the minds of Americans. Sustainable agriculture, for all aspects, is focused conservation and preservation while maintaining economic stability for producers. In relation to dairy farming, this concept is widely centered on the excreta and how to alter contaminants of excreta through dietary changes to lower the occasional excess amounts of certain substances, most notably phosphorous (P) and nitrogen (N). Excess P and N levels in the soil can lead to groundwater pollution, acid rain due to volatilization N into NH3, and formation of algal blooms which harm ecosystems and contaminate human drinking water. Current research is investigating the potential of reducing excess production of P and N through altering the nutrient intake of the dairy cattle and changing the excreta without adversely affecting milk production. Precision feeding management (PFM) is being utilized to achieve these efforts. Nutrient management through PFM is focused on 2 main points: analyzing forages for nutrient content and balancing the diet precisely to NRC requirements outlined for P and CP content. While most forages and concentrate mixes are analyzed, many producers choose to feed their cows more P than necessary due to the correlation previously reported between P and reproductive performance. Research has found this only be true at extremely deficient amounts. According to Ghebremichael and colleagues, it was found that decreasing excess dietary P by 22% resulted in a 25% reduction of P content in excreta (2008). Nitrogen excretion can be reduced by reformulating CP content in the diet, identifying those animals that require additional amounts of CP. Studies have shown that precision feeding for CP led to increased milk production due to more efficient use of dietary nutrients and additionally decreased feed costs associated with these animals. Ultimately, PFM is focused on efficiently feeding dairy animals the NRC required diet without feeding excess P and CP. In addition, this will enhance sustainability for dairy productions systems which, in turn, will ease consumer concerns and improve public perception.

Key Words: PFM, nitrogen, phosphorus

237 The benefits of anaerobic digestion as a waste management procedure on dairy farms. C. M. Munz*, A. C. Wilkie, and M. E. Sowerby, *The University of Florida*, *Gainesville*.

The increased urbanization of rural areas in addition to an increase in the concentration of intensive livestock operations have produced great awareness and concern for the proper storage, treatment and utilization of livestock manure. The waste management procedures on dairy farms are thus receiving a great deal of attention. Manure is not only a valuable source of crop nutrients, it is a substantial bioenergy resource if processed by anaerobic digestion. Anaerobic digestion refers to the decomposition of organic matter in an engineered methanogenic process that involves bacteria which decompose the manure in a way similar to the natural decomposition that occurs in a cow's stomach. The renewable resources produced are part of a closed carbon cycle and do not add to the atmospheric concentration of CO_2. In addition, quality fertilizer is still derived from the manure after digestion. Anaerobic digestion therefore boosts environmental quality as a waste management technology and is a sustainable energy-producing technology. Multiple studies have been conducted to determine the effects of implementing anaerobic digestion as a waste management protocol on dairy operations, as well as its economic feasibility. Benefits of using a digester on a dairy farm include waste treatment, reducing odors, flies, and pathogens, eliminating green house gas emissions, conserving nutrients, and recovering a significant amount of energy in the biogas that is captured. In addition, implementation of anaerobic digestion on dairy farms contributes to a socially desirable "green image" and to compliance with impending air emission regulations.

Key Words: anaerobic digestion, waste management, sustainability

238 Changing the attitude towards tail docking dairy cattle. B. A. Wenner* and E. L. Karcher, *Department of Animal Science, Michigan State University*, *East Lansing*.

A recent survey report listed that over 80% of dairies surveyed practiced tail docking in Midwestern states (Fulwider et al., 2008) and while this is commonly considered as a sanitary and time saving method among dairy farmers, this process is coming under increasingly harsh criticism. Tail docking was recently banned by the California legislature on October 12, 2009, and became official in California on January 1, 2010. This legislation will likely appear in many states to follow, including another big dairy state, New York, following the release of an undercover video depicting cows being tail docked (AP, 2010). The perceived purpose of tail docking is to improve milking comfort and udder health, and to decrease disease transmission for the cow by reducing contact between the tail, manure and the udder during milking. Additionally, the removal of the tail helps to prevent employee discomfort and illness from possible contraction of disease from contact with urine and tail during milking (Stull et al., 2002). In controlled studies, there is no significant impact of tail docking on udder cleanliness, cow cleanliness or udder health compared with dairy cattle with intact tails (Tucker et al., 2001). In another study no significant differences in udder health, bacterial prevalence, and milk production were found between docked or non-docked cattle, but significant farm differences were observed especially for contagious pathogens present (Schreiner et al., 2002). Further, on a farm research study in New Zealand, 33% of employees were found to have contracted leptospirosis. However, this was not linked to whether or not dairy cattle were tail-docked but rather correlated to clinical history of leptospirosis in the herd (Mackintosh, 1980). Also, the tail is used for communication between cows, vulvular protection, and to avoid insects. Fly counts were higher in those animals who were tail docked (Eicher et al., 2001). We suggest that cessation of tail docking as an industry practice will have no negative effects on cows or people and will serve a major positive public relations effect for the national dairy industry.

Key Words: tail docking, welfare

239 Improving freestall housing to address animal welfare and cow comfort. R. M. Smith*, D. R. Winston, and C. S. Petersson-Wolfe, *Virginia Polytechnic Institute and State University*, *Blacksburg*.

Animal welfare and cow comfort have become very hot topics among American dairy farmers. With the airing of a Northern New York dairy farm's "inhumane" treatment of cattle on a national network, consumers have been provided with information that is not representative of the entire dairy industry. Animal welfare is important to the producer because the better designed and managed facilities reduce the risk that cows will become sick or lame. Housing facilities such as freestall barns, pack barns, as well as conventional access to pasture have all been analyzed for the pros and cons related to cow comfort and well being. Bedding types, application rates, and usage have also been examined.

Research has been conducted on freestall design to examine the type and size is most desirable for cow comfort. Improving freestall design will improve cow comfort and in return may improve public perception of the dairy industry. Animals rested an average of 0.7 h less in stalls measuring 106 cm than in stalls measuring 116 or 126 cm (Tucker et al., 2004). A second experiment showed that the difference in lying time was 1.2 h in stalls measuring 112 cm versus 132 cm (Tucker et al., 2004). Overall, animals preferred wider stalls. The amount of fecal matter increased 2.4 times in stalls measuring 126 cm, and 1.6 times more for 116 cm in width, compared with 106 cm stalls (Tucker et al., 2004). Stocking density, bunk space, surface type, and barrier type all have different effects on the performance and comfort of the animal. Time spent lying can comprise 40 to 60% of a cow's life, and the surface is important for both the health and comfort of the animal (Tucker et al., 2003). Although cattle prefer deep bedding, deep bedding is more difficult for the producer to maintain and may cause more mastitis. Research generated by universities, professional organizations, research institutes, as well as personal experience should be considered when deciding on improvements or new facilities. Educated decisions on facility design will greatly improve cow comfort as well as the overall well-being of the animal.

Key Words: animal welfare, cow comfort, freestall

240 Off to a good start. J. C. Landry* and C. C. Williams, *Louisiana State University*, *Baton Rouge*.

Calves are the future lactating cows on the farm, so ensuring their health and well-being is vital to the dairy operation. A neonatal calf is born with an immature immune system, meaning that these animals are not able to produce antibodies when challenged with a disease causing pathogen. This type of immunity, called active immunity, is acquired and begins to develop after the first 2 mo of life. Therefore, the neonatal dairy calf relies on passive immunity to fight diseases during this early part of life. The passive transfer of immunity is obtained by gut absorption of the antibodies present in colostrum. Without this passive transfer of antibodies, or immunoglobulins, into the blood, the calf will be at greater risk for many diseases. Colostrum, the first and most important feed given to a newborn calf, is the primary source of nutrients for the calf and also provides essential and irreplaceable antibodies. The 3 essential factors to consider in colostrum feeding and management are quality, quantity, and time. The calf′s ability to absorb the antibodies declines within hours after birth, and by 24 h the intestine is closed to absorption. Failure of passive transfer may occur if the calf is not given enough high quality colostrum within the first 24 h of life. According to the latest National Animal Health Monitoring System (NAHMS) data, failure of passive transfer of immunity on US dairy farms has dropped dramatically since 1991–1992′s level of more than 40%. But passive transfer failure still occurs on US dairy farms at the rate of 19.2%. A successful heifer-rearing program begins with the proper management of the newborn calf. The quality, quantity, and timing of colostrum are critical for passive transfer of immunity to the neonatal calf. Using recommended management practices for feeding colostrum to the newborn calf will get these young animals off to a good start in life.

Key Words: calves, immunity, passive transfer

241 Hemorrhagic bowel syndrome: The mysterious killer. B. P. Cashell*, *Pennsylvania State University*, *University Park*.

Hemorrhagic bowel syndrome (HBS) is an acute sporadic enteric disease that affects the small intestine of mature dairy cattle. It has been estimated that HBS is responsible for 2% of cattle deaths in North America. The disease is characterized by dark bloody stools, bloody diarrhea, shock, depression, and acute death. The cow's extremities become cool, mucous membranes become pale, and rectal temperature is lower than normal. The disease occurs most frequently in the first 100 d of lactation. Sudden death is common, with large blood clots found in the intestinal area. It is estimated that 85% of HBS cases are fatal, and treatment methods are rarely successful. While the cause of HBS has not been specifically identified, there are many possible contributors to its onset. Several pathogens have been linked to HBS. *Clostridium perfringens* has been most strongly associated with the condition. According to Colorado State University, 82% of HBS cases had moderate to heavy growth of *C. perfringens* from fecal material. An Oregon State study implicated *Aspergillus fumigates,* a contaminant in fermented feeds, as another associated pathogen. Since treatment of HBS has been largely unsuccessful and its exact cause is unclear, current approaches to control HBS have included identifying and correcting management and environmental factors that may impair immunity. Other possible methods of prevention include vaccines and feed additives. Careful cost analysis associated with these measures is necessary before implementing expensive methods of HBS prevention that have undetermined effectiveness. The mystery of HBS will be unraveled through further research into the causes and risk factors associated with this condition.

Key Words: hemorrhagic bowel syndrome, *Clostridium perfringens*

242 Compost bedded pack barns: Opportunities, challenges, and management considerations. C. M. Sheaffer* and J. M. Bewley, *University of Kentucky*, *Lexington*.

A compost bedded pack barn, which relies on a large, open resting area, usually bedded with sawdust or dry, fine wood shavings, is a relatively new alternative for management of dairy cattle and their waste in a confinement setting. The soft, dirt-like texture of the compost absorbs shock, provides safe footing, and provides a comfortable resting surface for cows to lie down. Heat detection is improved as compared with concrete, because of less concern of slipping. The heating of the compost may kill some harmful bacteria, including mastitis-causing pathogens, which can help reduce the occurrence of environmental mastitis. When the compost is working properly and dry, it can also be conducive to cleaner cows. Properly composted material emits little odor and can be dried and spread onto fields. This may ultimately lead to better nutrient utilization and the dried compost is more easily handled than liquid manure. Adequate ventilation, achieved through high, open sidewalls, open-ridges, and appropriately placed fans, is essential. Daily turning and aeration of the compost is necessary to provide oxygen (12 to 16%) to the microbial population. Most producers use a cultivator, tines, or a rotary tiller attached to the rear of a skid steer or small tractor to stir the pack. The temperature of the pack should be monitored daily and must be maintained between 54 and 66°C to ensure an optimal environment for the bacterial population. For proper function, the amount of moisture added by cows through urination and defecation should be limited to 46 to 64% total moisture in the pack. To achieve this, an appropriate stocking rate is one cow per 80 to 100 ft^2. Bedding particle size is also an important factor and should be a balance between coarse wood chips and sawdust to maximize absorbency and available carbon. New bedding is added to the pack when existing bedding is moist enough to stick to the cows when they get up. Though applications for compost bedded pack barns may be limited because of limited sawdust supplies, they remain a viable alternative for small dairy herds or special needs groups within larger herds.

Key Words: compost bedded pack, dairy housing, composting

ADSA-SAD Undergraduate Competition: Undergraduate Original Research

243 The effects of metaphylaxis antibiotics on health and development of neonatal bull calves. K. G. DeHaan*, G. A. Holub, and M. A. Tomaszewski, *Texas A&M University*, *College Station*.

A study evaluating the effects of metaphylaxis antibiotics and milk replacer additives on the health and development of Holstein bull calves (n = 52; mean body weight = 42.28 kg + 3 kg; starting age < 3 d) was conducted. The calves were placed into a completely random 3 × 4 factorial design with each group receiving either tilmicosin phosphate (TIL), ceftiofur crystalline free acid (CEF), or saline solution (CON) injected subcutaneously into the neck area. For the duration of the study, the calves also received a commercial milk replacer powder (22% crude protein / 20% crude fat) fed at 1.1% BW. Within metaphylaxis treatment, calves were randomly assigned to receive either; 1) 4 g/d for 7 d and then 2 g/d for 14 d of an egg-based probiotic (PR); 2) 2 g/d of 96% betaine (BE); 3) both PR and BE (BP); or 4) no additives . The calves were housed in individual fiberglass hutches with commercial calf starter and water provided ad libitum. The body weight of each calf was recorded twice weekly in addition to daily recordings of fecal scores (1 = firm to 4 = watery) for 54 d. Medical treatments provided to each calf for scours, respiratory distress, or febrile events were recorded daily. The cumulative response of these incidences were analyzed and used as an index of morbidity. None of the additive effects were significant for any of the measured variables. The use of metaphylaxis did not significantly affect the average daily gain ($P > 0.60$) as the average daily gain was ~0.45 kg. However, when examining fecal scores, CEF and TIL significantly reduced teh average fecal score over the control ((1.85 vs. 1.97 vs. 2.20 respectively) ($P < 0.01$)). The incidences of fever nor respiratory issues ($P > 0.20$) were influenced dramatically by metaphylaxis. Overall, the average daily treatment for fever was only 0.66 events and 0.39 events for respiratory distress. Metaphylaxis did not influence the occurrence of scours (fecal score > 2) ($P > 0.87$). Other than fecal score, these results indicate the use of metaphylaxis did not enhance productivity or reduce morbidity of Holstein neonatal bull calves.

Key Words: calf, metaphylaxis

244 Effects of Purina Cornerstone 20 AMPLI-CALF DX30 on calf growth. A. A. Blasi*[1], C. C. Stanley[2], C. R. Krehbiel[1], D. A. Jones[2], and W. Hurst[1], [1]*Oklahoma State University*, *Stillwater*, [2]*Land O'Lakes Purina Mills LLC*.

Proper calf nutrition is key life-long productivity of the cow. Investments in a heifer during the first 12 weeks of life can affect her productive potential in adulthood. Proper milk replacer and calf starter that meets all of a calf's needs is essential for full growth potential. The objective of this study was to compare commercially available Purina Cornerstone 20 AMPLI-CALF DX30 to a mill prepared calf starter (contained 16.3 mg/kg Bovatec 68). Each had a similar composition on a DM basis with AMPLI-CALF containing 21.89% CP and the mill calf starter containing 21.23% CP. AMPLI-CALF was fed without oat hay until 12 wks of age with oat hay presented starting at 6 wks of age to the milled starter group. Twenty Holstein heifer calves born at the OSU dairy were placed at random in one of 2 feed treatment groups. Calves were housed individually in fiberglass hutches with wire panel runs and given free choice water. All calves received 3.79 L of premium colostrum within 24 h of birth. Calves were fed twice daily with Land O'Lakes 28:20 Cow's Match milk replacer. All calves were weaned at 9 wks old. Orts were recorded every day at 1600 and appropriate feed amounts were adjusted and fed ad libitum to allow for excess feed. Water was offered ad libitum. To determine calf growth, measurements of weight, heart girth, pelvic width, pelvic height and wither height were taken on 1, 28, 56 and 84 d. Measurements were taken in the afternoon before new feed was presented. There was no difference ($P > 0.10$) in ADG from d 1–28, 28–56 or 1–84. However, from d 56–84 ADG was greater ($P = 0.05$) for calves fed AMPLI-CALF (1.30 kg/d) compared with control calves (1.10 kg/d). There were no differences ($P > 0.10$) in body weight, heart girth, pelvic width, pelvic and whither heights, as-fed feed intake or gain efficiency on d 1–28, 28–56, 56–84 or 1–84. Although overall growth was not affected, AMPLI-CALF increased post-weaning ADG of heifer calves compared with the milled calf starter.

Key Words: calf nutrition, heifer growth, performance

245 Use of omega-3 fatty acid rich algae and their oil as a feed supplement for dairy cattle. D. M. Shepherd*[1], J. A. Stamey[1], B. A. Corl[1], M. J. de Veth[2], and D. R. Winston[1], [1]*Virginia Polytechnic Institute and State University*, *Blacksburg,* [2]*Balchem Corp.*, *New Hampton, NY.*

Studies have shown that ω-3 fatty acids can improve reproductive performance in dairy cattle. Microscopic algae are a source of ω-3 fatty acids that could be used as a supplement for dairy rations. Availability of ω-3 fatty acids from the diet is limited due to their biohydrogenation in the rumen. A potential solution is to encapsulate the algal biomass in a lipid coating, theoretically allowing ω-3 fatty acids, specifically docosahexaenoic acid (DHA) found in algae, to remain inert in the rumen for absorption and utilization post-ruminally. To examine the supply of DHA for incorporation into milk fat by lipid encapsulated algal supplements, 4 late-lactation Holstein cows were assigned to a 4 × 4 Latin Square design. Their rations were supplemented with treatments: 1X rumen-protected algal biomass, 1X rumen protected algal oil, or 0.5X rumen-protected algal biomass. Supplements were lipid encapsulated (Balchem Corp., New Hampton, NY). The control treatment was unsupplemented. The 1X supplements supplied 29 g of DHA/d and the 0.5X supplement supplied half this amount. Data were compared using orthogonal contrasts. Supplementation did not affect feed intake, milk yield, or milk composition. Algal biomass supplements increased DHA content of milk fat (0.47 vs. 0.10 g/d; $P < 0.05$). Algal biomass was more effective at transferring DHA to milk fat than algal oil (0.55 vs. 0.30 g/d; $P < 0.05$). Supplements increased the milk fat content of trans-18:1 fatty acids. The effect on trans-18:1 fatty acids suggests that some of the supplemented fatty acids may have influenced the rumen biohydrogenation microflora. The transfer efficiency of dietary DHA to milk fat across treatments ranged from 0.5% to 3%. In conclusion, there was a significant increase in the amount of DHA present in milk fat.

Key Words: omega-3 fatty acid, algal biomass, milk fat

246 Effect of rumen sampling on time budget of lactating Holstein dairy cows. J. Deming*, P. D. Krawczel, and S. E. Boucher, *W.H. Miner Agricultural Research Institute*, *Chazy, NY.*

There is increasing evidence that a relationship exists between a dairy cow's ability to maintain her time budget and her productivity. This suggests that sampling regimens that alter behavior could potentially mask treatment effects in nutrition trials. The objective of this experiment was to determine differences in the feeding, ruminating, and lying behaviors

of ruminally cannulated lactating Holstein dairy cows housed in tie-stalls during the adjustment and sampling periods of a dairy nutrition experiment. We hypothesized that sampling would decrease time spent feeding, ruminating, and lying. Thirteen cows were assigned to the concurrently conducted nutrition trial, and all cows were subject to the same sampling schedule. Time spent eating, ruminating, drinking, lying, standing, or in the milking parlor was quantified by direct observation. Behavior was recorded at 5-min intervals for 24 h during both the adjustment and sampling periods. Data were analyzed as a completely randomized design using the Mixed procedure of SAS. Due to differences in time outside of the pen during sampling period (63.0 ± 0.9 min/d) and adjustment period (80.3 ± 0.9 min/d; $P < 0.001$), feeding, ruminating, and lying behaviors were evaluated as percentage of time within the tie-stall. Feeding (18.7 ± 1.2%) and ruminating (40.3 ± 1.3%) were not affected by sampling ($P > 0.10$). Lying decreased from 55.0 ± 3.2% during the adjustment period to 49.3 ± 3.2% during the sampling period ($P = 0.003$). Ruminating while lying was also reduced by sampling (from 28.3 ± 2.9 to 24.7 ± 2.9%; $P = 0.03$). The results of this study suggest that sampling can impact some aspects of a dairy cow's time budget. The number of times cows are disturbed for the collection of samples should be considered when designing sampling regimens.

Key Words: dairy cow, behavior, sampling

247 Effect of coliform mastitis on osteopontin expression in mammary tissues of Holstein dairy cows. K. M. Jackson*[1], J. C. Gandy[2], L. M. Sordillo[2], and E. L. Karcher[1], [1]*Department of Animal Science, Michigan State University*, *East Lansing*, [2]*Department of Large Animal Clinical Sciences, Michigan State University*, *East Lansing*.

Mastitis caused by gram-negative bacteria is often characterized by uncontrollable inflammation. Osteopontin (Opn) is a proinflammatory factor that plays a role in initiating the innate immune response by promoting cellular adhesion and eliciting proinflammatory cytokines. The objective of this study was to evaluate Opn gene expression in the mammary tissue of Holstein cows naturally infected with coliform mastitis compared with healthy controls. Parencyhmal tissue was collected from 3 lactating cows killed for reasons relating to natural coliform infection and 3 lactating cows killed for non-infectious reasons. All animals were from a commercial herd. Real-time PCR was performed to evaluate the expression of the following cytokine genes in parenchymal tissue: Opn, tumor necrosis factor (TNF)-α and interleukin (IL)-1. Additional samples were collected from the external pudendal artery and analyzed for Opn gene expression. Osteopontin and IL-1 expression did not differ between the natural coliform infected parenchymal tissues and that of the control tissues. There was a trend for greater TNF-α expression in infected tissues compared with control tissues (20.5 ± 16.6 vs. 2.2 ± 1.9; $P < 0.07$). Variability within infected and control parenchymal tissue was high which may be a result of the collection periods and the heterogeneous population of cells. The severity and duration of coliform infection was not controlled in this study and expression of proinflammatory genes will be affected by these 2 factors. There was a 4.2-fold increase in Opn expression between the infected and control external pudendal artery samples (4.3 ± 0.5 vs. 1.0 ± 0.3; $P < 0.001$). Unlike the parenchymal tissue, the vasculature represents a more homogeneous population of cells. The variability between these samples was diminished compared with the parenchymal tissues. In conclusion, this is the first study to evaluate the presence of Opn in parenchymal tissue and external pudendal arterial samples. Further controlled studies are needed to reduce the variability observed between the infection groups.

Key Words: osteopontin, mastitis, mammary tissue

248 Evaluation of dairy cattle lying behavior in commercial freestall barns. C. Gravatte*, C. Coombs, and J. Bewley, *University of Kentucky*, *Lexington*.

Animal activity monitoring sensors have been developed to measure lying behavior and have been validated using direct visual observations. These sensors may prove useful for assessment of facility functionality and animal well-being. However, to properly evaluate results, within and across herd variations must be understood. The objective of this research was to describe physiological factors impacting automatically recorded lying times across multiple commercial dairy farms using freestall barns. The lying times of 247 Holstein cows were measured using an animal activity monitor in 12 commercial dairy herds in Kentucky. Herds were categorized by production level (high, medium, and low) using rolling herd average milk. Within herds, project cows were distributed equally among lactation stage (60 to 400 DIM, mid and late lactation) and production level (high, medium, and low) categories. Cows that exhibited clinical lameness were excluded. For cows exhibiting estrus, the day of and the day before breeding were removed. When hours lying or number of steps taken within an individual day differed from an individual cow's weekly average by 2 or more standard deviations, these observations were removed. An IceTag animal activity monitoring sensor (IceRobotics Ltd., Edinburgh, Scotland, UK), which measures posture (lying versus standing) and number of steps, was attached to the hind leg of each cow above the fetlock for 14 d. The MIXED procedure of SAS was used to develop models to describe hours lying. Mean lying time (n = 3298) was 11.19 2.70 h/d while mean locomotion score was 1.37 0.56. Cows that were in mid lactation (11.04 0.39 h/d) had significantly lower lying times than cows in late lactation (12.42 0.39 h/d, $P < 0.0001$). Lying time decreased with increasing milk yield ($P = 0.03$). Though the difference only approaches significance ($P = 0.11$), cows with a locomotion score of 3 spent more time lying (12.31 0.71 h/d) than cows with a locomotion score of 1 or 2 (11.16 0.14 h/d). Consideration of lactation stage, milk yield, and locomotion score is necessary for interpretation of results obtained from automatic activity monitoring sensors.

Key Words: lying behavior, activity monitor, precision dairy farming

249 Associations of DNA marker profiles for dry matter intake and efficiency with DNA marker profiles for fat-corrected milk yield and body weight. D. E. Brown*[1], C. D. Dechow[1], J. M. Daubert[1], W. Liu[1], and S. Bauck[2], [1]*Pennsylvania State University*, *University Park,* [2]*IGENITY Livestock Production Unit*, *Duluth, GA*.

The objective of this study was to estimate the associations of DNA marker profiles for dry matter intake (DMI) and dry matter efficiency (DME) with DNA marker profiles for fat-corrected milk (FCM) and body weight (BW). DMI and BW were recorded within 7 d of monthly DHI milk testing on 11 Pennsylvania tie-stall dairy farms. Farms were visited once per month over a 6-mo period to measure feed intake on all cows, and blood was collected for DNA extraction. Genotypes were obtained at 86 loci that had a major allele frequency of < 95 for 796 cows. There were 35,390 test day FCM, 3,999 test-day DMI, and 2,195 test-day BW records available for analysis. Test-day records were used to derive 305 d total FCM (3,558 records), average BW (1,095 records), 305 d DMI (994 records) and 305 d DME (993 records) for analysis. Two 3 trait models (FCM, BW and either DMI or DME) were used to conduct genetic evaluations that included marker genotypes as fixed effects and a random polygenic animal effect in ASREML. Correlations for DNA marker effects were positive between DMI and FCM (0.29), DMI and BW (0.63), and DME and FCM (0.80). Correlations were negative between DMI and DME (−0.33) and DME and

BW (−0.15). Correlations of the polygenic effects were also strongly positive between DMI and FCM, DMI and BW, and DME and FCM and negative polygenic correlation was found between DME and BW. This study also showed genetic variation for feed intake and for feed efficiency. These findings indicate that it may be possible to use DNA markers to select for higher DME.

Key Words: dry matter efficiency, fat-corrected milk, DNA marker profiles

250 Evaluating the effectiveness of "cow-side" tests to identify animals with a dominant follicle at the time of insemination in a TAI protocol. T. L. Crouch* and J. L. Fain, *Clemson University*, *Clemson, SC*.

This study investigated changes in metabolic functions and their tendency to correlate with an adequate preovulatory follicular size (>15 mm) and secondary signs of estrus to better determine whether insemination should be performed in a TAI protocol. A total of 26 non-pregnant lactating Holstein and Jersey dairy cattle (n = 21; n = 5, respectively) of unknown estrous cycle status were synchronized ($PGF_{2\alpha}$, d-18; GnRH, d-16; GnRH, d-10; $PGF_{2\alpha}$, d-3, GnRH,d-1) and were inseminated 12 h after the final GnRH injection, d0. Temperature, urine pH and milk weights were collected at 12 h intervals beginning 48 h before TAI with the final collection occurring at insemination. The size of the largest follicle for each animal was determined by transrectal ultrasonography 12 h before TAI. On d 0, milk samples were collected and progesterone concentrations analyzed using a rapid milk P4 test. The results were qualitatively recorded on a scale from 1 (P4 = 0–1 ng/mL) to 3 (P4 = 5 ng/mL). Secondary signs of estrus were recorded 12 h before and at TAI with scoring based on the following observations: 1 = behavioral change, 2 = mucosal discharge, and 3 = mucosal discharge and mounting or standing activity. No strong correlations (> ±0.4) were realized between any "cow side" sampling method and the incidence of a dominant follicle or increased estrus expression. No differences ($P > 0.05$) in parameters were found regardless of the presence of a dominant follicle at TAI. When reproductively inefficient cows, as indicated by > 250 DIM and > 3 previous services, were excluded from the results (n = 7), a moderate positive correlation of 0.57 was identified with urine pH increasing in the 24 h before TAI in animals with larger follicles 12 h before TAI. Animals with an identifiable dominant follicle also had a greater increase in urine pH 24 h before TAI when compared with animals with the largest follicle being <15 mm in diameter (0.32 and 0.02, respectively; $P < 0.05$). Anomalies within the data are being overcome with additional sampling and correlation with blood serum P4 concentrations as well as pregnancy rate data.

Key Words: cow side

251 Effects of temperature on X chromosome carrying compared to Y chromosome carrying bovine sperm cells: preliminary results. L. A. Krueger*[1], J. L. Herring[1], and R. Wilborn[2], [1]*Alabama A&M University*, *Normal,* [2]*Auburn University*, *Auburn, AL*.

Climatic conditions and slight differences in a female's internal environment can influence the gender of her offspring (Cameron et al., 2008; Bonier et al., 2007). An observation by Roche, et al. (2006) revealed that air temperature raised by 1°C at the time of breeding increased the likelihood of the conception of a male calf by 1%. This observation suggests that X and Y chromosome carrying sperm cells are affected differently by raised environmental temperature. The purpose of this experiment was to compare the effects of female body temperature against X chromosome and Y chromosome carrying sperm. Eighteen gender sorted bovine semen straws of Genex Bull AN01043 were subjected to time temperature treatments. Nine straws were sorted for the X chromosome (group A), and nine sorted for the Y chromosome (group B). Experimental Groups A and B each consisted of three subgroups (1, 2, and 3) of three semen straws each, so each subgroup contained three semen straws. The straws were incubated in randomly assigned water baths after thawing simultaneously for 40 seconds at 34°C according to the procedure recommended by Genex. The control (subgroups A1 and B1), was incubated at 37.94°C representing the normal internal body temperature of a cow. Subgroups A2 and B2 were incubated at 38.89°C and subgroups A3 and B3 at 39.72°C to represent the internal body temperature of a cow under increasing heat stress (McGhee et al., 2008). One straw was drawn from each subgroup at six hours, representing bovine sperm cell capacitation, at nine hours, and at twelve hours for examination of motility using Sperm Vision (minitube, Mt. Horeb, WI). Data were to be analyzed with an unpaired t-test at $P < 0.05$.
The test results at six hours of incubation revealed 10% motility for all subgroups, with all motile sperm cells labeled nonprogressives. Due to the nature of the data, time temperature treatments were stopped for all samples. This study is being revised to examine time temperature differences on fresh bovine unsexed semen. This revision will aid in the determination of adjustments necessary for continuation and retrial of this experiment.

Key Words: temperature, sperm, bovine

252 Corn grain and liquid feed as non-fiber carbohydrate sources in diets for lactating dairy cows: digestibility trial. E. M. Eilenfeld*, M. L. Eastridge, and J. L. Firkins, *The Ohio State University*, *Columbus*.

We hypothesized that sugars in liquid feeds would maintain or improve measures of ruminal fermentation and diet digestibility to a greater degree when corn grain is processed to have a lower rumen degradable starch concentration. Five rumen cannulated cows were used in a 5 × 5 Latin square design and fed a control diet with steam-flaked corn (SFC) or 4 diets with dry corn that was finely or coarsely ground (FGC or CGC at mean particle sizes of 0.8 or 1.9 mm, respectively) factorialized without or 3.5% liquid supplement (LF; Quality Liquid Feeds, Dodgeville, WI) replacing corn grain. All diets contained a constant 24% corn silage and 16% alfalfa hay and 6% grass hay that were adjusted to maintain 36% NDF and 20.3% forage NDF. Diets were formulated to contain 36% non-fiber carbohydrates. Each period consisted of 2 wk, cows were fed and milked twice daily, and chromic oxide was dosed via the rumen as a digestibility marker. Contrasts were SFC vs. dry corn (SFC vs. the 4 ground corn diets) and the main effects and interaction of particle size and LF. The SFC decreased ($P < 0.05$) ruminal acetate and increased ($P < 0.05$) propionate concentrations. Finer particle size reduced ($P < 0.05$) ruminal pH (5.99 vs. 6.16), reduced ($P < 0.10$) ruminal concentration of acetate, and increased ($P < 0.05$) propionate concentration. Liquid feed reduced ($P < 0.10$) acetate, and there was an interaction for butyrate (LF increased with FGC but no effect with CGC). Finer particle size ($P < 0.10$) and SFC ($P < 0.05$) reduced ruminal NH3 concentration. There were no treatment effects on digestibilities of DM (65.9%), OM (67.7%), or NDF (54.9%). The DMI was similar (24.6 kg/d), but SFC increased ($P < 0.10$) milk yield (38.0 vs. 35.9 kg/d). Milk fat (3.51%) was similar, but there was an interaction for milk protein - LF reduced ($P < 0.10$) milk protein with CGC but not with FGC. Milk urea N was lower ($P < 0.05$) with finer particle size (11.8 vs. 13.0 mg/dl). The SFC and finer particle size appeared to be more rapidly fermented in the rumen, without adversely affecting intake or apparent diet digestibility. Liquid feed appeared to be more beneficial with FGC than CGC.

Key Words: particle size

Animal Behavior and Well-Being: Poultry 1: Ducks, Layers, and Turkeys

253 Who did it and why: Floor laying by Pekin ducks. M. M. Makagon* and J. A. Mench, *University of California, Davis*.

Floor eggs, which are eggs laid outside of nest boxes, are a common problem in poultry production systems. We investigated factors contributing to the laying of floor eggs by Pekin ducks. In a 2 × 2 factorial design, 16 groups of 18-wk-old ducks (8 per group) were provided access to either 2 or 8 closed-topped or open-topped nest boxes in their pens. Egg locations were recorded daily for 16 weeks following nest box introduction. Video analyses were used to determine the sources of a sample of floor eggs laid during wk 1–4, 8, 12 and 16. An analysis of nontoxic dye deposition in the egg yolk was conducted on wk 12, 14 and 16 to determine each duck's contribution to floor laying. Repeated measures ANOVA revealed that the proportion of floor eggs decreased over weeks ($F_{3,9}$ = 29.29, P < 0.0001), and was greater among the groups with only 2 nest boxes ($F_{1,11}$ = 24.09, P = 0.0005), but was not affected by nest box design ($F_{1,11}$ = 0.08, P = 0.776). Not all available nest boxes were used on a given day. In 8-box pens, for example, on average only 3 to 4 boxes were used per day. Of the 202 floor eggs identified on video, 65% were laid in the 4 h after the lights went on (0300–0700). This corresponded to the time of highest nest box use and competition. However, 32% were laid during the dark phase (2100–0300) when nest box activity and competition were low, and 1% were laid in the afternoon. The remaining 2% of floor eggs were ejected from nest boxes by the ducks. Yolk stain analysis indicated that 67% and 52% of ducks housed with 2 and 8 boxes, respectively, laid floor eggs, although none laid exclusively on the floor. Taken together these results suggest that floor laying by Pekin ducks may in part be a product of competition for nests, and can be decreased by optimizing the nest box to duck ratio. However, since 33% of floor eggs were laid during periods of low competition and not all boxes were used each day, other factors probably also contribute to the problem.

Key Words: nesting behavior, domestic duck, floor eggs

254 Nest choices of Pekin ducks. M. M. Makagon*, C. B. Tucker, and J. A. Mench, *University of California, Davis*.

To encourage nest use by breeder flocks, it is important that nest boxes are attractive to hens. Few studies have evaluated factors affecting nest attractiveness and nest choices of ducks. We assessed the effects of nest box experience and features of nests on nest site selection by sexually mature Pekin ducks. Hens were tested individually in pens containing different nest box choices. Nest preferences were determined based on the locations of 14 successively laid eggs. Experiment 1 assessed the effects of nest box experience and degree of nest enclosure. Ducks (n = 24) were reared with access to either open-top (OP) or closed-top (CL) nest boxes. They were then allowed to choose between 4 nest boxes varying in level of enclosure: OP, CL, OP with a nest curtain (OP-C), or CL with a nest curtain (CL-C). Ducks laid twice the expected proportion of eggs in the CL-C boxes (t_{22} = 4.21, P = 0.0004), demonstrating a preference for a high level of enclosure that was independent of previous nest box experience (t_{21} = 0.65, P = 0.53). CL boxes were used as predicted by chance (t_{22} = −0.33, P = 0.746), while OP and OP-C contained only half the expected number of eggs (OP t_{22} = −2.64, P = 0.015; OP-CL t_{22} = −2.86, P = 0.009). Experiment 2 assessed the effect of the presence of an egg in the nest. Ducks (n = 24) were provided with 2 nest boxes, one of which contained a single egg from the previous day. Each day, the newly laid egg was marked and either placed back in the nest box where they were found (Handled) or moved into the adjacent nest box (Moved). Handled and Moved ducks laid 97.6% and 79.8%, respectively, of their eggs in boxes containing the previous day's egg. While ducks in the Handled group were consistent in their choice throughout the test, those in the Moved group developed this preference over time (Wilcoxon S = 17.5, P = 0.039), suggesting that the preference for laying in a nest containing an egg may be influenced by experience. These results indicate that nest box enclosure and the presence of an egg are important in determining the nesting choices of Pekin ducks. Incorporating these features into nest boxes may be useful for increasing consistency of nest use by breeder flocks.

Key Words: Pekin duck, nest site selection, nest design

255 The effect of human induced stressors on the vocalizations of commercial brown and white egg laying hens. E. Otu-Nyarko*[1], J. An[3], P. M. Scheifele[2], D. B. Miller[1], M. T. Johnson[3], and M. J. Darre[1], [1]*University of Connecticut*, *Storrs,* [2]*University of Cincinnati*, *Cincinnati, OH,* [3]*Marquette University*, *Milwaukee, WI*.

A study was conducted at a commercial cage layer poultry farm in Connecticut to determine the effect of human induced stressors on the vocalizations of brown and white egg layers of various ages. Vocalizations and behavioral data were collected from 13 groups of 320 hens per group. A uni-directional Shure 10L Prologue microphone with a frequency sensitivity of between 20Hz and 15,000Hz was connected to a Compaq laptop computer with Cool Edit Pro 2.0 sound analysis software to record and edit vocalizations. A Hidden Markov Model modified for use as a speech recognition algorithm and statistical tool was used to classify the vocalizations. The accuracy of the classification was determined using a confusion matrix. Three different human induced stressors were applied to them. These were abrupt noise, touch, and walking through the coop in front of the birds. Non-stressed vocalizations were also obtained for comparison with the treatments. Of the entire vocalization spectral envelope, the Greenwood Function Cepstral Coefficients were extracted for the determination of the level of accuracy with the classification of vocalization using the modified Hidden Markov Model and a confusion matrix. It was found that the non-stressful vocalizations were significantly different ($P \leq 0.05$) from the stress induced vocalizations for both breeds with classification accuracy of 77% and 75% for white and brown egg layers respectively. For the stress induced vocalizations there were significant differences in vocalizations made as a response to abrupt noise, touching, and walking through the coop at an accuracy level of 81.2%, 74.29% and 36.3% respectively with abrupt noise being the most stressful to the chickens, resulting in the most recognizable and repeatable vocal response. Both breeds at peak production (28–29weeks) had similar vocalizations under all the conditions as indicated by a lower accuracy of about 64% in comparison with all other age groups for both stress-induced and non-stressed vocalizations. The brown egg strain was less susceptible (89%) to the effect of the stressors than the white leghorn laying hens (92%).

Key Words: vocalization, stress, hidden Markov model

256 Influence of environmental management methods on the expression of glucocorticoid receptors in the laying hen's ovary. D. V. Arbona*, L. A. Bola, and J. B. Hoffman, *North Carolina State University*, *Raleigh*.

In commercial egg production, increasing public scrutiny regarding the welfare of laying hens has led to the development of alternative manage-

ment practices including free-range housing in addition to conventional battery style cages. To ascertain the effects of layer housing management methods on ovarian susceptibility to corticosterones via expression of follicular glucocorticoid receptors (GR), ovarian follicles were collected from 6 Hy-line brown layers reared in a free-range system with access to a forage covered area divided into 4 paddocks as well as an enclosed range hut with feed, water, and nests. For comparison, ovarian follicles were collected from 6 Hy-line brown layers reared in conventional battery style cages stacked directly on top of one another with troughs for feed and nipple waterers. Separated granulosa and theca tissues from the F1-F4 hierarchical, and combined granulosa and theca tissues from the small yellow and large white non-hierarchical follicles were collected by manual dissection for GR characterization. Characterization of the GR in the ovarian tissues was performed following Total RNA extraction followed by 2-step real-time PCR. Relative quantification of the GR was completed using the $\Delta\Delta C_T$ method and data was expressed as the fold-difference relative to the F1T sample. Differences in the expression were determined by ANOVA using the GLM procedure ($P < 0.05$). No significant differences in non-hierarchical follicular GR expression were noted between free-range (0.69 ± 0.11) vs. battery style hens (0.75 ± 0.16) ($P < 0.05$). However, total GR expression in the hierarchical follicles was significantly higher in the free-range hens (1.35 ± 0.05) compared with the battery style hens (0.69 ± 0.04) ($P < 0.001$). These observations combined with previous data showing significantly decreased production of grade A eggs by free-range hens suggest that the free-range environment may negatively influence reproductive fitness due to differences in follicular stress susceptibility caused by altered glucocorticoid receptor expression.

Key Words: glucocorticoid receptor, free-range, battery cages

257 The influence of cage housing system and laying hen strain on bone quality pre and post slaughter. A. McMillan[1], K. Juurlink[1], B. Rathgeber[2], and M. Jendral*[1], [1]*Nova Scotia Agricultural College*, *Truro, Nova Scotia, Canada*, [2]*Agriculture Agri-food Canada*, *Truro, Nova Scotia, Canada*.

The influence of cage housing system and laying hen strain on bone quality traits pre and post slaughter was determined for 3 strains of laying hens (Shaver White (SW), Lohmann Lite (LL), Lohmann Brown (LB)) housed in conventional cages, and furnished colony units, and processed under commercial conditions. During the laying period, hens were either housed in conventional cages (60cm × 45cm) (n = 24 cages per strain; 5 hens per cage) or furnished colony cages (240cm × 110cm) (n = 12; 4 per strain; 40 hens per cage). Furnished cages contained a nestbox (60cm × 55cm), 3 hardwood, semi-circular perches (240cm × 5cm) and a dustbathing facility (60cm × 20cm). At 80 weeks, all hens were palpated before slaughter to assess fractures to the furculum, keel, humerus, radius, ulna, femur, tibia and pubis bones. Post slaughter (no evisceration), 25 randomly selected hens per colony cage, and all 5 hens in 9 randomly selected conventional cages per strain were re-palpated for fractures of the above bones. Additionally, right femur, tibia and humerus bones were isolated from 6 randomly selected hens per colony cage and all 5 hens in 9 conventional cages per strain and frozen for later analysis of bone densitometry and breaking strength. Conventionally caged hens exhibited higher incidence of pre slaughter humerus and radius fractures ($P < 0.05$). Furculum breaks occurred most frequently post slaughter; however, no treatment or strain differences were determined for the furculum. LL and LB hens exhibited fewer wing and leg breaks pre and post slaughter ($P = 0.05$), however LL hens exhibited the highest incidence of keel fractures before slaughter. These results indicate that bone fractures throughout the laying period and at processing are more common in conventionally housed laying hens, and that strain differences are apparent.

Key Words: laying hen, bone quality, furnished cages

258 Astroturf as a dustbathing substrate for laying hens. G. Alvino*, G. Archer, and J. Mench, *University of California*, *Davis*.

During dustbathing bouts, birds distribute a friable substrate like sand through their feathers. This behavior helps to maintain good plumage condition and hence the insulative value of the feathers. Many designs of furnished cages for laying hens contain a dustbathing area comprised of an Astroturf (AT) pad, which may be sprinkled with feed with the intent of promoting both foraging and dustbathing. We evaluated the behavior of hens exposed to AT or AT plus feed to determine if these substrates stimulate dustbathing. Hy-Line CV20 laying hens (n = 30) that had no prior exposure to friable substrate were housed singly in 91.4cm x 45.7cm x 45.7cm cages beginning at 34 weeks of age. Groups of 10 hens were randomly provided with either sand (control); a 33 × 36.5cm AT pad; or an AT pad of the same size covered each day with 200 g of laying hen feed (ATF). After the hens had been exposed to these substrates for 17 d, behavior was video recorded from 0600 - 2200 h (photophase duration). Data were analyzed using Kruskal-Wallis and Dwass-Steel- Critchlow- Fligner non-parametric tests. There were significant differences in the total number of dustbathing bouts ($H_2 = 8.21$, $P = 0.017$), with control hens performing fewer bouts (mean = 3) than AT (13); ATF were intermediate (6). The proportion of bouts performed on substrate ($H_2 = 13.94$; $P = 0.001$) and the wire floor of the cage ($H_2 = 12.68$; $P = 0.0018$) differed, with the control hens that dustbathed performing a higher proportion in substrate (1.0) and a lower proportion on wire (0) than both AT (0.13; 0.87) and ATF hens that dustbathed (0; 1.0). There were also differences in total time dustbathing on wire ($H_2 = 12.32$, $P = 0.002$) and substrate ($H_2 = 9.32$, $P = 0.010$), with control hens dustbathing for significantly less time on wire (mean = 0 min) than both AT (26) and ATF (28) hens and significantly more time on substrate (19) than ATF hens (0). These findings need to be confirmed with additional observations, but suggest that an AT pad does not provide an adequate substrate even with feed added, since hens with AT dustbathe mainly on the wire floor of the cage rather than on the AT.

Key Words: Astroturf, sham dustbathing, chicken

259 The behaviour of laying hens in commercial aviary systems. M. P. de Villareal*[1] and I. Estevez[1,2], [1]*Neiker-Tecnalia*, *Vitoria-Gasteiz, Spain*, [2]*IKERBASQUE*, *Bilbao, Spain*.

Here we present preliminary results of a larger ongoing study in which we compare the behavior of laying hens maintained under different production conditions. For this part of the study, data were collected by video footage in 7 single tier aviary commercial farms with and without access to an outdoor park. Flock sizes ranged between 6,000 to18,000 birds. The lines used were Bovan brown, ISA brown, and Lohman white. Video recordings took place from 7.00 to 9.00, 11.00 to 13.00 and 17.00 to 19.00 for morning, midday and afternoon periods. Video sequences were imported into the software The Observer for visualization and analysis. From the recordings, behavioral time budgets and frequency of transitions, defined as the number of behavioral changes per unit of time, were obtained by continuous focal sampling of 3 randomly chosen hens in each video sequence. Data were standardized according to sequence duration. Means per farm, week and time period were calculated and used for statistical analysis, a mixed model repeated measures ANOVA (SAS, V 9.1). Results indicate differences in time budgets across layer line and housing system ($P < 0.01$), but

no effect of time period was detected ($P > 0.05$). Interactions across factors were non significant ($P > 0.05$). Lohman whites had the highest proportion walking and foraging whereas standing was most prominent in Bovan and ISA brown. Problematic behaviors such as aggressive pecks, threats and feather pecking were unusual events for all lines. The differences according to systems were important with higher frequencies of standing and foraging observed in aviaries without access to parks, and higher proportions of resting and less standing and foraging observed in free range. Behavioral transitions varied according to hen type and housing system only ($P < 0.05$). In conclusion, across strains the Lohman white hens were the most active, however no differences were detected related to problematic behaviors such as aggressive or pecking behaviors. Contrary to expectations, birds with access to an outdoor park were less active when indoors as compared with birds in aviaries without access to parks.

Key Words: laying hens, behavior, aviary systems

260 On-farm survey of beak characteristics in White Leghorns as a result of hot blade or infrared beak trimming. T. Gabrush[1], C. Carruthers*[1], K. Schwean-Lardner[1], T. Knezacek[1], C. Bennett[2], and H. L. Classen[1], [1]*University of Saskatchewan*, *Saskatoon, SK Canada*, [2]*Manitoba Agriculture, Food & Rural Initiatives*, *Winnipeg, MB Canada*.

Treating the beaks of White Leghorns is a common practice used primarily to reduce cannibalism. However, opposition to this procedure is based partially on the assumption that trimming may cause deformities, inhibiting the ability of hens to eat and perform normal behaviors. Infrared (INF) systems are currently becoming more prevalent in industry, replacing hot blade (HB) beak trimming. This on-farm survey examined the effects of HB or INF treatment on beak characteristics in commercial flocks. Hens on 3 farms were observed between 21 and 24 and between 53 and 60 weeks of age. Two farms housed hens of the same strain that had been HB trimmed at the hatchery while a third housed 2 strains that had been INF treated at the hatchery. Overall, 91% of the beaks measured were 10.0 to 13.9 mm in length, approximately 52 to 73% of the expected length of an intact beak. The remaining hens had beaks less than 10 mm (4%) or ≥14 mm (5%). HB trimmed beaks averaged 12.36 mm (SEM = 0.060) and 12.40 mm (SEM = 0.063) at 21–24 weeks of age, and 12.39 mm (SEM = 0.064) and 12.80 mm (SEM = 0.071) at 53–60 weeks of age. INF trimmed beaks averaged 11.33 mm (SEM = 0.058) and 11.14 mm (SEM = 0.043) at 21–24 weeks of age, and 12.03 mm (SEM = 0.053) and 11.35 mm (SEM = 0.059) at 53–60 weeks of age. Deformities were observed at low frequencies, and included abnormal re-growth (7.42%), blisters (0.54%), cracks (3.50%), angled beaks (not perpendicular; 2.88%) and cases where the bottom beak was longer than the top (BLTT) (11.63%). Although a direct comparison between HB and INF trimming was not possible because the hens were of different strains and were housed in different environments, cracks and abnormal re-growth were observed more frequently in HB (6.58% and 11.42%, respectively) compared with INF trimmed hens (0.42% and 3.42%, respectively). HB and INF treatment resulted in similar beak lengths and characteristics, however comparisons of treatment type within strain and environment is warranted.

Key Words: cannibalism, feather pecking, welfare

261 Effects of different infrared beak treatment protocols on chicken welfare and physiology. R. L. Dennis* and H. W. Cheng, *LBRU, USDA-ARS*, *West Lafayette, IN*

Infrared beak treatment (IR) provides an alternative to conventional hot blade beak trimming (HB), which purports to be more welfare friendly. To improve the efficiency of the IR system, different interface plates (25/23C and 27/23C) and lamp power settings (44, 48 and 52) were tested in this study. Infrared beak treatment was conducted at the hatchery and HB was performed at 7 to 10 d of age in a commercial setting. Physiological and behavioral measures were taken at 5, 10, 20 and 30 weeks of age after beak trimming (BT). Although all birds followed a similar growth curve, IR birds using 27/23C-48 protocol were the heaviest at 10, 20 and 30 weeks of age. Alternately, birds using the 25/23C-44 protocol were the lightest at 20 and 30 weeks of age. Upper and lower beak growth curves were also established showing birds trimmed with 25/23C interface plates to have a shorter upper and lower beak compared with 27/23C or HB trimmed birds. Birds trimmed using 27/23–44 and −48 consistently had the longest upper and lower mandibles among all birds. Feed wasted was greatest in HB and 27/23C-52 birds and tended to be less than HB in 27/23–48 and 25/23–48 and −52 trimmed birds ($P < 0.10$). Behavior analysis revealed that birds treated using 27/23C protocols walked and drank more than HB birds ($P < 0.05$). Feather scores (FS; scored 0–5; 0 = perfect plumage and 5 = bare with skin damage) taken at 20 and 30 weeks showed higher breast FS in HB and 25/23C-44 birds compared with 27/23C birds ($P < 0.05$). Back FS was the highest in 25/23C-48 birds compared with the birds trimmed using HB or other IR protocols ($P < 0.05$). At 5 and 10 weeks of age, 27/23C-44 and −48 birds pecked significantly more at the novel object (a synthetic feather) than the birds trimmed using HB or other IR protocols ($P < 0.05$). However, HB and 25/23C birds had the highest synthetic feather damage score (scored 0–5; 0 = no damage and 5 = completely stripped shaft; $P < 0.05$). Our data show evidence that welfare and traits affecting feed efficiency can be improved with IR over HB in laying hens and that the IR protocol used can be adjusted to optimize these measures.

Key Words: beak trim, infrared, laying hen

262 Brain and skull lesions in turkeys resulting from non-penetrating captive bolt, cervical dislocation, cervical crushing and blunt trauma. M. A. Erasmus*, P. V. Turner, S. G. Nykamp, and T. M. Widowski, *University of Guelph*, *Guelph, Ontario, Canada*.

Previously, live observations of brainstem reflexes and time to death were conducted on different weight classes of turkeys to assess the effectiveness of on-farm killing methods. Three experiments were conducted: 1) a non-penetrating captive bolt (Zephyr) and cervical crushing were examined in turkey hens (11.4 ± 0.1 kg) at a research facility; 2) the Zephyr and blunt trauma were examined in turkey toms (13.1 ± 0.2 kg) at 2 commercial farms; 3) the Zephyr, blunt trauma and cervical dislocation were examined in broiler turkeys (4.1 ± 0.3 kg) at a commercial farm. Immediate insensibility resulted when the Zephyr or blunt trauma were used, but not with cervical crushing or cervical dislocation. Based on these results, the objectives of the present study were to assess brain damage resulting from the different killing methods. The severity of skull fractures and subcutaneous and subdural hemorrhage was assessed using post mortem macroscopic scores. Samples in each weight category were submitted for CT scans and histology. Macroscopic scores were compared among treatment groups using a mixed model (Expt. One and 2) and general linear model (Expt. 3); subcutaneous hemorrhage was greater with the Zephyr (Hens: $F = 27.8$, $P = 0.01$; Toms: $F = 5.4$, $P = 0.02$; Broilers: $F = 11.6$, $P = 0.0003$) and skull fractures were more severe for toms and broilers killed with the Zephyr vs. blunt trauma (Toms: $F = 65.0$, $P < 0.0001$; Broilers: $F = 5.4$, $P = 0.03$). Subdural hemorrhage was present in all turkeys regardless of treatment. Microscopic brain damage was present in all turkeys killed with the Zephyr and blunt trauma, but only 1 of 4 turkeys killed with

cervical crushing and 1 of 4 turkeys killed with cervical dislocation. The Zephyr and blunt trauma likely caused death by directly disrupting brain function, whereas cervical crushing and cervical dislocation likely resulted in death from cerebral hypoxia and ischemia. Based on tests of sensibility and post mortem investigations into the degree of brain damage produced, the Zephyr and blunt trauma appear to be effective and humane for on-farm killing of turkeys.

Key Words: turkey, brain damage, humane killing

263 An experiment in transmission of *Mycoplasma bovis* in sand bedding to naive dairy calves. D. J. Wilson*[1], A. Justice-Allen[1], T. J. Baldwin[1], R. T. Skirpstunas[1], K. B. Cavender[1], and G. Goodell[2], [1]*Utah State University*, *Logan*, [2]*The Dairy Authority*, *Greeley, CO*.

The study evaluated possible transmission of *Mycoplasma bovis* from sand bedding to naive dairy calves. Screening of a closed herd showed 99% probability that the herd was free of mycoplasma in calves. Neonatal calves (n = 12) from the herd were blocked by weight and height and randomly assigned as controls (n = 6) bedded with quarry sand, or exposed (n = 6) bedded with *M. bovis*-positive bedding sand (confirmed by PCR) from another farm. Calves were housed at Utah State University in calf hutches, fed commercial milk replacer and calf starter, with strict biosecurity and separation between groups. Exposed group sand cultured positive for *Mycoplasma* spp. during weeks 1, 5, 6, 7, 11 and negative for the rest of the 15 week study; control group sand was always mycoplasma-negative. Exposed group calves were bedded on mycoplasmal bedding for 138 total calf-days. All 94 sera tested for antibody against *M. bovis* were negative. All 16 tracheal swabs and all 67 nasal and ear swabs collected from all calves were mycoplasma culture-negative. Two calves died and 3 were euthanized before the end of the study; the remaining 7 calves were euthanized after 15 weeks. All calves were necropsied and full diagnostic testing was performed. No exposed or control calves had any gross lesions of mycoplasma infection. All post-mortem culture (n = 60) and PCR (n= 48) tests on trachea (cultured only), deep lung, peri-bronchial lung, retropharyngeal lymph node, and carpal or tarsal joint fluid from all 12 calves were negative for *Mycoplasma* spp. The PCR could differentiate *M. bovis* if positive. Using test sensitivity and sequential probability, the probability of each calf being detected positive at least once if they had become infected with mycoplasma following 4 weeks of exposure was calculated. For the 9 calves that survived beyond 25 days of age, probabilities of detection were between 96.5% and 99.3%. There was no evidence that *Mycoplasma bovis*-positive bedding sand was a source of infection to naive dairy calves. Further studies in lactating cows are still indicated because of the possibility of infection through teat ends.

Key Words: mastitis, *Mycoplasma*, bedding

264 Effect of supplementing fatty acids to prepartum Holstein cows on transfer of passive immunity to calves. M. Garcia*, L. F. Greco, M. G. Favoreto, R. S. Marsola, L. T. Martins, D. Wang, W. W. Thatcher, J. E. P. Santos, and C. R. Staples, *University of Florida*, *Gainesville*.

The aim of this study was to evaluate supplementing linoleic acid (LA) to cows during the last 2 mo of pregnancy on transfer of passive immunity to calves. Cows (n = 89) were fed diets formulated to supply minimum amounts of LA and supplemented without fat, with saturated fatty acids (SFA; Energy Booster 100, MSC) at 1.75% of dietary DM, or with Ca salts of unsaturated fatty acids enriched in LA (UFA; Megalac-R, Church and Dwight, Co.) at 2% of dietary DM. Within 2 h of birth, calves were given 4 L of colostrum from their own dam or from a dam fed the same dietary treatment as the calf's dam using an esophageal feeder. Acquisition of passive immunity was assessed by measuring concentration of IgG in colostrum and in serum, as well as total protein concentrations in serum at 0 and 24 h of life. Apparent efficiency of absorption was calculated considering serum as 9.9% of BW. Body weight at birth did not differ among treatments (39.6 kg), however calves born from multiparous cows were heavier ($P < 0.05$) than those born from primiparous cows (42.6 vs. 36.5 kg). Concentration of colostral IgG was greater from multiparous cows fed fat than from those not fed fat prepartum (116 vs. 96 g/L) whereas the opposite was true for primiparous cows (83 vs. 101 g/L). As a result intake of IgG by calves born from multiparous cows fed fat prepartum was greater than that by calves born to cows not fed fat (459 vs. 383 g). Therefore serum concentrations of IgG tended to be greater ($P = 0.10$) at 24 h in calves born from multiparous cows fed fat compared with those not fed fat (26.7 vs. 21.1 g/L). Concentrations of serum protein did not differ among treatments (3.8 and 5.3 g/100 mL at 0 and 24 h, respectively). Calves born from cows fed fat prepartum tended to be more efficient at absorption of IgG (26.8 vs. 23.3%). Feeding supplemental fat prepartum to multiparous cows resulted in greater IgG concentration in colostrum and better efficiency of IgG absorption.

Key Words: calves, passive immunity, linoleic acid

265 Effect of a yeast autolysate combined with probiotics on performance and gut health of broilers. A. Ganner*[1], S. Masching[2], N. Reisinger[1], G. Schatzmayr[1], and T. Applegate[3], [1]*BIOMIN Research Center*, *Tulln, Austria*, [2]*BIOMIN Holding GmbH*, *Herzogenburg, Austria*, [3]*Purdue University*, *West Lafayette, IN*.

The present study was conducted to evaluate the efficacy of a product, consisting of yeast autolysate, lactobacilli, *Enterococcus* sp., *Pediococcus* sp. and bidifobacteria, on performance and jejunal structure of broilers. In a 35 d study, 300 1-d-old broilers were distributed to 2 experimental groups with 8 replicates: control group A, group B (1 kg yeast autolysate per ton feed combined with probiotic mixture of 10^8 CFU/kg feed). Directly after housing the chicks were supplied with the experimental diets. Feed and water were provided for *ad libitum* intake, feeding was done manually several times a day. On d 35 birds were killed and the distal jejunum taken from 8 chickens per group (1/pen). Paraffin sections were stained with periodic acid Schiff (PAS) and hematoxylin. The length of the villi and the depth of the crypt were determined with an ocular micrometer via light microscopy. The goblets cells were counted on 6 villi/ bird as well under the microscope and an average was taken. Similarly, 12 villi/ bird were measured for villus length and crypt depth. In the course of the feeding trial a positive influence could be observed by the product consisting of autolysate and probiotics. Weight on d 14 and daily weight gain (DWG) 1–14 were improved ($P = 0.0001$), as well DWG 15–35 ($P = 0.002$). Weight on d 35 (1433g) and DWG 1–35 (39.9g) were slightly improved in comparison to the control (1381g weight d 35, 38.4g DWG; $P = 0.08$). Mortality was reduced in the trial group (2.7%) in comparison to the control (5.3%). The goblet cell number was slightly increased by the trial group with 126 cells/villus (control 98cells/villus, $P = 0.1$). Villus height and crypt depth were not affected. Our results indicate that the product consisting of autolysate and probiotics is able to improve gut health and to enhance bird performance.

Key Words: yeast autolysate, probiotics, gut health, broiler performance

266 Effect of NuPro supplementation on intestinal *Clostridium perfringens* levels in broiler chickens. . R. Thanissery*[1], J. L. McReynolds[2], D. E. Conner[1], K. S. Macklin[1], P. A. Curtis[1], and Y. O. Fasina[1], [1]*Auburn University*, *Auburn, AL*, [2]*SPARC-USDA-ARS*, *College Station, TX*.

Clostridium perfringens (CP) is the causative bacteria for necrotic enteritis (NE) in poultry. Yeast extract contain immunomodulatory nucleotides, and may therefore serve as a non-antibiotic feed additive for reducing intestinal CP in broilers. In a 42-d floor pen trial, the efficacy of NuPro (a yeast extract) in reducing intestinal CP levels in broiler chickens was evaluated. Chicks (n = 600) obtained from a commercial hatchery were randomly assigned to 6 treatments. Treatment 1 (CX) consisted of chicks fed corn-soybean meal (SBM) diet without bacitracin methylene disalicylate (BMD) or NuPro added. Treatment 2 (MX) consisted of chicks fed corn-SBM basal into which BMD was added at 0.055g/kg. Treatment 3 (LN) consisted of chicks fed corn-SBM basal into which NuPro was added at 2% level throughout experiment. Treatments 4 (PCX), 5 (PMX), and 6 (PLN) consisted of chicks fed diets similar to those given to CX, MX, and LN treatments, respectively, and were additionally challenged with 3.5 mL of CP inoculum (10^8 CFU/mL) on d 14, 15, and 16 of experiment. Post-challenge (PC) assessment of intestinal CP levels was done on d 1, 7, and 21 PC. Growth performance (body weight (BW) and body weight gain (BWG)) was also assessed at 3 and 6 weeks. Results showed that by d 21 PC, the NuPro-containing diet significantly reduced intestinal CP levels ($P < 0.05$) in PLN treatment by 1.50 $\log_{10}$ CFU/g compared with NuPro-free PCX treatment. Also, the efficacy of BMD antibiotic and NuPro in reducing intestinal CP in PMX and PLN, respectively, was similar throughout the experiment. BW and BWG were similar ($P > 0.05$) among CP-challenged chicks (PCX, PMX, and PLN treatments), indicating that the NuPro-induced reduction of CP in PLN treatment occurred without any adverse effect on bird performance. In conclusion, dietary supplementation of NuPro at 2% level of diet effectively reduced intestinal CP during broiler production cycle.

Key Words: *Clostridium perfringens*, NuPro, broiler chickens

267 A modified in vitro larvae migration inhibition assay using rumen fluid to evaluate *H. contortus* viability. T. R. Whitney*[1], D. R. Klein[2], A. E. Lee[1], C. B. Scott[2], and T. M. Craig[3], [1]*Texas AgriLife Research*, *San Angelo*, [2]*Angelo State Univ.*, *San Angelo, TX*, [3]*Texas A&M Univ.*, *College Station*.

The objectives of this study were to evaluate how forage material added to an in vitro system affects rumen fluid parameters, which may unintentionally affect larvae viability (LV), and define effective concentrations of common additives, i.e., polyethylene glycol (PEG), quebracho tannins (QT), and ivermectin used in this modified in vitro larvae migration inhibition (LMI) assay. Rumen fluid was collected and pooled from goats (n = 3), mixed with buffer solution and a treatment (1 jar per treatment), and placed into an anaerobic incubator for 20 h. Ensheathed *H. contortus* larvae (<3 mo old) were then anaerobically incubated with treatment rumen and buffer fluid (repeated in 2 to 3 runs; 3 cups/treatment) for either 2, 4, or 16 h depending on the Trial; pH, ammonia N, and VFA were evaluated just before and after larvae were incubated. Larvae were then transferred into a well (n = 4 to 6 wells per treatment cup) containing treatment rumen fluid, within a Multi-Screen 96-well plate and incubated over night; larvae that passed through the 20-µm screen were considered viable. Data were analyzed using the MIXED procedure with run as the repeated measure and cup (rumen parameters) or well (LV) as the subject. Adding dry or fresh juniper material (representative of 40% of diet DM intake) reduced ($P < 0.05$) pH, ammonia N, and isobutyric, butyric, and isovaleric acids, and increased ($P < 0.001$) acetic, propionic, and total VFA. The PEG concentrations of 0, 0.4, 0.8, 1.4, and 2% w/v quadratically reduced ($P = 0.07$) LV. The QT concentrations of 0, 0.15. 0.6, and 1.2% w/v quadratically reduced ($P < 0.001$) LV; 89.4, 65.5, 22.8, and 9.2%, respectively. Ivermectin concentrations of 0, 0.05, 0.10, 0.50, 1, 1.5, 2, 3, 6 and 15 µg/mL quadratically reduced ($P < 0.001$) LV; 90.2, 82.6, 73.6, 66.3, 51.9, 56.5, 43.5, 41.9, 29.3, and 19.9%, respectively. Effects of altering in vitro rumen parameters and the use of PEG on LV needs to be further investigated. Concentrations of QT and ivermectin sufficiently decreased LV; thus, can be used in trials evaluating effects of in vitro rumen treatments on *H. contortus* viability.

Key Words: juniper, secondary compounds, internal parasites

268 Effect of feeding nitarsone medicated ration on the acquisition and development of nematode parasites in the chicken. F. D. Clark*[1], C. A. Tucker[1], J. Reynolds[1], T. A. Yazwinski[1], S. Clark[2], V. Smith[2], and K. Dobson[2], [1]*University of Arkansas*, *Fayetteville,* [2]*Alpharma, Inc*, *Bridgewater, NJ*.

This study was conducted to investigate the anthelmintic efficacies of nitarsone when fed at recommended dietary levels (Histostat at 0.01875%) to artificially infected chickens. Birds were obtained at 1 d of age (experiment d 1), and kept parasite free until artificially infected. Four experimental groups of chickens were established, 2 pens of 24 birds per pen in each group: TRT 1, non-medicated and uninfected; TRT 2, non-medicated and artificially infected on d 14, 21 and 28; TRT 3, medicated from d 42 to d 56 and artificially infected on d 14, 21 and 28; and TRT 4, medicated from d 7 to 56 and artificially infected on d 14, 21 and 28. For each day of scheduled artificial infection, each bird in a pen designated for infection was gavaged with a 1 mL suspension containing 500 *Ascaridia galli*, 500 *Heterakis gallinarum* and 1000 *Capillaria obsignata* eggs that contained infective larvae. Every 7 d from d 35 to 63, 5 fresh droppings were obtained from each pen, combined by pen and homogenized, and processed 3 times by homogenate for egg per gram counts (EPG). Additionally, randomly obtained birds from each pen were necropsied for nematode recoveries and counts on d 42 (3/pen; 6/exp grp) and 63 (12/pen; 24/exp grp). No ascarid eggs were found in any droppings during the study. *Capillaria* eggs were found in droppings from birds of treatment groups 2, 3 and 4 from d 35 to 63, with no quantitative effect of treatment on the EPG counts. *Heterakis* eggs initially appeared in droppings from birds of treatment groups 3 and 4 on d 42, but by d 63, a negative treatment effect was demonstrated for the respective EPG counts ($P < 0.05$). Worm counts performed on birds posted on d 42 and d 63 indicated a lack of treatment effect on total (larval plus adult) worm burdens as *Capillaria*, *Heterakis* or *Ascaridia*. However, for d 63 observations, negative treatment effects were noted for adult *Ascaridia galli* numbers, adult female sizes and the number of fully developed eggs per adult female ($P<0.05$).

Key Words: nitarsone, chickens, nematode parasitisms

269 Effect of a *Lactobacillus* probiotic and nitrate in feed on *Salmonella* colonization in broiler chicks. A. D. Wolfenden*, N. R. Pumford, M. J. Morgan, S. L. Layton, C. Kremer, G. Tellez, and B. M. Hargis, *University of Arkansas*, *Fayetteville*.

In our previous studies, we have found a consistent reduction of *Salmonella enteritidis* (SE) using a lactic acid probiotic culture (B11) in neonatal chicks. In vitro studies suggest that nitrate (NO_3) may potentiate this effect. An in vitro crop assay model was used to evaluate the effect of NO_3 in combination with B11 against SE. B11 with NO_3 at1000ppm reduced SE by 6.54 $\log_{10}$ as compared with non-treated control during a 24h incubation at 40C. Two in vivo studies were then initiated to determine if addition of NO_3 in the feed could further reduce SE colonization in the crop and cecal tonsils of broiler chicks. Briefly, 180 d-of–hatch chicks were randomly assigned to 6 groups: control, B11,

or B11with NO_3 at 1, 10, 100 or 1000 ppm. All groups were challenged by oral gavage with approximately 10^4 cfu of SE (n = 30/group). One hour later, all groups except control were treated by oral gavage with approximately 10^7 cfu of B11. Twenty-four hours and 72 h after treatment, chicks were humanely killed (n = 15/group), and crop and cecal tonsils were cultured for SE. In exp. 1, at 72h there was a significant ($P < 0.05$) decrease in the percent of SE positive crops from the B11+ $NO_3$100ppm (57%) and B11+ $NO_3$10ppm (67%) as compared with the control (93%). A significant reduction in the percent positive cecal tonsils in all groups was observed at 24h, however at 72h, only the B11 (47%) and B11+ $NO_3$100ppm (14%) were different from the control (93%). Exp. 2 was similar to exp. 1 with the following exceptions: chicks assigned to 3 groups (n = 40/group): control, B11, B11+NO_3 100ppm. In exp. 2, significant reductions of SE positive crops in both treated groups compared with control were noted: control: 24h 100%, 72h 100%; B11 24h 10%, 72h 65%; B11+ $NO_3$100ppm 24h 60%, 72h 10%. Similar results were noted in the cecal tonsil: control 24h 95%,72h 95%; B11 24h 10%, 72h 35%; B11+ $NO_3$100ppm 24h 15%, 72h 25%. These experiments indicate that the addition of NO_3 potentiated the effects of the lactic-acid bacteria probiotic in vitro and in vivo. It is postulated that this effect is through increased production of nitric oxide by the beneficial bacteria.

Key Words: *Salmonella*, nitrate, probiotic

270 Effect of food additives on intestinal microflora in caeca of broilers challenged with *Eimeria* species analyzed using 16S rDNA pyrosequencing. A. Nalian*[1], M. Manoharan[1], J. Bray[1], S. Dowd[2], and A. Martynova-Van Kley[1], [1]*Stephen F. Austin State University*, *Nacogdoches, TX,* [2]*Research and Testing Laboratory*, *Lubbock, TX*

The effect of food additives (coccidiostat and natustat) on composition of cecal microflora of *Eimeria* challenged broilers was studied using 454 pyrosequencing of 16S rDNA. We collected a total of 36 cecal samples from pre- and post-challenged birds from 4 treatment groups: natustat, coccidiostat, combination of both and control (no treatment). More than 170,000 sequences were obtained from pyrosequencing (~5000 sequences of an average 450 bp length per sample). The taxonomical lineage of the sequences was determined using RDP classifier and BLAST programs. Absolute majority of the sequences belonged to kingdom *Bacteria* and only 4 sequences belonged to kingdom *Archaea*. More than 94% of all the sequences belonged to phylum *Firmicutes* and 5% belonged to phylum *Proteobacteria*. Redundancy analysis of the relative percent abundance data from pre-challenged birds with Monte Carlo permutation test showed that there was no significant difference in microflora composition between different treatments. Whereas in post-challenged birds, we observed significant differences in microflora composition between treatment groups ($P = 0.01$) and also challenged and control groups ($P = 0.03$). In pre-challenged birds, the dominant taxa were *Lachnospiraceae* and *Faecalibacterium*. Generalized additive model showed that coccidiostat ($P = 0.001$) and combination of coccidiostat with natustat ($P = 0.002$) significantly lowered the number of bacterial taxa in ceca of chickens. In addition, in post-challenged birds, irrespective of treatment groups, the coccidia challenge lowered the relative percent abundance of *Faecalibacterium* taxa ($P = 0.001$). Our results show that pyrosequencing could be used to monitor the changes in microflora due to different treatments. We expect that pyrosequencing will be widely used in poultry for studying microbial communities and their interactions with the host and the environment.

Key Words: *Eimeria*, natustat, pyrosequencing

271 Genetic line and dietary immunomodulator effects on expression of CXCLi2 in chicken heterophils responding to *Salmonella enteritidis*. S. B. Redmond*, P. Chuammitri, D. Palic, C. B. Andreasen, and S. J. Lamont, *Iowa State University*, *Ames*.

The performance of leukocytes in the response to pathogens is influenced by genetic background and diet. Dietary immune modulation can alter the mechanisms by which leukocytes, such as chicken heterophils, respond to bacteria. This experiment evaluated the effects of genetic line and dietary immune modulation over time on chicken heterophil expression of interleukin-8 (CXCLi2), an important chemotactic chemokine which recruits leukocytes to the site of an infection. Chickens (n = 64) from highly inbred Leghorn and Fayoumi lines received basal or immune modulating diets enhanced with 0.1% β-glucans, 0.1% ascorbic acid, or 0.01% corticosterone from 8 to 11 weeks of age. Heterophils were isolated from blood samples pooled within line and diet (n = 4 birds/pool) on d 1, 3, 7, and 21 after the start of diet treatments, and then exposed to *Salmonella enteritidis* (SE) bacteria in vitro for 3 h. Heterophil isolates were assayed for CXCLi2 expression mRNA by quantitative RT-PCR. Cycle threshold values were analyzed by ANOVA for the fixed effects of genetic line, diet, and day post treatment, with hatch and plate as random effects. Collection day post treatment was not significant. Leghorn line heterophils expressed significantly higher levels of CXCLi2 than those from the Fayoumi line ($P < 0.01$), suggesting that the Leghorn response to SE relies more heavily on chemotactic signaling. Heterophils from birds fed the corticosterone diet expressed less CXCLi2 than those of birds fed the basal diet ($P < 0.05$), reflecting corticosterone's ability to inhibit immune response. This result suggests that stress-induced corticosterone increases can inhibit the ability of heterophils to produce chemotactic signals. There was no significant difference in CXCLi2 expression by heterophils of birds fed the β-glucans or ascorbic acid enhanced diets, indicating that these immune stimulants likely alter mechanisms other than chemotaxis to enhance immune response.

Key Words: dietary immune modulation, heterophils

272 Nitric oxide synthesis by chicken macrophages results in coordinated changes in the mRNA abundance of multiple arginine transporters. M. Moulds* and B. D. Humphrey, *California Polytechnic State University*, *San Luis Obispo*.

Nitric oxide (NO) is synthesized by macrophages when arginine (ARG) is cleaved by inducible nitric oxide synthase (iNOS). In mammals, ARG uptake for NO synthesis is controlled by CAT-2B, but in Aves the requisite system(s) are unknown. Therefore, ARG transporter mRNA abundance was quantified during a NO response from a chicken macrophage (HD-11) cell line and peripheral blood monocytes (PBM). PBM were isolated from Hyline W36 white leghorn hens (n = 3). PBM were cultured in RPMI complete media at 10^5/well (n = 3) while HD-11 cells were cultured in IMDM complete media at 4×10^5 HD-11 cells/well (n = 6). To induce NO production, cells were cultured with 0 (control) or 1 μg/ml *E. coli* lipopolysaccharide (LPS) for 48 h. NO was measured indirectly by means of media nitrite concentration. Total RNA was isolated from cultured macrophages and was reverse transcribed for measurement of iNOS and ARG transporter mRNA abundance by quantitative real-time PCR. LPS increased HD-11 nitrite concentration by 7,600% and PBM by 8.7% ($P < 0.05$). LPS also increased HD-11 and PBM iNOS mRNA abundance 8.5-fold and 2.6-fold, respectively ($P < 0.05$). CAT-2B mRNA was undetectable in both HD-11 and PBM cell types. In HD-11 cells, LPS induced CAT-1 and CAT-3 mRNA abundance from undetectable levels, and also increased CAT-2A mRNA abundance 1.6-fold ($P < 0.05$). The exporter y^+LAT1 mRNA abundance decreased by 71% in HD-11 cells ($P < 0.05$), but no change occurred in

y^+LAT2 mRNA abundance ($P > 0.05$). In PBM, LPS increased CAT-1 and CAT-3 mRNA abundance 11-fold and 13-fold, respectively ($P < 0.05$). In LPS treated PBM, mRNA abundance of y^+LAT2 decreased 67% ($P < 0.05$), but y^+LAT1 mRNA abundance did not change ($P > 0.05$). NO production increased ARG transporter mRNA in HD-11 cells (CAT-1, CAT-2A, CAT-3) and PBM (CAT-1, CAT-3) and decreased ARG exporter mRNA in HD-11 cells (y^+LAT1) and PBM (y^+LAT2). These data indicate that multiple ARG systems may be involved in ARG uptake for NO production in avian macrophages.

Key Words: arginine, macrophage, nitric oxide

273 Dietary cinnamaldehyde enhances intestinal protective immunity against *Eimeria acervulina*, *E. maxima* and *E. tenella* in broiler chickens. S.-H. Lee*[1], H. Lillehoj[1], S.-I. Jang[1], K.-W. Lee[1], M.-S. Park[1], and D. Bravo[2], [1]*Animal and Natural Resources Institute, Agricultural Research Service-U.S. Department of Agriculture*, *Beltsville, MD,* [2]*Pancosma S.A.*, *Grand Saconnex, Geneva, Switzerland*.

The protective effect of dietary treatment of cinnamaldehyde on challenge infection with *E. acervulina* (EA), *E. maxima* (EM), or *E. tenella* (ET) (20,000 oocysts/bird) was evaluated in broilers. Three days after hatch, broiler chickens were continuously fed with a standard diet (20/group) or standard diet supplemented with cinnamaldehyde (20/group) for 4 weeks and challenge infection was given at 2 weeks of age. Body weight gains, antibody titers, and cytokine gene expression were measured following oral challenge infection with EA, EM or ET. When body weight gains were measured at 5 and 9 d post infection (dpi), cinnamaldehyde-fed birds showed 10~30% increases over ($P < 0.05$) the untreated birds following challenge infection with EA, EM or ET. Cinnamaldehyde-fed chickens produced 2 folds higher IgY antibody titers ($P < 0.05$) against coccidia at 9 dpi compared with the control group. Finally, the levels of intestinal lymphocyte cytokine transcripts of IL-1β, IL-6, IL-15, and IFN-γ were 2–5 folds higher in the cinnamaldehyde-fed chickens compared with the controls. This study provides the first immunological evidence that dietary cinnamaldehyde significantly enhances host innate immunity against coccidiosis.

Key Words: Cinnamaldehyde, immunity, broiler

274 Immune system stimulation and sulfur amino acid intake alter the pathways of glutathione metabolism at transcriptional level in pigs. A. Rakhshandeh*[1], A. Holliss[2], N. A. Karrow[1], and C. F. M. de Lange[1], [1]*University of Guelph, Department of Animal and Poultry Science*, [2]*University of Guelph, Advance Analysis Centre*, *Guelph, Ontario, Canada*.

The synthesis rate of GSH increases during immune system stimulation (ISS) and is highly dependent on availability of sulfur amino acids (SAA). The expression of key regulatory genes was determined to evaluate the impact of ISS and SAA intake on pathways of GSH metabolism. Restricted-fed barrows (BW 21.5 kg) were allotted to one of 2 levels of SAA intake (1.1 and 3.2, g/d) and injected with either saline (n = 8) or increasing amounts of *Escherichia coli* lipopolysaccharide (n = 16) every 48 h for 7 d. Pigs were then killed to collect liver tissue for total RNA extraction. Liver and an internal standard (KANr) RNA were then reverse transcribed, and expression of selected genes was simultaneously determined by multiplex PCR amplification of cDNA from liver, the housekeeping gene (β-2-microglobulin) and the internal standard in the presence of their corresponding florescent labeled primers. The interactive effect (ISS × SAA) resulted in lower and higher expression, respectively, of GSH synthetase (GSH-S) and GSH reductase (GSR) at the low level of SAA intake in ISS animals ($P < 0.04$). Increased SAA intake decreased expression of GSH-S and GSR but increased expression of GSH peroxidase 3 (GPX3; $P < 0.03$). Expression of glutamate-cysteine ligase modifier (GCLM) was decreased by ISS ($P < 0.01$). However, ISS increased expression of glutamate-cysteine ligase (GCS), GPX1, GPX3 and GSR ($P < 0.4$). No treatment effect on expression of γ-glutamyl hydrolase (GGH) or GPX4 was observed. This study demonstrates that ISS and SAA intake alter GSH metabolism pathways at the transcriptional level in liver of pigs.

Key Words: sulfur amino acids, immune system stimulation, gene expression, multiplex PCR, glutathione

Animal Health-Johne's Disease (JDIP): Epidemiology and Transmission

275 Cost-effectiveness of diagnostic strategies to identify *Mycobacterium avium* ssp. *paratuberculosis* super-shedder cows in a large dairy herd. S. S. Aly*[1], R. J. Anderson[2], R. H. Whitlock[3], T. L. Fyock[3], S. McAdams[3], T. M. Byrem[4], J. Jiang[5], J. M. Adaska[6], and I. A. Gardner[1], [1]*Department of Medicine and Epidemiology, School of Veterinary Medicine, University of California, Davis*, [2]*California Department of Food and Agriculture, Animal Health Branch*, *Sacramento,* [3]*Johne's Research Laboratory, New Bolton Center, School of Veterinary Medicine, University of Pennsylvania*, *Kennett Square,* [4]*Antel BioSystems, Inc*, *Lansing, MI,* [5]*Department of Statistics, University of California, Davis*, [6]*California Animal Health and Food Safety Laboratory, Tulare*.

Paratuberculosis-infected cows that shed *Mycobacterium avium* ssp. *paratuberculosis* (MAP) in excess of 10,000 CFU/g of feces have been termed super-shedders and contribute the most to MAP bioburden on a dairy. Identification of super-shedders in a large dairy herd is challenging given their low prevalence, cost of MAP diagnostic tests, and hence, the large sample size needed. Several diagnostic strategies to detect super-shedders are possible given the different MAP organism- and antibody-detection tests and specimens available to test. The objective of this cross-sectional study was to compare the cost-effectiveness of diagnostic strategies to detect MAP super-shedders in a large dairy herd. The study herd of 3577 Jersey cows had a MAP seroprevalence of 3.5% based on routine testing at dry-off. Cows were housed in 14 freestall pens and the herd manager requested not to move cows between pens during the study. A whole herd survey (reference) and 14 other diagnostic strategies were evaluated and their cost-effectiveness calculated. The reference strategy included quantitative real-time PCR (qrt-PCR) on fecal pools, followed by qrt-PCR of the individual cow fecal samples from the positive pools and a random sample of individual cow fecal samples from suspect and negative pools. The remaining strategies included combinations of serum ELISA, milk ELISA and environmental and pooled fecal samples tested using qrt-PCR. Twenty super-shedders (0.5% of the herd; 2% of qrt-PCR MAP positive cows) were identified and had a mean of 82,040 colony-forming units (CFU)/g of feces. The whole herd survey using qrt-PCR was the most sensitive strategy but sensitivity was ≤ 80% for all 15 strategies. The most cost-effective strategy was to rank lactating cow pens by MAP bioburden, milk ELISA test cows in pens ≤ 32 CT followed by qrt-PCR testing of fecal samples from milk ELISA positive cows. Environmental samples collected using a standardized protocol as part of a diagnostic strategy can improve the cost-effectiveness of detecting super-shedders compared to a whole herd survey by qrt-PCR.

Key Words: cost-effectiveness, MAP super-shedder

276 Correlation between culture and quantitative real-time PCR results for *Mycobacterium avium* subspecies *paratuberculosis* in pooled fecal and environmental samples. S. S. Aly*[1], B. L. Mangold[2], R. H. Whitlock[3], R. W. Sweeney[3], R. J. Anderson[4], J. Jiang[5], Y. H. Shukken[6], E. P. Hovingh[7], D. R. Wolfgang[7], J. S. Van Kessel[8], J. S. Karns[8], J. E. Lombard[9], J. M. Smith[10], and I. A. Gardner[1], [1]*Department of Medicine and Epidemiology, School of Veterinary Medicine, University of California, Davis*, [2]*Tetracore, Inc.*, *Rockville MD,* [3]*Department of Clinical Studies-New Bolton Center, School of Veterinary Medicine, University of Pennsylvania*, *Kennett Square,* [4]*California Department of Food and Agriculture, Animal Health Branch*, *Sacramento,* [5]*Department of Statistics, University of California, Davis*, [6]*Section of Epidemiology and Quality Milk Production Services, Department of Population Medicine and Diagnostic Sciences, College of Veterinary Medicine, Cornell University*, *Ithaca, NY* [7]*Department of Veterinary and Biomedical Sciences, Pennsylvania State University*, *University Park,* [8]*Environmental Microbial and Food Safety Laboratory, ANRI, USDA-ARS*, *Beltsville, MD,* [9]*Centers for Epidemiology and Animal Health, Animal and Plant Health Inspection Service, USDA*, *Fort Collins, CO,* [10]*Department of Animal Science, University of Vermont*, *Burlington*.

Quantitative real-time PCR (qPCR) testing for *Mycobacterium avium* subspecies *paratuberculosis* (MAP) in fecal samples is a rapid alternative to culture on Herrold's egg yolk medium (HEYM), the traditional reference test for MAP. Although the sensitivity and specificity of these 2 tests has been described, the correlation between qPCR cycles-to-threshold (Ct) values and colony-forming units (CFU) on HEYM has not been evaluated. The objective of the present study was to estimate the correlation between qPCR and HEYM culture results in fresh and frozen pooled fecal and environmental samples and model the association between results of both assays. Quantitative HEYM culture results for 1997 pooled fecal samples from cows in 14 herds in 4 states, and 802 environmental samples from 113 dairies nationwide were correlated with their respective qPCR results. The Spearman's rank correlation between assays was good (−0.66) in both fresh and frozen pooled fecal samples and excellent (−0.76) and good (−0.61) in fresh and frozen environmental samples, respectively. Furthermore, the correlation varied from good (−0.53) to excellent (−0.90) depending on size of fecal pools. Truncated linear regression models indicated a significant negative association between CFU and Ct in fecal pools of all sizes and in both individual and pooled environmental samples. The use of qPCR instead of HEYM can yield more timely quantitative MAP detection on a herd basis and allow for incorporation of qPCR in many dairy herd testing strategies to reduce the risk of MAP transmission.

Key Words: culture PCR correlation, pooled and environmental samples, *Mycobacterium avium* ssp. *paratuberculosis*

277 Fecal culture and direct PCR in determining *Mycobacterium avium* ssp. *paratuberculosis* infectivity. C. C. Wu*[1], J. E. Williams[2], T. L. Lin[1], and G. R. G. Monif[3], [1]*Purdue University*, *West Lafayette, IN*, [2]*University of Florida*, *Gainesville,* [3]*Infectious Diseases Incorporated*, *Bellevue, NE*.

The present study was conducted to evaluate the utility of fecal culture, direct fecal real-time PCR, and direct fecal nested PCR in determining the status of *Mycobacterium avium* ssp. *paratuberculosis* (Map) infectivity in dairy herd. Eight hundred and 27 (827) fecal samples were collected from 2 dairy herds participating in Johne's Disease Demonstration Herd Program. Fecal culture was carried out by using Trek ESP system with IS900 PCR confirmation. Direct fecal Map real-time PCR uses heat shock protein gene (hsp) as the target in PCR (VetAlert TM Johne's Real-Time PCR, Tetracore). Direct fecal Map nested PCR is based on IS1311 (FecaMap, Infectious Diseases Inc.). The percentages of fecal samples positive for Map were 13.5% by culture, 11.6% by real-time PCR, and 21.8% by nested PCR. Using positivity by direct fecal culture as the gold standard, 35 samples were positive for Map by real-time PCR with 83.3% accuracy and 51positive for Map by nested PCR with 77.3% accuracy. Using positivity by culture or both PCR as the gold standard, 112 samples were positive for Map by culture with 97.3% accuracy, 49 positive for Map by real-time PCR with 85.0% accuracy, and 65 positive for Map by nested PCR with 78.8% accuracy. The results indicated that using positivity for Map by culture or both

PCR as the gold standard is a more accurate tool in determining the status of Johne's disease infectivity in dairy herd.

Key Words: *Mycobacterium paratuberculosis*, fecal culture, direct fecal PCR

278 Estimation of test parameters for fecal culture and serum ELISA for detection of *Mycobacterium avium* ssp. *paratuberculosis* fecal shedding. L. A. Espejo*[1], F. J. Zagmutt[2], H. Groenendaal[2], and S. J. Wells[1], [1]*University of Minnesota*, *St. Paul*, [2]*Vose Consulting*, *Boulder, CO*.

The objective of this study was to estimate the probability of the fecal culture and serum ELISA to correctly identify cattle that shed high, low, and no fecal concentrations of *Mycobacterium avium* ssp. *paratuberculosis* into the environment. The results of 12,957 parallel fecal culture (HEY media) and serum ELISA (IDEXX) from 8 dairy herds enrolled in the Minnesota Johne's Disease Demonstration Herd Program over a 9 year period were used for this study. The conditional probabilities that test results indicate high, low, and no fecal shedding, given the true shedding status of the animal P(test results|true status) were estimated using Bayesian Markov-Chain Monte Carlo methods. The model assumed no gold standard test, independence between both tests and Dirichlet distribution for the priors. The shedding levels using fecal culture were categorized as high with ≥ 50 colonies/slant, low with 0 < colonies/slant < 50, and no fecal shedding with no detectable colony growth on the slants. Likewise, levels for serum ELISA were established based on OD values, with ≥ 1.0 (high), ≥ 0.25 and < 1.0 (low), and < 0.25 (negative). Informative prior distributions of the conditional probabilities were given by one of the co-authors (SJW). The probability of the serum ELISA to correctly identify high fecal shedders (P(High| High)) was 69%, while the same probability for fecal culture was 59%. The probability of incorrectly identifying animals that were high fecal shedders as no shedding (P(No shedding| high)) was 10% for serum ELISA and 3% for fecal culture. The probability of correctly identifying animals that were not shedding (P(No shedding|no shedding)) was 99.8% for serum ELISA and 98.9% for fecal culture. These posterior conditional distributions improve understanding of the fecal culture and serum ELISA, and this information can be used to model the transmission of Johne's disease on dairy farms taking into account the uncertainty of these tests.

Key Words: Johne's disease, diagnostic tests, Bayesian inference

279 Effect of delaying exposure to Johne's disease until adulthood on development of new infections in adult dairy cows. S. J. Wells*, N. Kubat, L. A. Espejo, and S. M. Godden, *University of Minnesota*, *St. Paul*.

Control programs for Johne's disease (JD) in US dairy cattle are designed with focus on preventing exposure by *Mycobacterium avium ssp. paratuberculosis* (MAP) in young replacement cattle, as these cattle are considered to be at highest risk of infection. The objective of this study was to compare rates of subclinical and clinical MAP infection in cattle raised in an environment presumed free of JD to those of cattle raised in an infected environment. Through a survey of uninfected Minnesota dairy herds (Levels 3 or 4 of the Voluntary Johne's Disease Herd Status Program for Cattle), we identified JD infected herds that previously purchased replacement cattle from uninfected herds. Over a 3 year period, blood and fecal samples were collected in infected herds from 78 purchased replacement cattle that were raised in uninfected herds (exposed) and homebred cows of similar age and stage of lactation (non-exposed controls). Serum samples were tested using an ELISA (IDEXX) for detection of antibodies to MAP and fecal samples were tested for detection of MAP using bacterial culture (HEY media). While results from the first year of testing of cattle across multiple ages indicated that dairy cattle raised in JD low risk herds (Level 3 or 4) and introduced to Johne's infected herds were less likely to test positive for MAP than herdmates raised in infected herds, results over time from survival analyses showed that this difference in risk was reduced later in life. The hazard ratio point estimate from Cox regression for exposed compared with unexposed cattle was 0.70 (95% CI = 0.40,1.23) and 0.64 (95% CI = 0.33,1.24) for fecal culture and ELISA, respectively. These results suggest risk of MAP infection in adult dairy cattle which should be considered in development of comprehensive JD control programs.

Key Words: Johne's disease, susceptibility

280 Importance of latent infected animals in MAP infection dynamics in dairy herds. Y. H. Schukken*[1], A. K. Pradhan[1], R. M. Mitchell[1], Z. Lu[1], R. Smith[1], Y. T. Grohn[1], R. H. Whitlock[2], E, Hovingh[3], J. Smith[4], J. A. VanKessel[5], J. Karns[5], and D. Wolfgang[3], [1]*Cornell University*, *Ithaca, NY*, [2]*University of Pennsylvania*, *Kennett Square,* [3]*Pennsylvania State University*, *State College,* [4]*University of Vermont*, *Burlington,* [5]*ARS-USDA*, *Beltsville, MD*.

Mycobacterium avium ssp. *paratuberculosis* (MAP) is an important infectious disease of dairy cattle. Prevalence of test positive cows in dairy herds is often low. Prevalences between 0 and 10% are most common. Such low infection prevalences would be expected to result in infection die-out in a proportion of herds due to culling that is unrelated or related to MAP infection status. In reality MAP infection die-out in dairy herds is not observed. At the very least it is not reliably documented. This would imply that complex mechanisms play a role in MAP infection maintenance in dairy herds. The objective of this presentation is to investigate the role of latent infected animals in endemically MAP infected dairy herds. Animals with a latent infection are defined as animals that are not detected to shed the organism while being tested using common testing schemes used in MAP control programs, but that turn out to be tissue positive when sampled and cultured at slaughter. We studied the potential contribution of latent infected animals to the vertical transmission route of infection and the contribution to a low rate of low shedding of these animals while in a high stress period. High stress periods were assumed to occur when an animal was calving and when severe clinical diseases such as mastitis, DA and lameness occurred. The importance of latent infected animals was evaluated in a previously described MAP model. We used simulation modeling to evaluate scenarios with intermittent shedding of latent MAP infected animals, increased vertical transmission in these animals and shedding while in high stress periods. Modeling the potential contribution of latent infected animals resulted in a better description of long-term low test prevalence herds and a more accurate prediction of a very low probability of infection die-out in dairy farms.

Key Words: MAP, modeling, latent infection

281 Impact of Johne's disease vaccines on a dairy herd: a mathematical modeling approach. Z. Lu*, Y. H. Schukken, R. L. Smith, and Y. T. Gröhn, *Cornell University*, *Ithaca, NY*.

The objective of this study was to investigate the potential impact of Johne's disease vaccines on the dynamics of MAP infection in a dairy herd using a mathematical modeling approach. To reduce the prevalence of MAP infection, vaccination has been applied as a control measure in some dairy herds. However, Johne's disease vaccines are imperfect and

several types of vaccine efficacy have been observed, i.e., vaccines may provide a partial protection for susceptible calves, reduce infectiousness/shedding level of animals shedding MAP, lengthen the latent period of infected animals, slow the progression from low shedding to high shedding in infectious animals, or reduce clinical disease. To quantitatively study the impacts of Johne's disease vaccines, we developed a deterministic multi-group vaccination model consisting of 18 nonlinear ordinary differential equations. The model was parameterized using data from US dairy herds. An analytical expression of the reproduction ratio (R) incorporating several vaccine efficacies was obtained. Our analytical and numerical results show that Johne's disease vaccines may have a positive, zero, or negative effect in the reduction of prevalence. Some vaccine efficacies are beneficial to individual animals, but may not be useful to a herd-level control plan. We also studied the impact of multiple vaccine efficacies on the dynamics of MAP transmission. This work is helpful to understand various outcomes in field studies of Johne's disease vaccines and to provide a tool to evaluate vaccine efficacies in Johne's disease control.

Key Words: Johne's disease, vaccination, modeling

282 Estimating the efficacy of imperfect paratuberculosis vaccines in dairy cattle from longitudinal field data with Markov Chain Monte Carlo models. R. L. Smith*, Y. H. Schukken, Z. Lu, and Y. T. Grohn, *Cornell University*, *Ithaca, NY*.

The purpose of this study was to determine the efficacy of vaccination against paratuberculosis in dairy cattle. For this purpose, a statistical model has been developed to analyze longitudinal field data from dairy herds with endemic paratuberculosis and control programs involving vaccination. Infection with *Mycobacterium avium* ssp. *paratuberculosis* (MAP) is difficult to detect, due to the long latent period and imperfect diagnostics. In commercial dairy herds, many animals could be culled before their infection status can be verified diagnostically. Due to this uncertainty as to true prevalence, it is challenging to obtain an unbiased estimate of vaccine efficacy. In addition, vaccines can do more than just decrease susceptibility to disease; vaccination against MAP may also decrease infectiousness, increase the duration of latency, or slow progression of clinical disease. To overcome the observed complexity of early censoring (culling) and multiple potential vaccine efficacies, we developed a Markov Chain Monte Carlo model. The potential vaccine effects are inter-related, but may have different and even opposite economic impacts. Markov Chain Monte Carlo (MCMC) models have been used extensively to estimate parameters for stochastic models from data sets with missing information. These models allow for simultaneous estimation of several variables in the presence of nonlinear relationships. In this study we developed an MCMC model to estimate 5 different possible vaccine effects (on vertical transmission probability, horizontal transmission rate, duration of latency, duration of subclinical disease, and rate of progression to clinical disease), while correcting for missing information (such as true infection status and time of infection). The 50% confidence intervals of the model's posterior distributions contain the true value of the parameters of interest when simulated over a wide range of vaccine efficacies. This is an effective tool for estimating vaccine efficacy from field data.

Key Words: Johne's disease, vaccine, statistics

283 Molecular epidemiology of *Mycobacterium avium* ssp. *paratuberculosis* in three dairy herds in the northeastern United States. A. K. Pradhan*[1], R. M. Mitchell[1], A. J. Kramer[2], J. Dieguez[3], R. H. Whitlock[4], J. M. Smith[5], E. Hovingh[6], J. S. Van Kessel[7], J. S. Karns[7], and Y. H. Schukken[1], [1]*Cornell University*, *Ithaca, NY,* [2]*Utrecht University*, *Utrecht, the Netherlands*, [3]*University of Santiago de Compostela*, *Santiago de Compostela, Spain*, [4]*University of Pennsylvania*, *Kennett Square,* [5]*University of Vermont*, *Burlington,* [6]*Pennsylvania State University*, *University Park,* [7]*Environmental Microbial and Food Safety Laboratory, ANRI, USDA-ARS*, *Beltsville, MD*.

The objectives of this study were to evaluate (i) whether low shedders of *Mycobacterium avium* ssp. *paratuberculosis* (MAP) were passive shedding animals or whether they were truly infected, (ii) whether these animals could have been infected as adults by contemporary high-shedding animals (super-shedders), and (iii) whether animals in the herds shared the same MAP strains with that were obtained from environmental samples. The MAP isolates were obtained from a longitudinal study of 3 dairy herds in the northeastern United States. Selected isolates from fecal samples and tissues from all animals that were culture-positive at the same time that super-shedders were present in the herds and all environmental isolates were strain typed using a multilocus short sequence repeat technique. We found 15 different MAP strains from a total of 142 isolates from fecal samples and tissues. Eight different strains were found from a total of 102 environmental isolates; 6 of these strains were present in these selected animal isolates. Results indicated herd-specific infection patterns; a clonal infection in herd C with 89% of animals sharing the same strain, whereas herds A and B showed several different strains. Shedding levels and MAP strain typing showed that at least 50% of low shedders have the same strain as that of a contemporary super-shedder. About 57, 50, and 94% of environmental samples shared the same strains as super-shedders on Farms A, B, and C, respectively, which suggests that super-shedders may represent a risk of spreading MAP-infection among adult herd mates. Results suggested that in a dairy herd few cows could be classified as passive shedders whereas more low-shedding cows are truly infected. The sharing of same strain of low shedders with the contemporary super-shedders suggests that low shedders may have been infected as adults by super-shedders. Sharing of same strains of both environmental and animal samples suggests the spread of MAP-infection through environment.

Key Words: *Mycobacterium avium* ssp. *paratuberculosis*, longitudinal study, MLSSR analysis

284 Field evaluation of TG marker IS1311 PCR-REA for rapid differentiation of Indian Bison type *Mycobacterium avium* ssp. *paratuberculosis*. J. S. Sohal, S. V. Singh*, P. K. Singh, and A. V. Singh, *Central Institute for Research on Goats*, *Makhdoom, Farah, Mathura (UP), India, 281 122*.

The availability of MAP genome in the public database opened various areas including the analysis of native isolates (comparative genomics). Comparative genomics studies at our laboratory have identified some key variations in the genome of native MAP. Studies has highlighted that "Indian Bison type" may represent a new MAP Biotype so far not reported outside India. One important variation in the genome of Indian Bison type isolates is the deletion of TG in the IS1311 element. Taking advantage of this variation on specific PCR-REA based test using BsaJI restriction enzyme was designed to distinguish Bison type isolates of Indian origin from other isolates. Present study analyzed and evaluated the use of this new assay for its practical utility in field for molecular epidemiological investigations. In total 45 previously characterized Bison type DNA samples of Indian origin from different parts of the country were analyzed. Results of the present study showed that all isolates belonging to Bison type genotype from different host species and agro-climatic region of the country had TG deletion in the IS 1311 element. Presence of this variation in all the Indian isolates belonging

to Bison type genotype is indicative of the fact that this variation has been established in all Bison type isolates of Indian origin. Hence this assay can be used in future molecular epidemiological investigations. Also this assay should be used in other parts of the world in order to study the distribution of newly identified MAP biotype.

Key Words: *Mycobacterium avium* ssp. *paratuberculosis*, TG deletion, IS 1311 PCR-REA

285 Rising incidence of *Mycobacterium avium* ssp. *paratuberculosis* in the North Indian population of animal keepers suspected for IBD/CD. S. V. Singh*, A. Shishodiya, A. Panwar, B. Singh, and A. Kumar, *Central Institute for Research on Goats*, *Makhdoom, Farah, Mathura (UP), India, 281 122*.

Mycobacterium avium ssp. *paratuberculosis* (MAP) infection is highly endemic in domestic livestock population in India. However, limited information exist on the association of MAP with human's Inflammatory bowel disease (IBD)/Crohn's disease (CD) in the country. Therefore, present study aimed to investigate the association of MAP in animal keepers from peri-urban areas of North India (Ghaziabad and Saharanpur cities) with symptoms of IBD/CD, using multiple diagnostic tests. A total of 131 samples (25 stool, 53 blood and 53 serum) and 108 samples (14 stool, 47 blood and 47 serum) were collected from 54 animal keepers having clinical profiles indistinguishable to IBD (suspected for CD) and from 47 animal keepers without symptoms of IBD (not suspected for CD), respectively. Animal keepers were in contact with animals for variable duration and some of them had habit of raw milk consumption. Stool samples were screened by microscopy and specific IS 1311 PCR-REA. Blood and serum were screened by IS 1311 PCR-REA and indigenous ELISA kit, respectively. Of the animal keeper suspected for CD, 36.0 (9/25), 28.0 (7/25), 12.9 (7/54), and 12.9% (7/54) samples and of animal keepers without symptoms of IBD (not suspected for CD), 14.2 (2/14), 7.1 (1/14), 2.1 (1/47) and 4.2% (2/47) samples were positive for MAP by stool microscopy, stool PCR, blood PCR and indigenous ELISA kit, respectively. According to habits of animal keepers, results showed high occurrence of MAP in humans with habit of raw milk consumption and smoking. All MAP DNA samples were genotyped as 'Indian Bison type' (pre-dominant type of MAP in animals of India). Presence of 'Indian Bison type' genotype and higher prevalence of MAP infection in cases of suspected animal keepers as compared to not-suspected animal keepers, strongly indicated the role of MAP in causing CD.

Key Words: *Mycobacterium avium* ssp. *paratuberculosis*, Crohn's disease, inflammatory bowel disease

286 Herd-level prevalence of Johne's disease on dairy farms in Utah and the surrounding Intermountain West. D. J. Wilson*[1], K. A. Rood[1], and J. D. Trujillo[2], [1]*Utah State University*, *Logan*, [2]*Iowa State University*, *Ames*.

The objective was to determine dairy herd-level prevalence of Mycobacterium avium ssp. paratuberculosis (MAP) infection, the causative agent of Johne's disease (JD) in Utah and some surrounding states. A signed permission slip was required for participation in the study. Two milk samples were collected from each bulk tank on study farms, one month apart. The farms shipped milk to two major milk buyers in Utah, with all milk collected at one of two milk processors. Milk haulers collected an extra bulk tank milk sample for use in the study. Identity of the farms was coded for anonymity by milk plant personnel. An ELISA test for IgG1 antibody against MAP and a PCR to detect MAP, both designed for pooled bulk tank milk were performed on each milk sample. Each bulk tank was to be tested 4 times, twice on each of the 2 samples. The number of tank samples tested per farm ranged from 1 to 24 (most farms had 2 or 4 samples from one or two bulk tanks, respectively). The 2 farms with the most bulk tanks had 6 and 12 tanks, respectively. JD was detected at least once on 67/170 farms tested (39%). The most common positive test results were 1 or 2 positives/4 JD tests (n = 28 farms). The lowest proportions of all tests positive for JD on a given farm were 2/48, 1/8 (n = 3), and 2/12 (n = 2). Highest proportions of positive tests were 8/8, 4/4, 10/12, 9/12, 6/8, 7/12, and 13/24. The finding of 39% of herds positive for JD is similar to other recent estimates of herd prevalence, indicating increased levels of the disease compared with national estimates 15-20 years ago. Some herds were enrolled in a demonstration project to evaluate the effectiveness of using the individual cow JD milk ELISA test and culling to reduce prevalence of the disease. Analysis of data and reporting of results from that study will be completed in the future.

Key Words: Johne's disease, MAP, dairy cattle

Breeding & Genetics and Physiology & Endocrinology Symposium: Bridging the Gap Between Physiology and Genomics

287 Spanning research from QTL to functional unit of a gene. J. M. Reecy*, *Iowa State University*, *Ames*.

Since the dawn of modern genetics, researchers have been working toward the elucidation of genetic pathways that control variation in traits of interest. Along the way, new breakthroughs in technology have lead to new insights. The determination of the structure of DNA and the subsequent explosion in molecular biology, enabled researchers to identify genes responsible for many processes in a cell (e.g., glycogenesis, transcription, etc). Eventually, geneticists began to utilize these new molecular techniques to identify regions of the genome that contain genetic variation that was associated with phenotypic variation (quantitative trait loci; QTL). To date, molecular geneticists have identified almost 10,000 QTL in cattle, pigs and chickens. The speed with which new QTL are identified is ever increasing. Unfortunately, the identification of quantitative trait nucleotides (QTN) lags significantly behind. However, now that the genomes of all major livestock species have been sequenced a new suite of techniques have been unleashed. New genotyping and statistical techniques have made it possible to not only identify QTL and fine map them, but to also account for a large amount of total genetic variation associated with a trait of interest. For some traits there are a large number of small effect QTL (i.e., infinitesimal model), while for other traits there appear to be a limited number of QTL. In addition to genotyping and statistical breakthroughs, whole, or even partial, genome re-sequencing and transcriptomics (RNA-seq) are providing new insights into genome and gene structure. We can now combine phenotype, genotype and gene expression data to understand the mechanisms underlying traits of interest in greater detail than ever before. We have entered an era where molecular/quantitative genetic techniques need to be directed beyond production to consider animal health, animal welfare, climate change mitigation, and consumer health traits.

Key Words: genomics, transcriptomics, whole genome association

288 Advancing toward functional genomics. H. L. Neibergs*, *Washington State University*, *Pullman*.

Complex traits are difficult to identify at the molecular level. Because many genes are involved, many with modest effects, it is difficult for them to be detected in genomic studies. To identify loci responsible for complex traits, multidisciplinary collaborations between genetics and physiology are essential. Integration of computational biology, molecular biology and physiology enhances the genomics discovery process because the connections between the functions of the gene products will lead us to the genes involved in the phenotype. To make the link between genome and phenotype, tools such as gene set enrichment combined with single nucleotide polymorphism analysis offer approaches to evaluate biological pathways in the context of genomic variation. Evaluation of the unique transcription profiles of a cell at different points in the life of the animal, whether conducted with microarrays or RNA sequencing, adds information about the transcription regulation of the genome. Proteomics extends the transcriptional message to the proteins being produced in and around the cell and the post-translational modifications that affect the protein′s function. The identification of alternative splicing of the mRNA transcripts and the interaction of proteins with other protein and RNA molecules must also be investigated to determine how a phenotype is expressed. By understanding the biological process of transcription, translation, and interactions of the proteins, the variation present in the genome is placed in context to the phenotype. Progress toward solving the basis of complex traits may well begin with the biological process, rather than the QTL. Genetics may be the foundation of animal improvement, but true genetic progress will be made when we expand our field of view to include gene function.

Key Words: functional, genomics

289 Genomic analysis of data from physiological studies. D. J. Garrick*, *Iowa State University*, *Ames.*

Physiologists have long been undertaking research to discover and elucidate the mechanisms involved in particular metabolic processes such as maintenance, growth, reproduction, and disease. Animal breeders have focused their research endeavors on understanding genetics, the study of inheritance, to implement breeding programs that can systematically advance the genetic merit and phenotypic performance of food animal systems, by exploiting selection of above-average candidates to be the parents of the next generation. Prerequisite characterization of the genetic merit of selection candidates has principally been achieved by visualizing the genomes of the candidates solely through measurement of phenotypes on the candidate itself, or on its close relatives. The resulting artificial selection has made use of those genes that are responsible for variation in performance, without requiring or taking advantage of any knowledge of causality, in the same manner that natural selection can alter populations. Accordingly, selection could rightfully have been described as resembling a black-box. Leveraging on sequencing activities undertaken in various livestock genomes, high-density genotyping systems have become available that allow inheritance of individual genome fragments to be traced from one generation to another and related to variation in performance by quantifying their substitution effect. Genomic selection can then be undertaken by predicting merit by summing up the values of an individual's chromosome fragments. A by-product of this approach is that it identifies genomic regions contributing to variation in performance that can be queried in bioinformatic databases that accumulate knowledge of gene location and function. Collectively this information can extend the scope of physiological studies beyond the underlying mechanisms of average performance to explain the causes of variation in performance.

Key Words: genomic selection

290 Genomic information for physiologists. M. G. Thomas*, K. L. DeAtley, S. O. Peters, G. A. Silver, and A. M. Clayshulte, *New Mexico State University*, *Las Cruces*.

Furthering knowledge of genes and understanding their mechanistic-role is a focus of physiology research. Specifically, this research furthers understanding of transcripts that are translated into proteins and considers their relevance in the whole animal. Development of tools to work with genomic data have enhanced gene discovery for physiology and molecular biology research. Some of these tools also provide data for estimating genome-assisted breeding values for livestock improvement programs. For example, SNP-chip data can be used for QTL detection as well as genetic prediction. Once a QTL is discovered or queried from a database, the process of fine mapping to determine the DNA sequence inferring the physiology from the underlying genes involves numerous

strategies. These include resequencing and denser DNA marker association studies and (or) investigation of transcriptome and proteome reference resources to reveal candidate genes, which can be visualized in pathway software to help design studies to investigate their functions. An example of such a process involved detection of a QTL on chromosome 2 for heifer pregnancy (n = 830 and BovineSNP50 genotypes). Bioinformatic tools (animalgenome.org) were used to visualize 10 QTL and 10 annotations in a 4 Mb region flanking the SNP inferring this QTL. Since hypothalamus is part of the reproductive endocrine axis, RNA was harvested from this tissue of pre- and post-pubertal heifers and deep sequenced (RNA-Seq). Transcriptomes were aligned with the bovine genome (ver. 4.0) to evaluate presence and level of expression of candidate genes with Alpeus. Three genes with differing levels of expression were identified and their ontology suggested neuron function and cell signaling. Most importantly, these genes were new discoveries for this research program and provide opportunity for their visualization in pathways and consideration in design of experiments to decipher their physiological relevance. These considerations could also include evaluation of allele-specific variation. Advancements in genomics have expanded the ability of physiologist to discover genes and explore their functions.

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Key Words: candidate gene, physiology, RNA-Seq

Companion Animals Symposium: Microbes and Health

291 Introduction: Microbes and health. K. S. Swanson*, *University of Illinois*, *Urbana*.

Despite human claims to superiority, it can be legitimately argued that microbes rule the world. Whether it is an ocean reef, a landfill, or a gastrointestinal tract, invisible communities of highly active and adaptable microbes prosper. Over time, mammalian species developed a symbiosis with microbes that are now important inhabitants not only in the intestines, but also in the mouth, skin, and vaginal tract. In the gut, commensal microbes are a critical element for the development of the gut-associated lymphoid tissue, pathogen resistance, nutrient digestion (fermentation), and intestinal epithelial cell gene expression. Proper balance is key, however, as microbial imbalances contribute to inflammatory bowel diseases, gastrointestinal cancers, and other intestinal disorders. Microbial colonization also plays a crucial role in oral disease, which is now the most common form of disease in dogs and cats. Recent evidence also suggests a role of intestinal microbiota on the metabolic phenotype and disease risk (e.g., obesity, metabolic syndrome) of the host. A significant hindrance to studying gut microbiota has traditionally been the inability to effectively identify and quantify microbial species. Researchers have been reliant upon microbial culturing methods that are not only laborious, time-consuming, and often inaccurate, but also greatly limited in scope. High-throughput, DNA-based methods have been developed recently and have changed the research environment dramatically. Recent experiments using these techniques have begun to characterize the identity and metabolic activity of the entire gastrointestinal microbiota and their association with health and disease. Despite this recent progress, more research is needed to provide deeper coverage of the oral and intestinal microbiomes, evaluate effects of age, genetics, or environment (e.g., diet) on its composition and activity, and identify its role in disease.

Key Words: microbe, gastrointestinal health, oral health

292 Bacterial influences on mammalian gut development. R. K. Buddington*, *University of Memphis*, *Memphis, TN*.

The interactions between the gastrointestinal tract (GIT) and the resident bacteria play critical roles in influencing GIT development and the health and nutrition of young mammals and begin at birth when the sterile GIT is colonized by bacteria from the environment, particularly the maternal urogenital tract. Postnatal changes in the bacterial assemblages continue for months and are the result of shifts in dietary inputs, maturation of GIT and host physiology, and interactions among the resident bacteria. The interactions between the bacteria and the developing GIT are evident from the different patterns of GIT gene expression for gnotobiotic and conventional animals. Although postnatal development progresses smoothly for most animals, the overly reactive mucosal immune system of the immature GIT and the unstable assemblages of bacteria increase the risk of adverse and damaging inflammatory responses, such as neonatal necrotizing enterocolitis (NEC). Attempts to identify specific bacteria as causative agents of NEC have been inconclusive. The association of NEC with fermentation of undigested components of the diet and altered proportions of volatile fatty acids suggest bacterial metabolites may be better predictors of NEC risk than species composition. This presentation describes how the development, health, and disease resistance of the GIT are responsive to management of the bacterial assemblages. Antibiotic induced disturbances in the developing assemblages of bacteria can have profound and long-term adverse impacts on the GIT and the host. Encouraging results have been achieved by administration of probiotics to accelerate acquisition of bacterial assemblages that promote health. However, to be effective probiotics must be matched with the unique GIT environment of each host, and perinatal exposure is essential for colonization and long-term persistence. Prebiotics are an alternative that represent metabolic substrates for specific health promoting bacteria and include galactooligosaccharides, fructooligosaccharides and other complex carbohydrates.

Key Words: gastrointestinal, neonatal, infant

293 Microbes and gastrointestinal health of dogs and cats. J. S. Suchodolski*, *GI Laboratory, Texas A&M University*, *College Station*.

Recent molecular studies have revealed a complex microbiota in the canine and feline intestine, compromising several thousand bacterial, fungal, and viral phylotypes. The microbiota plays an important role in the development of the immune system. Studies have demonstrated a microbial dysbiosis in humans, cats and dogs with inflammatory bowel disease (IBD). In humans, the microbiota is implicated as inflammation develops in areas with the highest bacterial counts and antibiotic therapy improves clinical signs in a subset of patients. In rodent models with genetic susceptibility, intestinal inflammation develops only in the presence of bacteria. Current theories for the development of chronic intestinal inflammation favor a combination of environmental factors, the intestinal microbiota, and a genetic susceptibility of the host (e.g., polymorphism in the NOD2/CARD15 in Crohn's disease). New evidence suggests that genetic susceptibility predisposes to infection with enteric organisms. Polymorphisms in specific genes (e.g., interleukin-8, lactoferrin) have been associated with diarrhea in humans. It is suspected that intestinal inflammation causes a dysbiosis toward gram-negative bacteria, perpetuating the disease in genetically susceptible hosts. Most common microbial changes observed in intestinal inflammation are a decrease in the bacterial phyla *Firmicutes* and *Bacteroidetes*, with concurrent increases in *Proteobacteria*. Individuals with intestinal inflammation show a reduced diversity of *Clostridium* clusters XIVa and IV (i.e., *Lachnospiraceae*, *Ruminococcaceae*, *Faecalibacterium prausnitzii*), suggesting that these bacterial groups, important producers of short-chain fatty acids, may play an important role in promoting intestinal health. Similar changes (i.e., reduction in *Clostridium* clusters XIVa and IV) have been observed in dogs and cats with IBD. Boxer dogs with histiocytic ulcerative colitis harbor adherent and invasive *Escherichia coli* (AIEC) that share similarities to AIEC isolates obtained from ileal tissues of humans with Crohn's disease. Underlying genetic susceptibilities are currently an area of intense research in companion animals with chronic enteropathies.

Key Words: 16S rRNA gene, pyrosequencing, IBD

294 The oral microflora and periodontal health in dogs. Z. Marshall-Jones*, *Waltham Centre for Pet Nutrition, Waltham-on-the-Wolds*, *Melton Mowbray, Leicestershire, UK*.

The microbial ecology of the oral cavity is rich with over 500 species estimated to be represented. This diversity may be enhanced by the variety of niches available. Biofilms reside both on the dentition, as dental plaque, and the oral mucosa including the buccal mucosa and the tongue with its undulating papillae providing a range of microenvironments. Salivary microbial populations meanwhile exist in a planktonic niche outside of these biofilm communities.

Studies suggest periodontal disease is the most widespread oral health disease in dogs with between 56 and 80% of dogs estimated to have periodontal disease. Although the specific organisms or processes involved are unclear, the aetiological agent of periodontal disease is considered to be dental plaque. Virulence determinants including enzymes secreted by plaque bacteria are thought to initiate the host immune response, including the activation of host matrix-metalloproteinases, which are the major cause of tissue damage and inflammation. Despite the relatively detailed knowledge regarding plaque formation and the microorganisms associated with disease in humans, the oral microflora in dogs is relatively undescribed. Several studies have assessed the species in the canine oral cavity and detected substantial differences in the oral flora of dogs compared to humans. Studies of canine plaque and saliva have found as little as 28% of organisms identified by 16S rRNA gene sequence are indigenous to the human oral flora. In one such study over half of the taxa cultured were novel species with no similar organisms represented in the GenBank database. The classic human periodontal pathogens, including *Porphyromonas gingivalis, Tannerella forsythensis*, and *Aggregatibacter actinomycetemcomitans* were not detected in canine subgingival plaque. Disparity between *Porphyromonas* isolates from humans and companion animals were initially detected as differences in the catalase activity between human *P. gingivalis* (catalase-negative) and veterinary isolates. The veterinary *P. gingivalis*-like organisms are now thought to represent a related species *Porphyromonas gulae*. The potential of these species in disease causation is however unclear.

295 Using "humanized" mice to study the effect of diet on the human gut microbiome. P. Turnbaugh*, *Harvard University*, *Cambridge, MA*.

Unraveling the interrelationships between diet, energy harvest, and the gut microbial community (microbiota) and its gene content (microbiome) is confounded by large variations in microbial ecology between individuals. We created an animal model of the human gut ecosystem by transplanting fresh or frozen adult human fecal microbial communities into germ-free C57BL/6J mice. Metagenomic analysis of the temporal, spatial and intergenerational patterns of bacterial colonization showed that these humanized mice were stably colonized, and reproduced much of the bacterial diversity of the donor's microbiota. Switching from a low-fat, plant polysaccharide-rich diet to a high-fat/high-sugar "Western" diet shifted the structure of the microbiota within a single day, changed the representation of metabolic pathways in the microbiome, and altered microbiome gene expression. Reciprocal transplants involving various combinations of donor and recipient diets revealed that colonization history influences the initial structure of the microbial community, but that these effects can be rapidly altered by diet. Humanized mice fed the Western diet have increased adiposity; this trait is transmissible via microbiota transplantation. Humanized gnotobiotic mice will be useful for conducting proof-of-principle "clinical trials" that test the effects of environmental and genetic factors on the gut microbiota and host physiology.

Key Words: gut, microbes, diet

Dairy Foods Symposium: Microbiology and flavor of cheese: Impact of Lower Salt-In-Moisture Content of Low Fat and Reduced Sodium Cheeses

296 How model cheese composition, texture and structure influence aroma and salt mobility, release and perception. A. Saint-Eve*, M. Panouille, I. Deleris, C. Trelea, and I. Souchon, *UMR 782 Genie et Microbiologie des Procedes Alimentaires, INRA, AgroParisTech*, *78850 Thiverval-Grignon, France*.

To limit the impact of food on health issues as obesity, hypertension, or coronary diseases, the reduction of salt or fat content in food products without modifications of organoleptic properties remains a real industrial challenge. A better understanding of the mechanisms involved in release and perception could lead to a better formulation of diet dairy products. In this context, model dairy products with different contents of ultrafiltration retentate milk powder, milk fat and rennet were studied to better understand and quantify the role of texture and structure on physicochemical and sensory properties. The characterization of dairy products was performed by sensory methods (profile, time-intensity and temporal dominance of sensations) and by rheological (small amplitude oscillation tests, compression and texture profile analysis), structural (confocal microscopy) and physicochemical methods (determination of aroma and salt partition properties and diffusion coefficients). Salt and aroma releases in mouth (in vivo conditions) were also followed respectively by in-nose measurement (proton transfer reaction-mass spectrometry) or by measuring the evolution of saliva conductivity during consumption. A preponderant effect of fat on aroma and salty perceptions was observed, in agreement with aroma compounds and salt behaviour during in vitro and in vivo measurement.
However, relating sensory perception and food product properties is a complex issue, because of the variety of phenomena occurring in the mouth during consumption (dilution with saliva, break-down during mastication etc.). To identify main mechanisms explaining release in mouth, mechanistic models, based on the description of mass transfer of salt and aroma compounds in the mouth and taking both physiological and physicochemical parameters into account, have been developed. From the predicted release kinetics of stimuli (in agreement with experimental data), the respective roles of physiological parameters and of product properties can be established.

Key Words: modeling, release, flavor

297 Flavor development in low fat cheese. M. A. Drake*, *Southeast Dairy Foods Research Center, North Carolina State University*, *Raleigh*.

Flavor and flavor development in Cheddar cheeses with a fat reduction greater than 50% are markedly altered from full fat cheese. Similar alterations in flavor are noted with sodium reductions below 20%. Both a lack of flavor and the presence of off-flavors are generally noted and these changes are due to differences in flavor release as well as changes in the biochemistry of flavor development. Recent studies have highlighted homofuraneol and phenyl compounds (phenylacetic acid and phenylacetaldehyde) as sources of meaty/burnt/brothy and rosy off-flavors in low fat and reduced sodium cheeses. Concentrations and odor activity values of these compounds increased in Cheddar cheese with increased fat reduction. Addition of sodium gluconate to low fat cheeses decreased levels of these compounds up to 50% but did not impact sensory perception. Decreasing sodium in low fat Cheddar cheeses increased bitterness and aromatic off-flavors but interactions were noted between starter culture and salt concentration suggesting that strain selection would be beneficial for sodium reduction. Collectively, these results confirm the complexity of cheese flavor development and that a combination of approaches will be required to optimize cheese flavor with fat and/or sodium reduction.

Key Words: cheese flavor, fat reduction, sodium reduction

298 Influence of salt-in-moisture on starter and nonstarter lactic acid bacteria. J. L. Steele*[1] and J. R. Broadbent[2], [1]*University of Wisconsin-Madison*, *Madison,* [2]*Utah State University*, *Logan*.

The microbiota of ripening Cheddar cheese consists of the starter lactic acid bacteria (LAB) and non-starter LAB (NSLAB). Starter LAB are intentionally added to milk at the beginning of cheese manufacture, while non starter LAB (NSLAB) are adventitious microorganisms. These organisms have primary roles in the development of cheese flavor. Unfortunately, the mechanisms by which these organisms influence cheese flavor remain, in large part, unknown. This has made the development of cheeses with non-traditional compositions difficult, as it has not been possible to predict how changes in cheese composition would influence cheese flavor development. For example, flavor development in low-fat or low-sodium Cheddar cheeses is consistently troubled by a lack of desirable or characteristic Cheddar flavor, and by the emergence of pronounced undesirable "off-flavors." It is interesting to note that in both of these cheeses with non-traditional compositions the salt-in-moisture level is significantly reduced compared with Cheddar cheese with traditional composition. There are 2 primary hypotheses for how cheese composition can influence the development of cheese flavor: 1) that the microbiota of cheeses with non-traditional composition differs from that of cheeses with traditional composition; 2) that the microbiota is similar in both the traditional and non-traditional cheeses, but that the physiology of the SLAB and/or NSLAB is significantly different and hence they produced significant flavor compounds. Previous research in our groups and other groups worldwide have demonstrated that cheeses with intrinsic properties less restrictive to microbial growth accommodate a wider diversity of NSLAB, supporting the first hypothesis. Research is currently underway to evaluate the second hypothesis.

Key Words: cheese microbiota, cheese flavor, salt-in-moisture

299 Cheesemaking processes and strategies for manufacture of low fat and reduced sodium cheeses. T. P. Guinee* and K. N. Kilcawley, *Moorepark Food Research Centre, Teagasc*, *Fermoy, Co. Cork, Ireland.*

Cheese is a concentrated gelled product that structurally consists of a calcium-phosphate casein/para-casein matrix, enclosing fat and moisture. Both the concentration of the matrix and the level of interaction between the casein aggregates making up the matrix are key determinants of the physical properties. The quality of low fat cheese variants is not as acceptable as that of their conventional full-fat counterparts owing to their higher concentration of protein, higher degree of casein fusion, and unbalanced flavor. Hence, a key strategy in the manufacture of low-fat (<6%) fat cheese is to reduce the volume fraction of the casein matrix and to reduce the extent of casein aggregation. This may be achieved by dilution of the protein matrix on increasing moisture via manipulation of a range of process variables: including inter alia: heat treatment of milk, reduction in pH at rennet addition, gel firmness at cut, curd particle size,

scalding rate, scald temperature, length of time in vat, pH at whey drainage, salting and milling (Cheddar), rate of cheddaring, and pre-salting before plasticization (pasta-filata cheese). The degree of aggregation is particularly influenced by the ratio of denatured whey protein-to-casein, calcium-phosphate to casein, the ionic strength (affected by the level of NaCl and time of salting), and pH. Reducing the contents of fat and salt in cheese adversely affects both the development and release of key compounds associated with cheese flavor. Moreover, it is important to ensure that the ratios of degradation products of protein and fat per gram of protein or fat, respectively, in low-fat, low-salt cheese are altered to convey flavor perception similar to that of cheeses of normal fat and salt content. The regulation of these factors are critically influenced by the type of starter culture, the level and proteolytic activity of the rennet, curd washing, ripening condition, and rate of curd cooling.

Key Words: cheese, low-fat, low-sodium

300 The effect of intrinsic and extrinsic factors on the fate of pathogens in specialty and lower fat/reduced sodium cheese. J. B. Luchansky*, P. M. Tomasula, D. L. Van Hekken, and A. C. S. Porto-Fett, *USDA/ARS Eastern Regional Research Center*, *Wyndmoor, PA*.

Although the United States maintains one of the most abundant and wholesome food supplies in the world, based on the nature and number of recent illnesses and recalls, we should continue to improve our ability to recover, characterize, and control pathogenic microbes in foods, especially for specialty/ethnic products such as lower fat/reduced salt cheese. Pathogens of primary concern would include *Listeria monocytogenes*, Shiga toxin producing *Escherichia coli*, and *Staphylococcus aureus*. Various intrinsic and extrinsic factors can determine whether or not these microbes die, grow, or merely survive in cheese. A variety of biological (e.g., bacteriophage, bacteriocins), physical (e.g., high pressure processing, pasteurization), and chemical (e.g., organic acids, smoke, oxidizing agents) interventions have been used to better manage pathogenic microbes in cheese. However, salt, moisture, and fat content, as well as temperature, quite arguably have the most significant effect on the fate of pathogens in foods. The ability to optimize salt and fat levels to maintain product safety/quality without causing untoward effects on the attendant sensory properties of lower fat/reduced salt cheese will be the focus of this presentation. With a trend toward consumption of cheese that are more convenient, as well as lower in salt, fat, and preservatives, the sole barriers against microbial contamination, persistence, and/or proliferation may be adherence to Good Manufacturing Practices, formulation, and refrigeration, coupled with enhanced awareness.

301 Temperature and vacuum conditions for removal of added carbon dioxide from milk. D. M. Barbano* and J. H. Hotchkiss, *Cornell University*, *Ithaca, NY*.

Our objective was to determine the temperature and vacuum relationships for efficient removal of added CO_2 from raw milk. Added CO_2 in milk and dairy products inhibits the growth of spoilage organisms during refrigerated storage and shipping. As milk and milk concentrates are shipped over longer distances, the use of CO_2 is becoming more common to maintain raw milk quality. In most cases, some or all of the CO_2 needs to be removed from the milk before further processing. Raw milk before CO_2 addition typically contained about 100 to 200 ppm CO_2 and had a pH of about 6.9 at 4°C. In the present study, about 1600 kg of 4°C raw milk was continuously injected with CO_2 with a holding time of 15 s at 172 kPa to achieve a concentration of 2000 ppm. Milk containing added CO_2 was stored at 4°C for 24 h before initiating the CO_2 removal process. The cold milk containing CO_2 was pumped through a plate heat exchanger at 24.5 kg/min directly into the spray nozzle inlet of a pilot-scale APV vacuum deaerator system equipped with a spray nozzle that produced a cone shaped spray pattern into a vacuum chamber. Six different milk temperatures (51.5, 57.5, 63, 68, 74, and 79.5°C) and 5 different vacuum levels at each temperature (in the range of 621 to 1293 mmHg Torr) were evaluated. The CO_2 content (Mocon CO_2 analyzer) of milk and milk pH were measured for each treatment and control milk. The experiment was replicated 3 times with a new milk source each time. The CO_2 content of milk decreased and pH increased with increasing temperature and vacuum. As temperature increased, less vacuum was required to achieve complete CO_2 removal. Milk pH was highly correlated with CO_2 removal and pH can be used as a rapid measurement method to determine if CO_2 removal is near completion. A linear regression model (r-square 0.98) was developed that defines the relationship between temperature and vacuum required to reduce the CO_2 content of the milk to a level not significantly different form the milk before CO_2 addition.

Key Words: carbon dioxide, pH, vacuum

302 Processing factors that influence casein (CN) and serum protein (SP) separation by microfiltration (MF). E. E. Hurt* and D. M. Barbano, *Cornell University*, *Ithaca, NY*.

Our objective was to demonstrate the impact of skim milk composition, heat treatment of skim milk, concentration factor (CF) and diafiltration factor (DF), control of CF and DF, and SP rejection by the membrane on the performance of a MF system designed to process skim milk to separate CN from SP. A mathematical model of a skim milk MF process was developed with 3 stages, plus a 4th stage to standardize the micellar CN concentrate (MCC) to 9% true protein (TP) and allow calculation of yield of MCC (liquid, 9% TP) and milk SP isolate (MSPI) (90% SP on a dry basis). The model predicted the effect of the 5 factors on: retentate and permeate composition, SP removal, and MCC and MSPI yield. When the TP of skim milk increased from 3.2 to 3.8% MCC and MSPI yield increased by 19% and 18%, respectively. Increased heat treatment (73 to 85°C) of skim milk caused CN as a percentage of TP in skim milk as measured by Kjeldahl analysis to increase from 82 to 86% and the yield of MSPI to decrease by 22%. A CF and DF of 2X gave a 3rd stage retentate TP concentration of 5.38% compared to 13.13% for a CF and DF of 5X and 3rd stage cumulative SP removal increased from 89 to 99%, respectively. Variation in the balance between CF and DF (instead of equal CF and DF) caused a progressive increase or decrease in TP concentration in each stageâ€™s retentate depending on whether CF > DF (increasing TP in retentate) or CF < DF (decreasing TP in retentate). Increased rejection of SP by the membrane from a SP removal factor of 1 to 0.6 caused a 17% reduction in MSPI yield and 3rd stage cumulative SP removal decreased from 97 to 80%. Within the ranges of the factors studied, the TP content of the 3rd stage retentate was most strongly impacted by the target CF and DF and skim milk composition. Cumulative SP removal was strongly impacted by heat treatment of skim milk, SP removal factor, and target CF and DF. Yield of MCC and MSPI was strongly impacted by skim milk composition. Yield of MSPI was also impacted by the heat treatment of milk and SP removal factor.

Key Words: microfiltration, serum protein

303 Multistage process with ceramic graded permeability (GP) microfiltration (MF) membranes to produce high casein content micellar casein concentrate (MCC) with low lactose. J. Zulewska*[2], M. W. Newbold[1], and D. M. Barbano[1], [1]*Cornell University*, *Ithaca, NY,* [2]*University of Warmia adn Mazury*, *Olsztyn, Poland*.

The objective was to determine if 0.1 μm Membralox GP membranes perform differently than 0.1 μm Membralox uniform transmembrane pressure (UTP) membranes. The 4th, 5th and final stage were run as finishing stages with purpose of lowering the lactose content of the final retentate to < 0.2% and adjusting the final protein concentration to > 9%. Raw milk was cold (4°C) separated and then the skim milk was pasteurized (72°C, 16 s) and microfiltered (320 kg) in a continuous bleed-and-feed 3X process using 0.1 μm ceramic GP membranes at 50oC. The retentate from stage 1 was diluted with pasteurized reverse osmosis (RO) water in 1:2 ratio and microfiltered (stage 2) with GP system. This was repeated 3 more times with total 5 stages (Stage 1 = MF; Stage 2 to 5 = diafiltration (DF)) of processing. To bring the protein content of the retentate to at least 9%, the final retentate from stage 5 was microfiltered using the same membrane at 1.75X CF without addition of RO water. The experiment was replicated 3 times. Data for the UTP system were obtained in a separate experiment from the GP data. Flux was significantly higher in GP than UTP system (72.5 vs. 54.0, 84.5 vs. 54.0, 92.7 vs. 54.6 kg/m^2 per hour in 1st, 2nd and 3rd stages for GP and UTP, respectively). The average retentate recirculation flow for GP and UTP were 714 and 644 L/min, respectively. The SP removal was higher in 1st stage of the UTP system than GP (63.7 vs. 56.0 for UTP and GP, respectively) with 2nd and 3rd stage being higher for GP system (26.7 vs. 21.9%, 13.8 vs. 9.7%, respectively). No difference in cumulative percentage of SP removal was detected for GP and UTP membranes, 96.5 and 95.2%, respectively. GP membranes had higher SP removal rate (kg/m^2 per hour) for 3 stages than UTP membranes: GP 0.69 and UTP 0.46 kg/m^2 per hour. Final retentate contained 0.09% lactose and 9.82% of crude protein.

Key Words: microfiltration, graded permeability, micellar casein concentrate

304 Functional modification of whey protein concentrate by microfiltration. H. Somni* and V. V. Mistry, *Midwest Dairy Foods Research Center, South Dakota State University*, *Brookings*.

Microfiltration (MF) (0.1 μm) of raw milk results in a permeate stream (MFP) with composition similar to cheese whey. The objective of this study was to compare ($P \leq 0.05$) the functional properties (gelation,

emulsion, and foaming) of whey protein concentrate (WPC) obtained from different sources. Clarified Cheddar cheese whey was pasteurized and split into 2 parts (3 replications); one part was ultrafiltered (UF) to 10X concentration and spray dried (CWPC), remaining was MF (0.1 μm) before process like CWPC (DWPC). MWPC was manufactured from MFP by UF and spray drying similar to CWPC and DWPC except that none of the stream was pasteurized (4 replications). The moisture, protein, fat, and ash content were, respectively, 6.4, 34.8, 2.8, and 5.4% in CWPC, 7.2, 37.2, 1.4, and 5.6% in DWPC, and 6.6, 48.7, 1.6, and 4.5% in MWPC. Gelation measured as 'least concentration endpoint' was lower for CWPC and DWPC. Emulsion stability of DWPC (1.3%) and MWPC (1.6%) was lower than CWPC (5.4%). While CWPC failed to produce stable foam, the overrun of DWPC (1059.7%) was higher than MWPC (952.7%). However, the foam stability after 30 min for MWPC (51%) was higher than DWPC (29%). Thus, the functional properties of WPC were different. In addition, protein solutions of DWPC and MWPC in water were devoid of turbidity unlike WPC manufactured by conventional process. Such differences are caused by major and minor compounds like glycomacropeptide (GMP), minerals, and MFGM associated compounds like phospholipids and lipoproteins. While some of these compounds like MFGM associated compounds could be removed by MF and removal of minerals depends on their state, substances like GMP are not removed by MF alone. Such compounds affect the functional properties. Microfiltration also improves shelf stability of products by removal of microorganisms and suspended matter. This opens an avenue for WPC in beverage application.

Key Words: microfiltration, whey protein concentrate, functional properties

305 Ultrafiltration of milk at high temperature. M. Lewis*, A. Grandison, N. On-Nom, and D. Wang, *University of Reading*, *Reading, Berkshire, UK*.

UF of milk has been performed at temperatures between 30 to 120°C to examine the effects on mineral partitioning, permeation rate (PR) and membrane fouling. Experimental protocols were developed to measure PR and fouling of membranes at different temperatures over a period of 40 min for milk UF, followed by water rinsing for 5 min. These initial UF runs were replicated 3 times. It was found that pH, ionic calcium and soluble calcium decreased in permeates, as temperature increased, whereas freezing point depression increased. Similar trends were found when milk was dialyzed at similar temperatures. The initial PR increased as UF temperature increased up to 100°C, but rapid PR decline was observed at 80 and 100°C. In contrast, at 50°C there was no noticeable decline in PR over a 40 min period. After about 20 min, PR was higher at 50°C compared with 80°C and it was even lower at 100°C, suggesting more severe membrane fouling at higher temperatures. When average PR was measured over a period of 30 min between 50 and 80°C, it was found to increase to a maximum at 60°C and declined thereafter. During water rinsing, PR recovered much more quickly at 50°C, compared with 80 and 100°C. Ultrafiltration at high temperature is a useful tool for measuring pH and ionic calcium of milk at high temperatures and showed that pH and ionic calcium of milk were highly temperature dependent. In contrast, the properties of permeates produced at high temperature, showed little change of pH and ionic calcium with temperature, but only at temperatures below that which they had been separated by UF. Measurement of pH and ionic calcium at high temperatures will permit a better understanding of their role in heat stability of milk.

Key Words: ultrafiltration, pH, ionic calcium

306 A method for spirulina production using cheese whey. K. M. Miranda[1,2] and L. M. Fonseca*[1], [1]*Federal University of Minas Gerais*, *Belo Horizonte, MG, Brazil*, [2]*Fundação Centro Tecnológico de Minas Gerais*, *Belo Horizonte, MG, Brazil*.

Cheese whey is a product with high nutritional value. However, because of processing costs in several countries it has limited use in the dairy industry. The objective of this work was to evaluate the use of cheese whey as an alternative media for spirulina production. spirulina (*Arthrospira platensis*), a blue-green algae used as a supplement and as whole food, has a protein content of up to 70% in the dry matter. One of the media used for spirulina production is the Zarrouk media. For this experiment, cheese whey reconstituted to 3g/100mL and 6g/100mL was clarified by heating and centrifugation, and the pH corrected to pH 9.0. Samples containing 500 mL of whey, clarified or not, were inoculated with 0.1 g/L and 0.2 g/L of spirulina and submitted to alternated 12-h photoperiod (3.0 Klux) at 25°C, during 10 d. The experiment was repeated in 5 batches. The algae growth was monitored by turbidimetry (560nm). After growth, the material was filtered, washed, pressed, and dried (50°C/8 hours). The biomass final composition was analyzed using standard methods, and the results submitted to analysis of variance. Spirulina did not grow well in non-clarified cheese whey, due to turbidity and low light transmittance through the medium. The maximum growth of spirulina was obtained with clarified cheese whey reconstituted to 3g/100mL with production of up to 1.83 g of spirulina for 1000 mL of medium. This production was reached in the sixth day, and was approximately 80% higher when compared to standard Zarrouk media. It is concluded that spirulina production using cheese whey is a feasible and low cost method, with higher production when compared to the standard industrial media. However, because of turbidity, a clarification step is necessary.

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Key Words: cheese whey, spirulina, protein

307 Investigation on coagulant properties of *Calotropis procera* and stabilization of its proteolytic enzymes. G. Belvedere[1], F. La Terra[1], M. Manenti[1], S. Lortal[2], J. C. Codjia[3], S. Doko[4], and G. Licitra*[1,5], [1]*CoRFiLaC, Regione Siciliana*, *Ragusa, Italy*, [2]*UMR Science et Technologie du Lait et de L'Oeuf*, *Rennes Cedex, France*, [3]*University of Abomey-Calavi*, *Benin*, [4]*University of Parakou*, *Benin*, [5]*DACPA, Catania University*, *Catania, Italy*.

Coagulant properties present in the latex extracted from *Calotropis procera* (fam. Asclepiadaceae) are well known. This extract is used by Peuhl community in Benin to produce Wagashi, a cheese known in West African states. From literature it is known that a wide number of chemical compounds were extracted, including cardiac glycosides, flavonoids, phenol compounds, terpenoids, and 2 proteolytic enzymes: calotropain FI and calotropain FII. Proteolytic enzymes that are present in the latex of *Calotropis procera* undergo easily oxidizing phenomena and for this reason their activity declines after 1 or 2 d. The aim of this study was to investigate whether the proteolytic enzyme present in *Calotropis procera* is the only factor influencing milk coagulation, and finally if it can be stabilized. The extract from Calotropis was autoclaved at 100°C to denaturate the proteolytic enzyme used for the milk coagulation. Its gelation activity was also verified. Several trials on the stabilization of the proteolytic enzyme, which contained active sites of cystein, were performed using extract from potato or natural flour from tapioca, gari, carob gum, and an antioxidant compound rich in cystein, glycin, and glutamic acid. The best results were obtained

with extract from potato tuber and the antioxidant compound. Results showed clearly that the coagulation process of milk was exclusively enzymatic. The proteolytic enzymes calotropain FI and calotropain FII present in *Calotropis procera* were stabilized successfully for several months and preserved their proteolytic activity in both types of trials. This would allow in the future to have a proteolytic enzyme readily available to produce Wagashi cheese in a traditional way.

Key Words: Wagashi cheese, proteolytic enzymes, *Calotropis*

308 Quality of raw and pasteurized milk (invited Pioneer speaker, 30 min presentation). C. H. White*[1,2], [1]*Mississippi State University*, *Mississippi State,* [2]*Randolph Associates, Inc.*, *Birmingham, AL*.

Milk must be safe and of high quality. Fortunately, high quality milk is normally safe, especially by microbiological standards. The definition of high quality milk must encompass the various pertinent standards and testing protocols. While raw milk is being sold to consumers under certain conditions in some states, from a microbiological standpoint this practice is questionable. Raw milk is considered by some to have more cheese flavor than cheese made from pasteurized milk. Is this a safe and reasonable practice even though it may result in a delicious cheese? Raw milk quality also impacts the shelf-life of pasteurized milk. The shelf-life is the length of time milk retains desirable sensory properties at a specified temperature. In the past 50 years, the shelf-life of commercial pasteurized milk has increased from 3 or 4 d at 7°C to 21 or more days. Extended shelf-life milk, as well as, ultra high temperature (UHT) milk can last for many weeks (even under non-refrigerated conditions for UHT products). How do dairy processing plants determine a products shelf-life? What are the key factors affecting this shelf life? Beneficial bacteria, such as certain member of the genera *Lactobacillus* and *Bifidobacterium* are routinely added to selected fluid milk for the nutritional well being of the consumer. These bacteria are thought to aid in the digestive processes and are believed to prevent or at least combat various diseases. These bacteria at least help to ensure a healthy microflora in the gut, a most desirable situation. What then is the overall quality of pasteurized milk? How is this quality determined? Does the dairy industry have enough new workers entering the field to ensure this quality? The dairy industry, in general, has well trained people producing the milk, and is fortunate have a dairy processing industry that been at the foundation of our food supply.

Key Words: milk quality, shelf-life, raw milk

Growth and Development Symposium: Intestinal Development and Growth

309 Strategies to alter intestinal development, health and function of poultry to improve growth performance. T. J. Applegate*, *Purdue University*, *W Lafayette, IN*.

The gastrointestinal tract (GIT) in chickens, turkeys and ducks is a dynamic organ system. During early posthatch growth, there is a tremendous energetic allocation to GIT growth. While most research has focused on ontogenic changes to nutrient transporter and/or enzyme production, the structural aspects of intestinal maturation often is not studied in tandem, which may be more limiting to growth. Similarly, researchers often use simple morphometric measures of intestinal structure (villus height, crypt depth, goblet cell numbers). However, these crude measures may not be as reflective of enterocyte proliferation, migration, apoptosis, and necrosis. Remarkably, the turnover of the bird′s intestine ranges from less than 2 to over 5 d, but our knowledge of what factors affect cell cycle and functionality are largely lacking in poultry. Recent work has noted that appearance of indigestibility by the young bird is due in part to changes in the pH of the proventriculus and endogenous secretion differences. For example, 60 to 80% of the apparent digestibility differences in amino acid utilization during the first week and later in life are due to differences in basal endogenous amino acid losses. Recent research has also focused on the maintenance needs of the intestine, particularly as it relates to preserving its barrier functionality with or without sub-therapeutic antibiotics. The GIT barrier is far from being static and responds to many challenges through changes to: a) peristalsis, b) enterocyte turnover, c) mucin production, adaptation of commensal microflora, d) innate immune responsiveness (including inflammation and acute phase response), and/or e) alterations to secretions. The extent and duration of each of these responses encompasses the nutrient and growth cost for maintenance of this barrier function. While most antibiotic replacement strategies are not capable of similar physiological and microbiological responses, some probiotic bacteria and plant extracts are able to modify mucin production, preserve intestinal tight junctions and enterocyte cell cycle, as well as alter inflammatory responses within the intestine.

Key Words: intestine, poultry

310 Nutritional support of intestinal health: Insights from a piglet model. J. Odle*, S. K. Jacobi, A. J. Moeser, and A. T. Blikslager, *North Carolina State University*, *Raleigh*.

Early postnatal morbidity and mortality of mammalian neonates represent significant challenges to the agricultural and medical sciences. While many stressors impinge on the newborn, gastrointestinal maladies predominate. This is not surprising given the quiescent state of the intestine in utero and the rapid ontogeny that ensues following birth. Furthermore, the intestinal mucosa, initially sterile, must be protected from viral and bacterial pathogens that are ubiquitous in the postnatal environment. Because the intestine is a "supply organ," overall vitality of the neonate hinges on its proper function. Our studies have employed rotaviral-gastroenteritis and ischemic-injury models to examine the effects of various nutrients on intestinal restitution and recovery. We have been unable to measure beneficial effects of enteral glutamine or alanyl-glutamine. However, supplemental arginine increased intestinal protein synthesis via mTOR signaling, increased crypt depth, and improved transepithelial resistance (TER). Supplemental plasma-protein also effectively abrogated gastroenteritis following rotaviral challenge. Most recently we investigated prophylactic intervention with dietary long-chain polyunsaturated fatty acids using an ischemic-injury model. Arachidonic acid (ARA) reduced initial villus denudation and accelerated acute restitution, measured as increased TER. Restitution effects of ARA were attenuated by indomethacin, suggesting possible prostaglandin mediation. Our collective findings suggest positive (but modest) effects of selected nutrients on intestinal repair. Further research is needed to understand better the complex interplay between nutrients, growth factors, immunological, and bacterial determinants which impact intestinal health and ultimately neonatal vitality.

Key Words: rotavirus, arachidonic acid, arginine

311 Integral role of the gut in growth signal transduction between the environment and host. D. G. Burrin*, *USDA Children's Nutrition Research Center, Department of Pediatrics, Baylor College of Medicine, Houston, TX.*

The gut epithelium serves as a vital biological interface between the environmental microbiota, luminal dietary factors and the mammalian host. The function of the gut barrier is especially critical during early neonatal development and weaning when the diet changes markedly and the immune system is immature in rapidly growing animals. In addition to functioning as a physical barrier, the gut epithelium contains specialized cells and receptors that serve to recognize specific molecules derived from the diet and microbes. The enteroendocrine cell comprises a small proportion (<5%) of gut epithelial cells, but their effects are magnified via release of several hormones that positively impact animal growth and development. The endocrine L-cell is capable of sensing multiple luminal molecules, including glucose and bile acids that trigger the secretion of gut hormones, such as glucagon-like peptide 1 and 2. These 2 hormones have an important stimulatory effect on insulin secretion, insulin sensitivity, glucose absorption and gut epithelial growth. Recent studies also have show that bile acids taken up by enterocytes can activate the nuclear receptor, farnesoid X receptor (FXR), stimulating the release of fibroblast growth factor 19 (FGF19). FGF19 functions as a hormone that alters hepatic lipid metabolism and bile acid homeostasis. In addition to nutritionally significant molecules, the gut epithelium also senses the presence of the microbiota through toll-like receptors (TLR) that transmit signals to the underlying cells within the immune and neuroendocrine systems. The activation of TLR by bacterial products can result in negative feedback on key elements of growth, such as appetite, gut motility, and anabolic hormone signaling. The presentation will discuss the essential role of the gut in novel aspects of these growth signal transduction pathways in the developing animal.

Key Words: glucagon-like peptides, bile acids, toll-like receptors

312 Nutrient transporters in support of ruminant growth and development: novel and updated findings. J. C. Matthews*, *University of Kentucky*, *Lexington*.

This literature review summarizes recent findings in cattle (primarily) about urea, SCFA, thyroid hormones, amino acid, and calcium transporters. In ruminants, the relationship between diet and urea cycling is complex. Expression of urea transporter-B (UT-B; SLC14A1) is upregulated throughout the rumen in response to high vs low concentrate diets, but apparently not increased levels of rumen ammonia. In growing lambs, the relative tissue content of UT-B in gastrointestinal tract epithelia, liver, kidney, and parotid salivary glands, was not affected by varying dietary CP. Monocarboxylate transporters (MCT) 1 (SLC16A1) and 4 (SLC16A3) are expressed throughout the ruminant gastrointestinal

tract and are likely responsible for the absorption of SCFA across these tissues, especially the rumen. However, a recent finding suggests that at least rumen tissue content of MCT4 mRNA and fractional rate of SCFA absorption appear insensitive to increased rumen fluid SCFA concentrations in cattle fed high vs low concentrate diets. Regarding the fate of absorbed ruminal SCFA during lactation, the cellular localization of MCT1 and 4 in the mammary gland of lactating Holsteins has been identified, along with a thyroid hormone transporter (MCT8, SLC16A2), and the aromatic amino acid transporter TAT1 (SLC16A10). In Belgian Blue cattle, association mapping has identified a mutation in the neuronal glycine transporter GLYT2 (SLC6A5) that leads to a decrease in presynaptic accumulation of glycine and is likely the cause of congenital muscular dystonia 1. Similarly, a mutation in $Ca2^{+}$ATPase (ATP2A1) results in decreased cytosolic $Ca2^{+}$, thus impaired fast-twitch muscle function. In summary, several recent and important findings have been made in delineating existing relationships between nutrient transporter expression and specific physiological states of cattle. When combined with results of additional functional capacity studies, these findings will lead to a greater understanding of ideal physiological conditions required to support optimal nutrient use by cattle.

Key Words: biological transport, nutrient-gene interaction, SLC

313 Out of the black box and back to the future: New frontiers and challenges for rumen microbiology to advance animal growth and development. M. Morrison*[1,2], [1]*CSIRO, St. Lucia, Queensland, Australia*, [2]*The Ohio State University*, *Columbus*.

Ruminant microbiology has been studied for more than a century, initially via microscopic examinations of rumen fluid providing morphological and compositional descriptions of the microbiota. Cultivation techniques for obligate anaerobes were developed in the mid-20th Century, and the principal way of studying rumen microbiology shifted, to culture and isolate as many species as possible then study select physiological processes. In the late ‘80s and ‘90s, with the development of tools such as PCR, and the application of reverse transcriptase and DNA polymerases, the field of rumen microbial ecology was transformed to a largely cultivation-independent field of inquiry, using 16S rRNA and/or the gene encoding that molecule as a semantide. During this period, recombinant DNA technologies also made an impact on the field of rumen microbiology, principally via a level of reductionism that provided deeper knowledge about fewer rumen microbial interactions and processes. In the first decade of the 21st Century, microbial biology has advanced from the sequencing of individual genomes, to comprehensive assessments of microbial diversity and the genetic potential resident within entire microbial communities. This has been driven largely by the appreciation that culturable microbes represent only a small percentage of the microbial world and advances in high throughput sequencing technologies. As such, there has been a renewed interest in the interrogation of rumen and other gut microbiomes via (meta)genomic approaches. So, are these efforts resulting in more of the same, or something “new” in relation to our understanding of the microbial biology underpinning rumen function, nutrient availability, and animal growth and development; and from which, new opportunities might emerge? This presentation will examine some of the latest observations and findings arising from the study of individual rumen bacteria, as well as rumen microbiomes. The field of rumen microbiology still has something to offer the animal industries, as well as other sectors of science and industry.

Key Words: rumen microbiology, growth and development, microbial genomics

314 The human intestinal microbiome—Applications to animal agriculture. D. N. Frank*, *University of Colorado*, *Boulder*.

Advances in DNA sequence-based technologies now permit genetic analysis of complex microbial populations without the need for prior cultivation. My talk will summarize the molecular methods of culture-independent microbiology (“metagenomics”) as exemplified by their application to studies of the human gastrointestinal tract in both health and disease. Such culture-independent metagenomic surveys reveal unprecedented microbial biodiversity in the human intestine. Large-scale shifts in gut commensal populations (“dysbiosis”), rather than occurrence of particular microorganisms, are associated with several gastroenterological conditions, including antibiotic-associated diarrhea, Crohn’s disease, ulcerative colitis, and obesity. These findings demonstrate the importance of commensal microorganisms in maintaining GI health and suggest that redress of disease-associated imbalances may ameliorate human pathogenic conditions. Metagenomic techniques are readily applicable to animal agricultural science and are likely to provide important new microbiological perspective, as they have in human biomedicine.

Key Words: microbiome

Lactation Biology Symposium: Novel Mechanisms Regulating Milk Secretion and Mammary Involution

315 High fat diet suppresses de novo fatty acid synthesis in mammary epithelial cells independent of SREBP regulated gene expression. S. M. Anderson*, M. C. Rudolph, E. A. Wellberg, and M. C. Neville, *University of Colorado School of Medicine*, *Aurora*.

The lipid component of milk is an important energy source and a critical nutrient for proper development of the newborn. The lactating mouse secretes her entire body weight in fat during a normal lactation period. Fatty acids in milk triglyceride are blended from preformed sources (dietary and adipose stores), and de novo synthesized fatty acids. Factors that control lipogenic differentiation of mammary epithelial cells have not been identified. Gene expression profiling has identified potential controller genes including SREBP1c, Src, Spot14 (THRSP), Akt1, and the long form of the prolactin receptor. Metabolic genes that increase at parturition include the glucose transporter GLUT1, citrate synthase (CS), malic enzyme 1 (ME1), citrate transporter (SLC25a1), ATP citrate lyase (ACLY), acetyl-CoA carboxylase 1(ACC1), fatty acid synthase (FASN), and stearoyl-CoA desaturase 2 (SCD2). SREBP1c regulates transcription of several of these genes in the liver; however, SREBP1c knockout mice do not display a lactation defect. Mice deficient in SCAP (SREBP Cleavage Activation Protein) have a significant lactation defect characterized by a 25% decrease in de novo synthesized fatty acids in milk and a 50% decrease in pup growth. Expression of FASN, Insig1, SLC25a1, and SCD2 in mammary epithelial cells is reduced, but there is no change in ACC1 and ACLY. This suggests SREBP-dependent and -independent regulation of lipid biosynthetic enzymes in mouse mammary epithelium. To compensate for loss of de novo fatty acid biosynthesis in SCAP null dams, we fed them a high fat diet (45% kCal). Although pup growth improved, lactation competency was not restored completely. Interestingly, the mRNA levels of ACC1, ACLY, FASN, SCD2, and SLC25a1 did not change, but the protein levels of ACC1, ACLY, and FASN were significantly reduced. This implies post-transcriptional regulation of fatty acid biosynthetic enzymes in mammary epithelial cells in response to dietary fat, rather than at the transcriptional level. Current efforts are focused upon understanding aspects of this post-transcriptional regulation in mammary epithelial cells.

Key Words: lactation, triglyceride, SREBP

316 Serotonin: A homeostatic regulator of bovine lactation. N. Horseman*, *University of Cincinnati*, *Cincinnati, OH*.

Serotonin, a central neurotransmitter and peripheral hormone, was discovered in the mammary glands of mice using molecular genetic and gene expression profiling approaches. Physiological studies demonstrated that serotonin functions as a homeostatic regulator in the mouse mammary gland. Studies in human and bovine mammary gland experimental systems permitted us to generalize that serotonin is a conserved homeostatic regulator of lactation among mammals. Based on a foundation of basic science that has elucidated fundamental physiological, cellular, and molecular aspects of serotonin signaling in lactation, we have embarked on a variety of studies to understand the practical implications of serotonin signaling in human and bovine lactation, and in breast cancer. An extraordinary variety of drug targets and non-drug interventions can selectively impact serotonin signaling, providing a rich resource for modifying mammary gland cell functions.
This project was supported by National Research Initiative Competitive Grant no. 2009-35206-05178 from the USDA Cooperative State Research, Education, and Extension Service.

Key Words: serotonin

317 Stanniocalcin-1 and local control of mammary involution. P. Lacasse*, *AAFC-Dairy and Swine R&D Centre*, *Sherbrooke, QC, Canada*.

Stanniocalcin-1 (STC-1) is a hormone that was first identified in fish and recently in mammals. In euryhaline teleost fishes, gill calcium uptake is decreased by STC-1, an action opposed by prolactin. In mice, some evidence suggests that STC-1 is implicated in lactation. Indeed, STC-1 is only detectable in blood during gestation and lactation, wild-type pups suffered growth retardation when fed by transgenic mothers overexpressing human STC-1, and passive immunization against STC-1 induced an alteration of milk composition and caused growth retardation of pups. Therefore, we have initiated a research program on the role of STC-1 in the regulation of bovine lactation. We have first demonstrated that injections of estradiol to lactating cows, while reducing milk production, increased the expression of STC-1 by the mammary cells and increased by several fold the concentration of STC-1 in milk. In a second experiment, we have measured STC-1 levels in blood and milk during lactation. We found that, as lactation progressed, STC-1 concentrations increased in milk but not in blood. In another experiment, cows were milked differentially for 8 wk, with half of the gland milked 1X and the other half milked 3X daily. Milk production and lactation persistency were greater in the udder half milked 3X while indicators of mammary involution, such as milk BSA and proteinase activity, increased in the udder half milked 1X. Milking 1X caused an increase in milk concentration of STC-1, an effect that persisted beyond the treatment period. Using unilateral milking, we have investigated the role of STC-1 during involution. Milk STC-1 concentration increased in the unmilked quarters and was correlated with milk proteinase activity and BSA. Mammary epithelial cells cultured in the presence of milk from the involuting quarters had more apoptotic cells and a reduced metabolic rate as compared with those cultured in milk from the milked quarters. Interestingly, the metabolic rate was negatively correlated with the STC-1 concentration in milk. These results suggest that STC-1 is implicated in the progression of involution. Nevertheless, more research will be needed to determine the target and function of this hormone.

318 The role of Ca^{2+}-ATPases in milk secretion and involution. T. A. Reinhardt*, *National Animal Disease Center, ARS/USDA, Ames, IA*.

The means by which calcium is transported into the milk is a poorly understood process. An older hypothesis is that calcium arrives in milk via exocytosis of secretory products from the Golgi pathway. This is consistent with more recent data showing that the secretory pathway Ca^{2+}-ATPases (SPCA1 and 2), are induced in lactating mammary tissue. However, greater expression of the plasma membrane Ca^{2+}-ATPase isoform 2bw (PMCA2bw) occurs during lactation. PMCA2bw expression is more strongly correlated with increases in milk calcium secretion and PMCA2bw's apical location suggested that calcium might be secreted directly into milk via this pump. This hypothesis was confirmed by examining calcium secretion in PMCA2 gene knockout mice compared with wild type controls. Milk from PMCA2-null mice have 60% less calcium than milk from wild-type mice. Total milk protein concentration was lower, and an indirect measure of milk production (litter weights) suggested that the PMCA2-null mice produce significantly less milk. These data demonstrated that PMCA2bw is required for maximal milk production and secretion of much of the calcium in milk. This major secretory function represents a novel biological role for the PMCA's, which were previously regarded as premier regulators of intracellular

Ca^{2+} for cell signaling and general fine control of cell calcium homeostasis. The data available to date suggest that calcium transport into milk involves both the Golgi secretory pathway via the activities of SPCA1 and 2 as well as a major role for the apical pathway via PMCA2. It follows that lactating mammary cell calcium homeostasis is maintained by the high expression of PMCA2, SPCA1 and 2. Within 24 h after abrupt cessation of lactation, PMCA2 and SPCA1 and 2 expression decreased 80–95%. The abrupt loss of Ca^{2+}-ATPases, required by the mammary gland to maintain cell calcium homeostasis, could lead to accumulation of cell calcium, mitochondria Ca^{2+} overload, calcium mediated cell death and thus may play a part in early signaling of mammary involution.

Key Words: mammary calcium transport, Ca^{2+}-ATPase, involution

319 Effect of vitamins E and C on collagen turnover by bovine intramuscular fibroblasts. A. C. Archile*[2,1], I. B. Mandell[1], S. P. Miller[1], M. C. Cha[1], and P. P. Purslow[1], [1]*University of Guelph*, *Ontario, Canada*, [2]*University of Zulia*, *Maracaibo, Venezuela*.

Intramuscular collagen contributes to the variation in background toughness of meat. Vitamin E may reduce intramuscular collagen maturity, while vitamin C has been reported to improve meat texture in beef. The objective of this study was to investigate whether vitamins E and C are able to regulate collagen turnover in bovine intramuscular fibroblasts, the cells responsible for its synthesis and degradation by secretion of matrix metalloproteinases (MMPs). Fibroblasts were isolated from *longissimus dorsi* (LD) and *semitendinosus* (ST) muscles from a yearling animal and grown in DMEM + 10% FCS. Fibroblasts were treated with vitamins E and C for 24 h as follows: 1) with 50 or 100 μ*M* of vitamin E, 2) 50 μ*M* of vitamin C, 3) either 50 μ*M* vitamin E+50 μ*M* vitamin C, or 100 μ*M* vitamin E+50 μ*M* vitamin C. Control cells received no vitamins. After treatment for 24 h, media were collected and analyzed for MMP-2 activity by zymography. Cell lysates were tested for total collagen synthesis (TC) using the Sircol assay. Data were analyzed by 2-way ANOVA, Fisher's LSD and Pearson bivariate correlation. Vitamins E and C each increased ($P < 0.05$) the activity of MMP-2 secreted by fibroblasts from both muscles, but the effect was stronger ($P < 0.05$) in cells derived from LD than from ST. A synergistic effect between vitamins E and C on MMP-2 activity was observed for cells from both muscles. Both vitamins increased TC in cells from both muscles above the controls to a different extent; higher TC values ($P < 0.05$) were found for ST cells versus LD cells. There was a strong positive correlation ($P < 0.05$) between MMP-2 activity and TC synthesis. These results confirm the hypothesis that both vitamins may increase collagen turnover in intramuscular fibroblasts, which could have direct implications for the response of these muscles to the animal's diet, affecting collagen turnover in vivo. A high rate of collagen turnover may lead to increased collagen solubility in muscles which can affect meat tenderness.

Key Words: vitamins E and C, collagen turnover, meat tenderness

320 Fatty acid composition of Jersey beef was affected by finishing diet and tissue type. T. Jiang*[1], C. J. Mueller[2], J. R. Busboom[1], M. L. Nelson[1], J. O'Fallon[1], and G. Tishida[2], [1]*Washington State University*, *Pullman,* [2]*Oregon State University*, *Corvallis*.

Our objective was to determine the impacts of finishing diet energy level and tissue type on fatty acid composition and palatability of Jersey beef. Steers (n = 20) were assigned to a randomized complete block (RCB) design with initial weight as blocks (Light, 228.0 vs. Heavy, 261.4 ± 0.4 kg) and finishing diet (70 vs. 85% corn) as treatments. Ribeye steaks were collected for sensory evaluation and were dissected to obtain muscle, seam, and subcutaneous (s.c.) fat. In addition, fat samples were collected from s.c. tissue (BF), kidney (KPH), and the intestinal tract (VIS). Data for fatty acids and sensory evaluation were analyzed as a split-plot design and a RCB design, respectively. Saturated fatty acid (SFA) level was lower ($P < 0.05$) and monounsaturated fatty acid (MUFA) was higher ($P < 0.05$) in s.c. fat than in muscle or seam fat, which could be explained by higher ($P < 0.05$) myristoleic and vaccenic acid levels in s.c. fat. Oleic acid (C18:1) level was higher ($P < 0.05$) in s.c. fat than in seam fat, accompanied by a higher ($P < 0.05$) Δ9 desaturase index in s.c. fat. Trans fatty acid (TFA) and CLA levels were lower ($P < 0.05$) in muscle than in seam or s.c. fat. Increased concentrate in the diet decreased ($P < 0.05$) n-3, n-6 and total polyunsaturated fatty acid (PUFA) levels in muscle; however, n-6: n-3 ratio remained the same. SFAs and TFAs, n-6: n-3 ratio, and elongase index were lower ($P < 0.05$) in BF than in KPH or VIS. Increased concentrate in the diet increased ($P < 0.05$) TFA in BF, KPH, and VIS and linolenic acid (C18:3n-3) and elongase index in BF. Finishing diet did not impact sensory attributes of the beef steaks ($P > 0.05$). All the steaks were acceptable in palatability with an initial tenderness score of 6.4 ± 0.2 and a beef flavor score of 5.5 ± 0.1 based on a 10 cm scale. In conclusion, fatty acid composition differed depending on fat location in the body. The lower concentrate diet produced beef with a more health-beneficial fatty acid composition, without affecting beef eating quality.

Key Words: finishing diet, tissue, fatty acid composition

321 Effects of frame size and animal age on beef carcass quality and tenderness. S. K. Duckett*[1], J. P. S. Neel[2], R. M. Lewis[3], W. Swecker[3], M. L. Wahlberg[3], J. P. Fontenot[3], and W. Clapham[2], [1]*Clemson University*, *Clemson, SC,* [2]*USDA-ARS*, *Beaver, WV,* [3]*Virginia Tech University*, *Blacksburg*.

Angus-cross steers (n = 96) were used to determine the effects of frame size (medium, MED or small, SM) and animal age on beef carcass quality and tenderness in a forage finishing system. Steers grazed mixed pastures (bluegrass/white clover) and were slaughtered at 16.6, 18.6, and 20.3 mo of age in a 2-yr study. At 24 h postmortem, carcass traits were collected and a rib from each carcass obtained for Warner-Bratzler shear force (WBSF) analysis. In yr 1, postmortem aging treatments included 14 and 28 d. In yr 2, postmortem aging treatments included 2, 4, 7, 14, and 28 d. Hot carcass weight, fat thickness, and skeletal maturity scores increased ($P < 0.05$) with animal age. Marbling scores, quality grades, and yield grades were greater ($P < 0.05$) for 20.3 than 16.6 mo. Longissimus muscle color was lighter ($P < 0.05$) and less red ($P < 0.05$) in 16.6 than 20.3 mo. Subcutaneous fat color was lighter ($P < 0.05$) and yellower ($P < 0.05$) for older than younger carcasses. Hot carcass weight and ribeye area were greater ($P < 0.05$) for MED than SM. Frame size did not alter other carcass parameters. In both years, the interaction between animal age and postmortem aging was significant. In yr 1, WBSF values at d 14 were lower ($P < 0.05$), indicating greater tenderness, for 16.6 mo than 18.6 and 20.3 mo. Extending the postmortem age to 28 d did not change ($P > 0.05$) WBSF values in young and intermediate ages but did improve tenderness ($P < 0.05$) for the older age group. In yr 2, WBSF values were lower ($P < 0.05$) at d 2 of postmortem aging for 16.6 mo than 18.6 or 20.3 mo. At 14 d postmortem, steaks from 16.6 and 18.6 mo were more tender ($P < 0.05$) than 20.3. By d 28, WBSF values did not differ ($P > 0.05$) among animal ages. In pasture-based beef finishing systems, increasing animal age results in larger carcasses with more external fat and marbling; however tenderness of ribeye steaks decreases with advanced age such that longer postmortem aging times are required to achieve similar tenderness level.

Key Words: beef, forages, tenderness

322 Effect of skeletal separation and moisture enhancement on eating quality of cull cow beef. P. Streiter*, C. Campbell, and I. Mandell, *University of Guelph*, *Guelph, Ontario, Canada*.

Sixty-two cull beef cows of known age and breed were slaughtered without electrical stimulation to investigate skeletal separation and moisture enhancement effects on eating quality. Carcass sides were designated to one of 4 postmortem processing treatments: 1) No

additional processing (Control), 2) prerigor skeletal separation (SS) after carcass dressing, 3) moisture enhancement (ME) using calcium ascorbate (CaAsc) 24 h postmortem and 4) Combination of SS and ME. Skeletal separation involved severing the pelvic bone at the narrowest part of the body of the ilium, and detaching vertebrae and connective tissue between 6th and 7th thoracic and 5th and 6th lumbar vertebrae. At 24 h postmortem, longissimus muscle from the ribeye (RE) and loin along with semimembranosus and semitendinosus (ST) muscles were excised from each carcass side with designated muscles injected with CaAsc (11% by wt). All muscles were cut into steaks for subsequent meat quality evaluation including shear force (SF) determination of tenderness for 7, 14, and 21 d aged product. A 10 member trained taste panel assessed treatment differences in palatability attributes for 14 d aged RE steaks as well as comparing sensory findings for cull cow vs. red branded beef from AA (USDA Select) and AAA (USDA Choice) quality grade carcasses. Skeletal separation reduced SF ($P < 0.001$) for RE steaks while moisture enhancement reduced SF ($P < 0.021$) for RE and ST. Postmortem aging for 14 vs. 7 d reduced SF to a lesser extent for SS vs non-skeletal separated sides, resulting in a SS by postmortem aging interaction ($P < 0.01$). Skeletal separation and moisture enhancement improved ($P < 0.01$) taste panel ratings for tenderness with an additive effect when combining SS with ME. Moisture enhancement tended to improve ($P < 0.07$) juiciness scores. While beef flavor was not affected by postmortem processing, ME increased ($P < 0.0001$) off-flavor scores. The combination of SS and ME may provide an additive effect for enhancing tenderness in the longissimus but at the expense of undesirable off-flavors.

Key Words: cull cows, skeletal separation, calcium ascorbate

323 Accuracy of real-time ultrasound for body composition traits for evaluating carcass traits in medium wool crossbred lambs. F. R. B. Ribeiro*[1], J. A. Carter[1], C. A. Hughes[1], W. S. Ramsey[2], J. W. Savell[2], R. R. Riley[2], C. Sharpton[2], and R. G. Tait Jr.[3], [1]*Texas A&M University-Commerce*, *Commerce,* [2]*Texas A&M University*, *College Station,* [3]*Iowa State University*, *Ames, IA*.

The objective of this study was to evaluate the accuracy of real-time ultrasound (RTU) measurements of body composition for evaluating lamb carcass traits. Data for this study were obtained from 25 medium wool crossbred lambs. Animals were scanned 2 to 5 d before harvest. The RTU measured traits were ultrasound BW (uBW, mean = 59.2 kg), 12–13th rib fat thickness (uBF, mean = 0.50 cm), and 12–13th rib *longissimus lumborum* muscle area (uLMA, mean = 18.6 cm^2), and carcass traits were HCW (mean = 35.3 kg), 12–13th rib fat thickness (cBF, mean = 0.56 cm), and 12–13th rib *longissimus lumborum* muscle area (cLMA, mean = 19.3 cm^2). Measurements were collected using an Aloka 500 with a 12-cm 3.5MHz transducer, each animal′s wool was clipped to no longer than 0.64 cm, and vegetable oil was used as a coupling agent to increase image quality. In addition to these traits, body condition score (BCS), hip height (HH), and ultrasound-measured rump fat thickness (uRUMP) also were collected. Data were analyzed using the PROC REG and PROC CORR procedures of SAS. Accuracy of RTU was determined by calculating the correlation, mean bias, and standard error of prediction (SEP) between RTU measurements and carcass measurements. The correlation, mean bias, and SEP between uBF and cBF were 0.90, −0.06 cm, and 0.09 cm, respectively, and for uLMA and cLMA were 0.66, −0.65 cm^2, and 2.12 cm^2, respectively. BCS was correlated ($P < 0.05$) to uLMA, uRUMP, and HH (0.62, 0.43, and 0.43, respectively). HH was correlated ($P < 0.05$) to uBF, uLMA and uRUMP (0.53, 0.41, and 0.60, respectively). These results suggest that RTU can be used as a non-invasive technique to accurately measure carcass traits in live lambs.

Key Words: ultrasound, carcass composition, lambs

324 Farming system changes fatty acids profile and lipid oxidation in meat of Sarda-breed suckling lambs. A. Nudda*, G. Battacone, M. G. Manca, R. Boe, A. Fenu, G. Spanu, and G. Pulina, *Dipartimento di Scienze Zootecniche, University of Sassari*, *Sassari, Italy*.

A study was carried out to evaluate the fatty acid composition of meat of suckling lambs raised in different breeding systems. Thirty-six pregnant ewes grazing on natural pasture (8 h/d) were divided into 2 groups supplemented with low (200 g/d; group L) or high (600 g/d; group H) amounts of concentrate. At lambing the ewes were divided in 2 subgroups (12 lambs each) balanced for single animals and twins: lambs kept indoor during the grazing time of the ewes (group I) and lambs which followed the mother on pasture (group O). Lambs were slaughtered at 27 d of age. After 24 h of refrigeration at 4°C, the tight muscles were dissected from each right half-carcass. Fatty acid profile and lipid oxidation (thiobarbituric acid test, TBARs) were studied. The data were analyzed with a linear model that included the fixed effects of supplementation (L vs H) and management (O vs I) and their interaction. In general, lamb meat from L ewes did not ($P > 0.10$) differ from the lamb meat from H ewes for the fatty acids analyzed, except for t11 C18:1 ($P < 0.01$). Management had relevant effect on the level of several fatty acids. The meat from O lambs had a lower ($P < 0.05$) content of C14:0, C16:0 and a higher ($P < 0.05$) content of C18:2 n6 and C18:3 n3 than that from I lambs. The content of DHA, PUFA n3 and PUFA n6 tended ($P < 0.10$) to be higher in O lambs than I lambs. The TBARs were not ($P > 0.10$) influenced by the 4 breeding systems. Interaction effects were significant ($P < 0.05$) for C18:0, C18:1 t10, C18:1 c9, C18:2 n6, PUFA n6, n6/n3 and TBARs. In conclusion, the dose of 600 g/d of concentrate supplemented to the ewes did not modify the FA profile and the lipid oxidation of the meat of their suckling lambs compared with the dose of 200 g/d of concentrate. Lambs, which followed the mother on pasture, produced meat with a higher content of C18:3 n3, probably because of the presence of grass in their diet.

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Key Words: suckling lamb, fatty acid, farming system

325 Comparisons of different muscles metabolic enzymes and muscle fiber types in Jinhua and Landrace pigs. J. Guo*, T. Z. Shan, T. Wu, Y. F. Zhang, and Y. Z. Wang, *Institute of Feed Science*, *Hangzhou, Zhejiang, China*.

Western and indigenous Chinese pig breeds show obvious differences in muscle growth and meat quality. However, the underlying molecular mechanism remains unclear. The objective of the present study was to investigate the variations in meat quality, muscle fiber type and enzyme activity of local Jinhua and exotic Landrace pigs at the same age (180 d of age, 4 animals individually). Using real-time RT-PCR, we detected the mRNA levels of myosin heavy chain isoforms such as oxidative (type I and type II a), glycolytic (type II b), and intermediate (type II x) fibers in longissimus dorsi and soleus muscles. Furthermore, the metabolic enzyme activities of lactate dehydrogenase (LDH), succinic dehydrogenase (SDH) and malate dehydrogenase (MDH) in longissimus dorsi and soleus muscles were also detected. The results showed that the Jinhua breed exhibited a higher intramuscular fat ($P < 0.01$) content and lower drip loss compared with Landrace ($P < 0.05$). Meanwhile, the

mRNA levels of oxidative and intermediate fibers were elevated in the Jinhua breed, whereas the glycolytic fibers were more highly expressed in the Landrace ($P < 0.01$). Furthermore, the Jinhua pigs possessed a higher oxidative capacity than did the Landrace ($P < 0.05$). These results suggested that the elevated expression of the oxidative and intermediated fibers in Jinhua breed is related to higher activities of oxidative enzymes and meat quality as indicated by a higher intramuscular fat and lower drip loss. These results may provide valuable information for understanding the molecular mechanism responsible for breed specific differences in growth performance and meat quality.

Key Words: Jinhua pigs, myosin heavy chain, meat quality

326 Effects of cage versus floor litter environments on blood parameters and meat quality in broilers. J. Yuan*, C. H. Huang, B. Wang, S. H. Zhou, and Y. Guo, *State Key Laboratory of Animal Nutrition, China Agricultural University*, *Beijing, China*.

The study was conducted to determine the effects of cage vs. floor rearing on some blood parameters and meat quality in broilers. At 3-wk of age broilers were allocated into 2 pens (9 birds/0.7 m^2/pen) of litter floor pens; one-story cages and battery cages, separately. At the end of 7 wk the experiment was terminated. Nine birds of every treatment were harvested. Breast muscle yield, muscle fiber characteristics, meat quality and blood parameters were determined. We observed that the breast muscle yield was lowered ($P < 0.05$) in broilers reared in the battery cages compared with those on floors. There were no ($P > 0.05$) differences for myofiber density of breast muscle among different rearing systems. Birds reared in battery cages, however, tended ($P < 0.10$) to be smaller in diameter of breast myofibers and exhibit lower drip loss than birds reared on floor. The pH (24h) of breast muscle was lower ($P < 0.05$) in broilers reared in one-story cages than those reared on litter floors or in battery cages. Higher ($P < 0.01$) levels of serum Insulin-like factor-1 (IGF-1) and plasma triglyceride (TG) were observed in broilers reared in one-story cages than birds on litter floor or in battery cages. No ($P > 0.05$) differences were found in the activities of plasma lactate dehydrogenase, creatine kinase, glutamic oxalacetic transaminase, glutamate-pyruvate transaminase (GPT), concentrations of plasma pyruvic acid (PA), lactic acid, triglyceride, nonesterified fatty acids, malonaldehyde, glucose and uric acid and serum corticosterone. Rearing in one-story cages and battery cages, however, tended ($P < 0.10$) to lower the concentrations of plasma GPT and PA in boilers. The results suggest that one-story cages do not affect the breast muscle yield and meat quality of broilers, and the energy, protein and lipid metabolisms of broilers. Battery cages rearing lowers myofiber diameter and consequently reduces breast muscle yield, which can be attributed to the lower protein synthesis and negative energy balance.

Key Words: rearing environment, meat quality, broilers

327 Effect of dietary selenium yeast (Sel-Plex) and vitamin E supplementation to broilers on meat quality characteristics of raw and marinated breast fillets. A. D. Quant*[1], A. J. Pescatore[1], J. L. Pierce[1], K. M. McClelland[2], G. R. Rentfrow[2], A. H. Cantor[1], M. J. Ford[1], and W. D. King[1], [1]*Alltech-University of Kentucky Nutrition Research Alliance*, *Lexington,* [2]*Department of Animal and Food Sciences, University of Kentucky*, *Lexington*.

A study was conducted to evaluate the effects of dietary supplementation of selenium (Se) and vitamin E (Vit.E) to broilers on meat quality characteristics of raw and marinated breast fillets. This study utilized 576 Cobb500 broilers that were randomly allotted to 4 treatments with 48 pens of 12 birds/pen in a 2x2 factorial design (12 replicates/treatment). Broilers were fed a corn-soybean meal control diet with no added Se or Vit. E, supplemented with either 0.3 mg Se/kg diet as Se yeast (Sel-Plex, Alltech, Inc., Nicholasville, KY), or 30 IU Vit. E/kg as all-rac-α-tocopheryl acetate, or a diet supplemented with both Se and Vit. E. Broilers were humanely harvested at 49 and 56 d of age (raw and marinated portion, respectively) and breast fillets were sampled for analysis of meat quality characteristics. Marinated breast fillets were soaked in a 3.2% sodium pyrophosphate and 4% NaCl solution for 13 h (marinade pH: 9.74). In raw breast fillets, Se yeast supplementation significantly decreased drip loss at 3d compared with the control ($P = 0.049$) and Vit. E ($P < 0.01$) treatments, however by 7d, the only observed improvement was Se yeast compared with Vit. E ($P < 0.01$). Oxidative stability at 7d (as indicated by thiobarbituric acid reactive substance values) of the raw breast fillets was improved by Se yeast supplementation with ($P = 0.095$) or without added Vit. E ($P < 0.01$) compared with the control treatment. In the marinated breast fillets, there was no effect of dietary treatment on drip loss, however oxidative stability at 7d was significantly improved by all 3 antioxidant containing treatments ($P < 0.01$) compared with the control. Antioxidant supplementation did not affect color stability, carcass yield (WOG, front half, saddle), breast fillet pH, cooking loss, and tenderness values in both the raw and marinated breast fillets. These results indicate that dietary supplementation of Se yeast in broiler diets decrease drip loss and improve oxidative stability in raw breast fillets, and greatly improve oxidative stability in marinated breast fillets.

Key Words: selenium, meat quality, marination

328 Effect of three different postmortem electrical stimulation methods on quality of early-deboned broiler breast meat. H. Zhuang*, E. M. Savage, and K. C. Lawrence, *USDA-ARS*, *Athens, GA*.

The present experiment was carried out to evaluate the effects of electrical stimulation (ES) immediately pre-scalding (PS), ES immediately post-defeathering (PD) or PS combined with PD (PSPD) on the quality of early-deboned (2 h) broiler breast muscles, pectoralis (p.) major (fillets) and p. minor (tenders). No stimulation, early-deboned (2 h) and 24 h deboned (24 h) fillets were used for the comparison. The 42-d-old broiler carcasses were electrically stimulated with pulsed current at 200 V for 30s (1min total for PSPD), and breast meat was deboned 2 h postmortem. Quality indicators evaluated were: CIELAB L*, a* and b* color and pH of the raw fillets; Warner-Bratzler (WB) shear force (cooked meat) and cook yields of the fillets and tenders. There were no differences in raw fillet color and pH between the 3 ES treatments. Effects of different ES methods on meat WB shear force values and cook yields varied with breast muscles. For the fillets, the average WB shear force values of both the PS and PSPD samples, which were not different from each other, were significantly lower than those of the PD samples. There were no differences in cook yields between the PS and PD, or between the PS and PSPD, although cook yield of the PD samples was significantly higher than the PSPD samples. For the tenders, there were no differences in the average shear force values and cook yields between the 3 ES treatments. Regardless of ES method and muscle type, early-deboned broiler breast meat from ES carcasses required significantly less force to shear than the 2 h control, and more force than the 24 h control. These results indicate that ES can tenderize early-deboned poultry breast muscles; however, the effectiveness of ES tenderization varies with ES method for the fillets. Single PS is more effective in reducing fillet shear values than single PD, and there is no further reduction in shear values with double PSPD compared with the single PS.

Key Words: broiler, electrical stimulation, breast meat

329 Optimization of the time of marination for early deboned broiler breast fillets. V. A. Kuttappan*, V. B. Brewer, J. F. Meullenet, and C. M. Owens, *University of Arkansas*, *Fayetteville*.

Marination is an effective method which can be used to improve the tenderness of the early deboned breast fillets. However, there is little information available on the impact of the time at which fillets are marinated. The present study was intended to optimize the time of marination for chicken fillets deboned at 2h postmortem (PM). In this study, a total of 300 broilers (43–46days) were processed using an in-line system and deboned at 2h PM over 5 replications. Fillets were marinated at either 2.5, 4, 6, 8 or 24h PM. A non-marinated control was included. The fillets were vacuum tumbled (20 min) with a 15% marinade (final concentration of 0.5% salt and 0.45% phosphate). The left fillets were held for 24h in cooler before freezing while the right fillets were frozen immediately after marination to simulate various commercial practices. Marination pickup, retention, thaw loss, cook loss and Meullenet Owens Razor Shear energy (MORSE) values were measured. There was a significant increase in marinade pickup as the time of marination increased from 2.5 to 24h PM. Marination retention varied slightly among treatments. Thaw loss was significantly higher for fillets marinated and immediately frozen compared with those held until 24h PM before freezing, with the exception of fillets marinated at 8 and 24h PM. There was a significantly higher cook loss for the control fillets when compared with all marinated fillets suggesting that marination resulted in better water holding capacity. There was no significant difference between MORSE values of the non-marinated control and the fillets marinated at 2.5h PM. However, the MORSE values for the marinated fillets significantly decreased as the time of marination increased from 2.5 to 24h PM. The tenderizing effects of marination were only observed when marinated at 4h PM and later in this study. The fillets marinated at 8 and 24h PM had significantly lower MORSE than other treatments. Freezing immediately after marination did not impact MORSE values. The results of this study suggest that time of marination can impact marination pickup and quality factors such as tenderness.

Key Words: marination, early deboned, broiler fillets

330 Consumer acceptance of visual appearance of broiler breast meat with varying degrees of white etriping. V. A. Kuttappan*, J. F. Meullenet, and C. M. Owens, *University of Arkansas*, *Fayetteville*.

White striping is a condition associated with heavier broiler breast fillets and is observed grossly as white striations seen parallel to the direction of the muscle fibers. The present study was intended to assess the consumer acceptance of broiler fillets with different degrees of white striping condition. High resolution digital images of fillets, representative of varying degrees of white striping, were shown to 75 consumers in a blind study. Individual images were presented using a completely balanced randomized design. There were 4 replicates of individual fillets within each white striping category (Normal-NORM, Moderate-MOD, and Severe-SEV) and one picture of tray pack (3 fillets) for each category. The consumers were asked to express their overall liking for appearance with a 9-point hedonic scale (9 = like extremely; 1 = dislike extremely), purchase intent using a 5-point scale (5 = definitely would buy; 1 = definitely would not buy). An open ended comments section was also included. The results showed that NORM fillets had a significantly higher ($P < 0.05$) hedonic score (6.9) than the MOD fillets (6.1) which was also significantly higher ($P < 0.05$) than the SEV fillets (4.5), indicating that as severity of white striping increased, the consumer acceptance decreased. From the distribution of the responses, 10.7, 22.4 and 56.7% of the consumers disliked the NORM, MOD, and SEV fillets, respectively. Furthermore, the average purchase intent score for the NORM fillets (3.6) was significantly higher ($P < 0.05$) than those with 2 degrees of white striping (2.4 and 2.5, respectively), suggesting that the consumers were more likely to buy NORM fillets. Over 50% of the consumers indicated that they would probably/definitely not buy MOD or SEV fillets. The open-ended comments revealed the major reasons for the dislike of the white striped meat were that the fillets looked more fatty or marbled and/or that they thought the meat would be “tough.” The results of the study suggest that the white striping does affect the consumer acceptance based on the appearance of the fillets.

Key Words: white striping, consumer acceptance, broiler fillets

Nonruminant Nutrition: Enzymes 1

331 Efficacy of a thermally processed exogenous enzyme cocktail on broiler performance. K. R. Beaman*, K. G. S. Lilly, L. K. Shires, S. A. Loop, and J. S. Moritz, *West Virginia University*, *Morgantown*.

Feed ingredient price has influenced nutritionists to maximize diet nutrient availability through use of exogenous enzymes. Poultry are almost exclusively fed pelleted diets that entails feed being subjected to conditions of high moisture, temperature and pressure that could partially denature added enzymes. Exogenous enzyme efficacy may be decreased or completely lost if enzymes are not able to survive the pelleting process. The objective of the current studies was to properly assess the efficacy of a commercially available exogenous enzyme cocktail subjected to increasing steam conditioning temperatures during pelleting (82, 88, 93oC). All studies used male Cobb 500 broilers obtained from the same commercial hatchery. The experimental period was from d 3–21 with 8 birds per pen and 8 replications per treatment. Study 1 established significant differences between the Positive Control (PC) and Negative Control (NC) diets ($P < 0.05$). However, the exogenous enzyme cocktail did not show improved performance. Study 2 was designed to improve the opportunity for the exogenous enzyme cocktail to demonstrate a benefit. This study utilized increased mixer-added lipid addition in the diet formulation that may decrease frictional heat production in the pellet die, and a decreased metabolizable energy difference between the positive and negative control. Again, performance differences were observed between the PC and NC control diets ($P < 0.05$), with no beneficial effect demonstrated for the exogenous enzyme at any temperature ($P > 0.05$). In Study 3, diet formulations were similar to Study 2; however, temperatures were decreased (71, 77, 82oC) and an additional unconditioned mash (UCM) treatment was added. Significant differences were obtained between NC diets with and without exogenous enzyme cocktail in the UCM for live weight gain and feed conversion ratio (FCR) and at 82oC for FCR ($P < 0.05$). However, only numerical differences in performance were shown between the PC and NC diets.

Key Words: exogenous enzyme cocktail, enzyme efficacy, broiler performance

332 Growth performance and nutrient utilization of broiler chickens fed diets supplemented with phytase alone or in combination with citric acid and multi-carbohydrase enzyme. T. A. Woyengo*[1], B. A. Slominski[1], and R. O. Jones[2], [1]*Department of Animal Science, University of Manitoba*, *Winnipeg, Canada*, [2]*Canadian Bio-Systems Inc.*, *Calgary, Canada*.

An experiment was conducted to determine the effect of supplementing a corn-soybean meal-based diet with phytase alone or in combination with citric acid (CA) or multi-carbohydrase, a preparation of non-starch polysaccharide-degrading enzymes (MC) or both on growth performance and nutrient utilization. A total of 360 one-day-old broiler chicks were assigned to 6 dietary treatments, each consisting of 12 pens of 5 birds each, and were fed experimental diets from 1 to 21 d of age. The diets included a positive control (PC) (0.46% non-phytate P; 1.1% Ca), a negative control (NC) (0.26% non-phytate P; 0.89% Ca), and NC without or with phytase (600 U/kg) alone, phytase plus CA (5 g/kg), phytase plus MC (Superzyme OM; 0.6 g/kg), or phytase plus CA and MC. Birds fed the PC diet had higher ($P < 0.05$) BWG (764 vs. 594 g/21 d) and tibia ash content (50 vs. 38%) than those fed the NC diet. Phytase improved ($P = 0.03$) BWG (632 g/21 d), which increased further ($P = 0.018$) to 673 g/21 d for the phytase plus MC diet. In contrast to phytase alone, phytase plus MC supplementation improved ($P < 0.05$) FCR of the NC diet from 1.37 to 1.32. Tibia ash content for the NC diet increased ($P < 0.05$) from 38 to 42% due to phytase and a trend ($P = 0.136$) in its further increase to 44% was noted for the phytase plus MC diet. Phytase improved ($P < 0.05$) ileal digestibility of P from 29 to 43%, and the addition of CA or MC or both to phytase-supplemented diet further increased ($P < 0.05$) P digestibility to 52, 53 and 54%, respectively. Phytase addition improved ($P < 0.05$) diet AMEn content from 2959 to 3068 kcal/kg, which tended ($P < 0.06$) to increase further following CA (3150 kcal/kg) or MC (3142 kcal/kg) addition. No interactions were detected between CA and MC on all response criteria measured. The results show that addition of MC to the phytase-supplemented broiler diets can result in improved nutrient utilization and growth performance.

Key Words: broiler, enzyme, citric acid

333 Intestinal histology and amino acid digestibility of broilers fed increasing dietary phytic acid during a live coccidia vaccination. R. N. Lehman*[1], A. J. Cowieson[2], C. L. Walk[1], and A. P. McElroy[1], [1]*Virginia Tech*, *Blacksburg,* [2]*AB Vista*, *Wiltshire, Marlborough, UK*.

Day-old Cobb 700 male broilers were obtained from a commercial hatchery, weighed, and half were spray-vaccinated with a live coccidia vaccine (Coccivac-B) before placement into one of 72 floor pens with clean pine shavings (35 chicks/pen). Vaccinated and non-vaccinated birds were given one of 3 diets with different phytic acid (PA) levels (low = 0.20% phytate-P; medium = 0.28% phytate-P; high = 0.36% phytate-P) for a total of 6 vaccination X diet treatments (12 replications/treatment). The non-vaccinated birds received no coccidiosis control. On d 21, ileal digesta was collected for amino acid (AA) digestibility and duodenal, jejunal, and ileal tissue samples were collected for histological examination. In the duodenum, there was a significant diet by vaccination interaction ($P < 0.05$) on villus height (VH) with non-vaccinated birds having a shorter VH than vaccinated birds on the low PA diet, but a greater VH than the vaccinated birds when fed the medium and high PA diets. The VH to crypt depth (CD) ratio (VCR) remained constant for the non-vaccinated birds as dietary PA increased, whereas VCR decreased ($P < 0.05$) in the vaccinated birds as PA increased. Vaccinated birds and birds given the medium PA diet had deeper ($P < 0.05$) crypts compared with all other treatments. In the jejunum, vaccinated birds had deeper ($P < 0.05$) crypts and larger VCR. Vaccinated birds fed the low PA diet had larger VH than non-vaccinated birds, but a smaller VH than non-vaccinated birds fed the medium and high PA diets. In the ileum, vaccination alone caused a larger ($P < 0.05$) VH, CD, and VCR. Vaccination caused a decrease in total AA digestibility ($P < 0.05$), and the high PA diet resulted in the highest AA digestibility. These results suggest that interactions between the level of dietary PA and coccidia vaccination could alter intestinal morphology and subsequently have an effect on AA digestibility in broilers. An improved AA digestibility seen with the high PA diet may be due to exceeding a critical PA:protein ratio that may cause protein insolubility at intermediate levels.

Key Words: phytate, vaccination, histology

334 Effects of NSP-enzymes on in vitro digestibility and intestinal microbiota activity in broilers fed two different wheat cultivars. B. Bouza, C. Clavaud, P. A. Geraert, and E. Devillard*, *ADISSEO SAS*, *03600 Commentry, France*.

Non-starch polysaccharide (NSP) enzymes or carbohydrolases are commonly used in poultry diets to improve feed digestibility. These enzymes modify substrates reaching the different parts of the gastrointestinal tract and thus could have similar effects to that of prebiotics on intestinal microflora. The aims of the present study were to determine in vitro the effects of carbohydrolase complex (Rovabio Excel) on the digestibility of 2 wheat cultivars, Caphorn (Ca) and Isengrain (Is) differing by their NSP composition, and on the consequences on broiler intestinal microbiota activities. A first in vitro incubation step was carried out to mimic digestion in the upper digestive tract with pepsin/HCl and pancreatin incubations with supplementation or not with carbohydrolases (Rovabio Excel AP at 0.5 mg/g substrate). In vitro digestibilities of energy (dE) of the 2 cultivars were different, with Ca being less digestible than Is (−3%, $P < 0.009$). The effects of Rovabio depended on wheat cultivars, with an improvement of dE of 6.4% ($P = 0.005$) and 2.1% ($P = 0.081$) for Ca and Is, respectively. The resulting materials were used in an anaerobic incubation with ileal contents from broilers. More gas (+38 mL, $P = 0.0004$) and more short chain fatty acids (SCFA) (+164 m*M*, $P = 0.025$) were produced with Ca than Is in relation with dE of the wheat cultivars (Is > Ca). When carbohydrolases had been used in the first incubation step, there was a decrease in gas and SCFA productions. These effects were more important for Ca than for Is. Finally, the enzymes effects were also observed on SCFA profile, with more butyrate and less propionate produced from enzyme-treated substrates than from untreated substrates. In conclusion, this study showed a positive effect of NSP-enzymes on the in vitro digestibility of energy of both wheat cultivars, which leads to changes in intestinal microbiota characteristics. There were also differences between cultivars, in term of effects of NSP-enzymes, probably linked to NSP composition of the two substrates.

Key Words: NSP-enzymes, wheat digestibility, ileal fermentation

335 Assessment of phytase in broilers undergoing a coccidiosis challenge. A. L. Shaw*, J. P. Blake, and K. S. Macklin, *Auburn University*, *Auburn, AL*.

An experiment was conducted to assess the effects of a phytase enzyme on broilers undergoing a coccidiosis challenge through 21 d of age. Twenty one days before the experiment, 120 chicks were placed in 24 of 48 floor pens to produce a coccidia challenge. At 10 d of age they were orally dosed with a cocktail containing 100,000 and 5,000 sporulated *E. acervulina* and *E. tenella* oocysts, respectively, for litter seeding. Straight run broiler chicks (1008) were placed across 48 floor pens (21 birds/pen, 6 reps/trt) on either fresh or seeded litter. All birds were fed a corn-soybean meal diet (22% CP, 3087 kcal/kg) adequate in all nutrients but Ca and available phosphorus (aP). Treatments were created using a combination of 2 Ca-aP levels (0.9% Ca, 0.45% aP vs. 0.7% Ca, 0.25% aP and 500 FTU Optiphos), 2 coccidia challenges (unchallenged vs. challenged), and 2 vaccination strategies (unvaccinated vs. vaccinated with CoccivacB prior to placement). On d 10, 18, and 21 bodyweight (BW) and feed consumption (FC) were recorded for each pen. Five birds/trt were sacrificed and intestinal samples were obtained for visual and microscopic lesion scoring on d 10 and 18. At 21 d 18 birds/trt were selected for removal of left tibia to assess bone strength. BW and FC were unaffected (P>0.05) by inclusion of phytase or vaccination strategy. From 0-10d birds exposed to the seeded litter had a higher FCR (P<0.05). Upon conclusion of the experiment, birds exposed to coccidia had lower BW and FC, as well as a higher feed conversion (P<0.05) in comparison to those not challenged. Regardless of treatment, bone breaking force as well as visual and microscopic scoring of the duodenum and ceca showed no differences (P>0.05). Although there were no statistical differences in cocci scoring, incidence of cocci was greater in challenged vs. unchallenged birds. Results indicate that phytase was ineffective in improving the performance or P utilization of birds vaccinated and/or subjected to a coccidiosis infection.

Key Words: Broiler, *Eimeria* spp., phytase

336 Dietary supplementation of *Peniophora lycii* phytase improves mineral bioavailability in broiler chickens. A. Kollanoor Johny*[1], K. Syam-Mohan[1], T. V. Viswanathan[1], and A. Jalaludeen[2], [1]*Department of Animal Nutrition, College of Veterinary and Animal Sciences, Kerala Agricultural University*, *Mannuthy, Kerala, India*, [2]*Centre for Advanced Studies in Poultry Science, College of Veterinary and Animal Sciences, Kerala Agricultural University*, *Mannuthy, Kerala, India*.

An investigation was carried out to study the effect of dietary *Peniophora lycii* phytase on the growth and mineral bioavailability in broiler chickens. Day-old, straight run commercial broiler chicks (n = 96) were randomly divided into 8 identical groups containing 12 birds each, reared under deep litter system for 8 weeks. The groups were randomly allotted to 2, maize-soy based diets: control and experimental, with 4 replicates per treatment. Birds in the control group received a standard broiler ration (SBR) whereas, the treatment group received SBR supplemented with phytase at 750 U/kg diet. Feed and water were supplied *ad libitum.* Body weight and feed intake were recorded, and feed conversion ratio (FCR) and protein efficiency ratio (PER) were calculated. Two birds from each replicate were sacrificed at sixth and eighth week and, liver, spleen, tibia and blood samples were collected for analyses. At the end of 8 weeks, a 3-d metabolism trial was carried out using 2 birds selected randomly from each replicate, and housed in individual metabolism cages with facilities for feeding, watering and collection of droppings. Body weight, dry matter (DM) intake, FCR and PER did not differ significantly between the groups ($P > 0.05$). Also, DM and nitrogen retention between the groups were not different. However, the availability of calcium (Ca), phosphorus (P), magnesium (Mg), copper (Cu), and iron (Fe) was significantly improved ($P < 0.05$) with phytase supplementation and were 39, 55, 54, 24, and 65% more, respectively compared with the control. The concentration of Fe in the liver was significantly higher ($P < 0.05$) in the phytase-treated groups at sixth and eighth week of trial, whereas its concentration in the spleen did not differ between groups. Tibial weight and tibial ash content at sixth week were significantly higher ($P < 0.05$) for the phytase-treated groups. However, serum concentrations of Ca, P, Mg, Cu, Fe and Zn did not differ between the groups. Results of the study indicate that *Peniophora lycii* phytase could potentially improve the bioavailability of minerals in broiler chicken.

Key Words: *Peniophora lycii* phytase, mineral bioavailability, broiler chicken

337 Mineral excretion and bone mineral content as affected by phytase and feed additives in broilers. M. R. Dalmagro*[1], E. O. Oviedo-Rondón[1], A. Mitchell[2], A. B. Leytem[3], N. A. Barbosa[4], N. K. Sakomura[4], J. W. Wilson[5], and C. Paulus[5], [1]*North Carolina State University*, *Raleigh,* [2]*USDA-ARS, BARC*, *Beltsville, MD*, [3]*USDA-ARS*, *Kimberly, ID*, [4]*Universidade Estadual Paulista, UNESP*, *Jaboticabal, SP, Brasil*, [5]*DSM Nutritional Products Inc.*, *Parsippany, NJ*.

One broiler study was conducted to evaluate the effects of feed additives (FA) in diets containing phytase on mineral excretion and bone mineral content (BMC) for broilers up to 43 d of age. Corn-soybean diets with 5% inclusion of DDGS were used as basal diets. All diets contained ionophore Coban. The treatments evaluated consist of a control without phytase (C), and 7 treatments that contained phytase Ronozyme P

formulated to release 0.1% of phytate phosphorus (P) to have an equal amount of available P compared with C. These 7 treatments included diets without any other FA (PC), GP antibiotic (BMD), 3 probiotics: BC30 (*B. coagulans*), B2B (*B. licheniformis*, *B. subtilis*), and Calsporin (*B. subtilis*), and 2 EO: Crina POULTRY Plus (CPP) at 300 ppm and Crina PoultryAF (CPF) at 100 ppm. Day-old Ross 708 broilers were randomly assigned to 96 floor pens with previously used litter. Ten males and 10 females were placed in each pen. Fresh excreta were collected at 40 d and one male per pen was sacrificed at 44 d of age to collect bones. Data were analyzed as a completely randomized block design with 12 replicates per treatment. The highest excretion of P (Pex) and water extractable P (WEP) was observed in C chickens. Excreta from C chickens had the highest moisture, but the lowest K and Mg. These chickens also had the lowest tibia and femur BMC. The Pex was reduced by addition of phytase in all diets. GP and the EO did not cause further reductions on Pex, but all probiotics reduced Pex. WEP was reduced by PC, GP and CPP. Excreta of chickens fed diets containing only phytase had the highest concentration of Ca, Mn, and Mg. Calcium excretion was reduced by probiotics and EO. The highest tibia and femur BMC was observed in B2B chickens. The excreta of these B2B chickens had the highest concentration of K and the lowest concentrations of Na, Zn, and Mn. Concentrations of Cu in the excreta were not affected by treatments. It was concluded that FA may affect mineral metabolism in chickens fed diets with phytase. Probiotics seem to have a positive effect on P retention and bone mineral deposition.

Key Words: probiotics, essential oils, growth promotants

338 Use of the precision-fed rooster assay and a chick AME trial to determine the best method for enzyme efficacy. J. Brandon* and A. B. Batal, *The University of Georgia*, *Athens*.

The beneficial effects of exogenous enzyme addition to poultry diets have been well documented. However, the results have been variable depending on the in vivo method used. The most common methods employed to assess the bioefficacy of exogenous enzymes in vivo are performance trials and metabolism studies, such as the precision-fed rooster assay. There has been criticism of the use of the precision-fed rooster assay. Thus, the objective of these studies was to compare the precision-fed rooster assay with the chick AME trial to determine which method best measures enzyme efficacy. In 2 studies 6 different enzymes mixed in a complete diet (as well as a control diet with no enzyme, for a total of 7 treatments per study) were evaluated using the precision-fed rooster TME assay alongside a more conventional chick AME trial. The rooster assays were traditional precision-fed rooster assays in which 8 birds per diet were fasted for 24 h then crop intubated with 35 g of the test diet and excreta was then collected for 48 h. However, to keep consistent with the chick AME trial, the roosters were 'primed' on the experimental diets. They were allowed ad libitum access to the experimental diets for 5 d before the fasting and crop intubation. The chick AME trials used 728 d old Cobb 500 by-product male chicks (7 replications per treatment, 8 chicks per replication) that were fed the same experimental diets for 5 d and excreta was collected at 18 d of age for the determination of AME. Regardless of the method used, in both studies no significant increase was observed due to exogenous enzyme supplementation on the TME values determined from the precision-fed rooster assays or the AME values determined from the chick digestibility trials. The determined TME values were significantly higher than the AME values. However, no correlation was observed between the determined ME values for the control or enzyme diets between the rooster and the chick assay, suggesting the assay used could affect the measured efficacy of the enzymes.

Key Words: enzymes, TME, AME

339 The effects of the addition of phytase and an enzyme cocktail to high and low nutrient density diets with DDGS or MBM in laying hens during phase II. D. Hahn*[1], S. Scheideler[1], E. E. M. Pierson[2], and C. L. Novak[3], [1]*University of Nebraska-Lincoln*, *Lincoln,* [2]*Danisco Animal Nutrition*, *St. Louis, MO,* [3]*Land O' Lakes Purina Feed, LLC*, *Kansas City, MO, and Lincoln, NE*.

The objective was to test the addition of Avizyme 1502, a blend of protease, amylase and xylanase (Danisco, UK Ltd.) in laying hen diets containing dried distillers grains (DDGS) or meat and bone meal (MBM) during phase II of egg production. All diets contained phytase (300 FTU minimum; Phyzyme XP 5000 G Feed Enzyme). Three hundred eighty-four Hy-Line W-36 laying hens were used in this study, from 35 to 52 weeks of age. There were 12 replicate pens with 4 hens per pen. The experiment consisted of 8 dietary treatments arranged in a 2 × 2 × 2 factorial design: diets (DDGS or MBM), metabolizable energy (ME) levels (2880 Kcal/kg or 2800 Kcal/kg), and 2 enzyme levels (0 or 0.0375% Avizyme) to provide protease at 8000U/g, amylase at 800U/g and xylanase at 600 U/g of product. All diets contained Phyzyme at 60 g MT (~300 FTU) and were formulated to contain 0.30% avP and a Ca adjustment as recommended by Phycheck software tool (10% decrease). Response variables measured included: daily egg prod, biweekly egg wt, weekly feed intake; body wt, Haugh unit, yolk wt, albumen wt, shell wt, shell strength and specific gravity were taken monthly. There was a significant effect for feed intake between high and low ME diets ($P = 0.0349$), with diet 3 (2880 Kcal/kg, MBM, Phyzyme) having significantly lower intake when compared with the other 7 treatments. However, there were no differences noted between treatments for hen weight, egg production and egg quality parameters ($P > 0.05$). Thus, reducing ME, P and Ca with the addition of enzymes had no negative effect on egg production and quality. Given Nov 2009 commodity prices, there was a cost savings shown in regards to high (2880 Kcal/g) vs low (2800 Kcal/g) energy diets when MBM was in the diet. There was a cost savings with the addition of Avizyme.

Table 1. Kg feed cost/Doz. eggs produced

	DDGS		MBM	
ME	-Avzym	+Avzym	-Avzym	+Avzym
2880	$0.253	$0.227	$0.322	$0.240
2800	$0.251	$0.238	$0.269	$0.261

Key Words: metabolizable energy, Avizyme1502, laying hens

340 Justifying phytogenic feed additive matrix values in conjunction with exogenous feed enzymes. L. K. Shires*, S. A. Loop, C. K. Gehring, K. R. Beaman, and J. S. Moritz, *West Virginia University*, *Morgantown*.

Phytogenic feed additives (PFA) are purported to possess antimicrobial properties as well as nutrient sparing characteristics that may aid in alleviating high diet costs; however, in order for PFAs to assist nutritionists in decreasing diet cost, matrix values must be determined and implemented in feed formulation. On d4, 1,344 male Cobb 500 broilers were weighed and randomly allotted to 1 of 64 floor pens. Floor pens were located in 2 separate rooms, composed of one block each. Study 1 evaluated proposed matrix values for a commercially available PFA and assessed nutrient sparing when the product was combined with commercial phytase, carbohydrase and protease. The most remarkable proposed matrix values were 14.6 kcal/lb for metabolizable energy and 0.07% for Ca and AP. The objective of Study 2 was to determine true amino acid digestibility (TAAD) and nitrogen corrected true metabolizable energy (TME_n) using 32 cecectomized SCWL roosters. Dietary

treatments for both studies included a basal, basal with phytogenic product matrix value, basal with phytogenic product matrix value and phytogenic product, and similar treatments evaluating the phytogenic product matrix with exogenous enzyme products. Decreasing the basal diet by the proposed phytogenic matrix values decreased broiler live weight gain and increased feed conversion ratio ($P \leq 0.05$). However, when the same diet included the phytogenic feed additive, live weight gain and feed conversion ratio were restored to that of the basal diet ($P > 0.05$). The proposed matrix values of the specific PFA tested were justified; however, the PFA was not additive or synergistic with exogenous enzymes. Nitrogen corrected true metabolizable energy and TAAD data did not differ when the diets varied based on the PFA per se ($P > 0.05$). However, when the PFA was incorporated using proposed matrix values and used in conjunction with exogenous enzyme matrix values, several tested TAAD values were decreased ($P \leq 0.05$). Decreased nutrient digestibility may involve reductions in gut microflora due to the PFA as well as simultaneous reduction in substrate concentrations.

Key Words: phytogenic feed additives, matrix values, true amino acid digestibility

341 The effect of phytase and energy enzyme inclusion on growth and bone ash in low phosphorus diets. J. R. Coppedge*[1], J. Klein[1], K. Jessen[1], A. Jordan[1], B. Brown[2], F. Ruch[2], and J. T. Lee[1], [1]*Texas A&M University*, *College Station,* [2]*Enzyvia LLC*, *Sheridan, IN*.

An experiment was conducted to evaluate the effect of varying levels of phytase with and without NSPase inclusion on broiler performance when supplemented in corn/soybean meal diets low in available phosphorus. The objective was to determine if NSPase inclusion enhances phytase activity in relation to growth parameters and bone ash in broilers reared in batteries through 14 d of age. Four diets with selected available phosphorus levels of 0.15%, 0.20%, 0.25%, and 0.30% were included in the experimental design to develop a dose response curve to calculate phosphorus release from experimental treatments. An additional 6 treatments were evaluated that included 3 levels of phytase (150, 200, and 250 FTU/kg) with and without NSPase inclusion in a diet containing 0.15% available phosphorus. Evaluated parameters included body weight, feed conversion ratio, mortality and bone ash percentage. Body weight and bone ash percentage were positively influence with increases in available phosphorus levels. Phytase inclusion positively influenced growth performance and bone ash percentage. Broilers fed the 200 and 250 FTU/kg phytase inclusion levels outperformed the broilers fed the 150 FTU/kg inclusion level. Addition of NSPase with 150 FTU/kg phytase resulted in increased broiler body weight as compared with the 150 FTU/kg phytase diet alone. Using regression equations determined from dose response treatments for body weight, bone ash (mg), and bone ash percentage, NSPase inclusion increased phosphorus release at the 150 FTU/kg level from 0.06% to 0.09%. These data indicate that NSPase inclusion may increase phytase effectiveness when co-administered during early stages of growth.

Key Words: bone ash, phytase, broiler

342 Transforming coccidiosis mediated lesion score effects into estimates of performance and calorific costs in the form of ADG, FCR, malabsorption and effective caloric value throughout the broiler growth curve to 48 days of age. R. G. Teeter*[1], A. Beker[1], C. Brown[1], C. Broussard[2], F. Fitz-Coy[2], J. Radu[2], and L. Newman[2], [1]*Oklahoma State University*, *Stillwater,* [2]*Schering-Plough Animal Health*, *Summit, NJ*.

Methodologies enabling the conversion of intestinal lesion score into calorific cost estimates have been developed. Coccidiosis, the major disease challenge for broilers, reduces ADG and elevates FCR. Birds normally develop immunity during the production cycle, but uncertain timing can lead to intestinal lesion scores ranging throughout the growth curve. Vaccination at hatch speeds immunity development, reduces lesion score severity and shifts lesion scores to the early weeks. To examine the caloric cost of immunity development 2 groups of birds were reared in cocci free environments with one vaccinated at hatch (Coccivac-B) and the other maintained as naive to cocci. Birds were selected from the 2 backgrounds at 5 weekly intervals for metabolic chamber placement. The 5 challenge periods consisted of an oral dose of sterile saline or a mixture of 3 *Eimeria* species as oocysts. Metabolic costs of cocci challenge included appetite suppression, maintenance energy cost, malabsorption as excreta calorie elevation and reduced performance. Though immunity development occurring early in the production cycle, had energy costs, birds with late growth curve immunity development exhibited significantly higher costs in all categories. In this study coccidiosis mediated lesion scores 6 d post oocysts challenge at 14, 21, 28, 35, and 42 d, exhibited highly significant deleterious impact with marked elevation late in the growth curve (35, 42 d). Lesion score 1 and 2 reduced the dietary effective caloric value from an initial 3,200 kcal/kg ration by 125 and 596 kcal for 800 g broilers and by 625 and 2,277 kcal/kg for 3000g birds, respectively. Calorimetry data substantiated the lesion consequence with increased maintenance energy need, heat production and malabsorption. Timing of immunity development is critical to performance as late growth curve cocci challenges markedly exacerbated energy costs for birds lacking immunity.

Key Words: coccidiosis, immune response, energy

343 Mintrex-Zn improves tibia Zn deposition and antioxidant status of broilers under stress with coccidiosis challenge. S. D. Bun* and Y. M. Guo, *China Agricultural University*, *Beijing, China*.

An experiment was conducted to investigate the beneficial effects of the organic zinc (Mintrex-Zn) vs inorganic zinc for broilers chicks reared under stress with coccidiosis challenge. Tibia Zn, bone breaking strength, and oxidative enzymes were examined during study. A total of 480 one day-old male chicks were randomly placed into 80 cages of 6 chicks each. A corn-soybean meal diet containing Zn 29.64 mg/kg was used as a basal diet for the negative control group, supplemented with Zn at 20, 40 and 60 organic Zn per kg of diet, respectively. Treatment 2 is the positive control supplemented with reagent-grade zinc sulfate at 40 mg/kg while Mintrex-Zn (a methionine hydroxyl analog chelate) was used as an organic source for the treatment 3, 4 and 5. Half of the chicks in each treatment were inoculated by gavage with 1.5×10^4 *E. tenella* sporulated oocysts at 21 d of age. For the non-infected group, the tibia Zn deposition and bone breaking strength of chicks fed Mintrex-Zn was higher ($P < 0.05$) than those fed inorganic Zn at the same levels (40 mg/kg). Similar tendency, supplementation of Mintrex-Zn resulted in significant increase in GSH-Px activity ($P < 0.001$), and tended to elevate ($P = 0.08$) Cu/Zn-SOD activity while LPO (lipid peroxidation) was markedly decreased ($P < 0.05$). For the infected group, tibia Zn retention, bone breaking strength of chicks fed Mintrex-Zn at 40 mg/kg were highest among the treatments ($P < 0.001$) and reached the plateau thereafter. The maximum Cu/Zn-SOD and GSH-Px activities and decreased LPO were also observed in the chicks fed diet supplemented with Mintrex-Zn vs inorganic corresponding. It can be concluded that Mintrex-Zn enhanced tibia Zn deposition and could be considered to be more protective than zinc sulfate in terms of reducing the negative effect of oxidative stress induced by coccidiosis infection.

Key Words: organic zinc, antioxidant enzymes, broilers

344 Effects of type and level of dietary fiber on digestive traits and nutrients digestibility in broilers. E. Jiménez-Moreno*[1], J. M. González-Alvarado[2], S. Chamorro[3], C. Romero[1], R. Lázaro[1], and G. G. Mateos[1], [1]*Universidad Politecnica de Madrid*, *Madrid, Spain*, [2]*Universidad de Tlaxcala*, *México*, [3]*Consejo Superior de Investigaciones Científicas*, *Madrid, Spain*.

The effects of inclusion of oat hulls (OH) and sugar beet pulp (SBP) in the diet on total tract apparent of retention (TTAR) of nutrients were studied in broilers from 1 to 21 d of age. A control diet based on cooked rice that contained 3,260 kcal AME_n/kg and 1.6% crude fiber (CF) was diluted with 0, 2.5, 5.0, and 7.5% of either OH or SBP. Each treatment was replicated 6 times (a cage with 12 chicks). Digestive traits and nutrient retention were recorded at 7, 14, and 21 d of age, and jejunal histology at 14 d of age. Broilers fed additional fiber had heavier gizzards with higher digesta contents and lower pH than those fed the control diet ($P \leq 0.001$). As the level of fiber increased the relative weight of the gizzard increased linearly ($P \leq 0.001$) and gizzard pH was reduced ($P \leq 0.05$). Broilers fed OH had heavier gizzards ($P \leq 0.001$) with less digesta content ($P \leq 0.001$) and higher pH ($P \leq 0.01$) than those fed SBP. Villus height was reduced ($P \leq 0.05$) and crypt depth tended to be shorter as the level of fiber increased. Also, the inclusion of SBP but not OH, reduced villus height: crypt depth ratio linearly ($P \leq 0.05$). Fiber inclusion affected TTAR of nutrients in different manners depending on nutrient, type, and level of fiber considered. In general, the inclusion of 2.5% fiber improved nutrient digestibility with the effects being more pronounced with OH ($P \leq 0.001$ for DM, N, and AME_n). However, the inclusion of 7.5% fiber reduced nutrient digestibility ($P \leq 0.001$), especially when OH was used. We conclude that the inclusion of up to 7.5% OH or SBP increases the weight the gizzard and reduces its pH. The inclusion of 2.5% fiber improves TTAR of nutrients. However, a further increase to 7.5% has negative effects. Young chicks have a minimal requirement of at least 2.3% CF in the diet.

Key Words: fiber sources, nutrient digestibility, broiler

345 The effects of 1.2 ppm T-2 Toxin on performance, lesions, and general health of male broilers and the efficiency of an organoaluminosilicate (mycotoxin binder). J. C. Medina[1], J. A. Fierro*[1], J. Lara[1], V. Brito[2], and M. Forat[2], [1]*NUTEK S.A de C.V.*, *Tehuacan, Puebla, Mexico*, [2]*EURO-NUTEK Premix S.A. de C.V.*, *El Marques, Queretaro, Mexico*.

Mycotoxin presence has become a major problem in the Mexican livestock industry; thus producers trend is towards the use of binders to alleviate its effects. T-2 toxin is a mycotoxin that affects broilers health and performance (CAST, 2003). A trial was performed to evaluate the

toxic effect of a contamination (1.2 ppm) of T-2 and the efficiency of a commercial organoaluminosilicate. Ninety Ross 308 male broilers were randomly allocated in five groups: group 1 (negative control group), group 2 positive control (1.2 ppm T-2 toxin), group 3 (1.2 ppm T-2 toxin + 1.5 kg/ton organoaluminosilicate binder), group 4 (1.2 ppm T-2 toxin + 3.0 kg/ton organoaluminosilicate binder), and group 5 (3.0 kg/ton organoaluminosilicate binder). 18 replicates with one bird each. The birds were fed their respective diets from 10 days of age, up to 39 days, date in which they were sacrificed. We recorded the individual weight of the birds at the beginning and end of the experiment. At day 39 consumption and weight gain, feed conversion and mortality were calculated. Mean weights were: Group 1: 2307.7 g (a), Group 2: 2031.9 g (b), Group 3: 2254.3 g(a), Group 4: 2234.1 g (a), Group 5: 2246.3 g (a). Lesions of the oral cavity were scored. The results shown statistical significantly differences in weight gain, and numerical differences in feed intake, feed conversion and mortality. The effects of the T-2 toxin in the broilers were practically eliminated by the incorporation of any of both doses of the organoaluminosilicate in the diet. The weight difference between the control group and the intoxicated group is of 11.2%. The weight of the challenge group (organoaluminosilicate + T-2 toxin) represents a weight recovery of 83%. We observed that T-2 toxin is of dermal toxicity and that the oral lesions reduce feed intake. The organoaluminosilicate in the diet of the animals that were given T-2 toxin, reduced the negative effects caused by the aforementioned mycotoxin.

Key Words: organoaluminosilicate, T-2 Toxin, mycotoxin binder

346 Strategies to reduce preharvest *Salmonella* in organic broilers. K. G. S. Lilly*, K. R. Beaman, B. N. West, L. K. Shires, S. A. Loop, P. J. Turk, G. K. Bissonnette, and J. S. Moritz, *West Virginia University*, *Morgantown*.

Antibiotics are popularly used to combat bacteria, such as *Salmonella*. However, due to the concern of antibiotic resistant bacteria, organic poultry products have gained consumer interest. Outdoor rearing requirements for organic poultry could increase exposure to bacteria, including *Salmonella*. The objective of this USDA NIFSI funded project was to assess the effects of prebiotics and probiotics (Study 1) and acidifying water treatments (Study 2) on organic broiler performance and the presence of *Salmonella*. Study 1: A prebiotic (MAN), 2 probiotics (PRO1 and PRO2) and a control treatment (CON) were implemented. Study 2: Raw apple cider vinegar (RACV), organic acid blend (OA), hydrogen peroxide (H2O2) and a control treatment (CON) were incorporated into watering systems. For both studies, 300 1-d-old Cobb 500 male chicks were randomly assigned to treatment and pen. On d-21 birds were weighed and designated to one of 13 weight classes for each treatment and allocated 13 per pen within each of the 5 housing locations which included pasture access at the West Virginia University Certified Organic farm. Data collection occurred from d-21–49. For Study 1, PRO1 and MAN demonstrated the highest d-21 bird weight (BW), followed by CON and then PRO2 ($P < 0.05$). Study 1 treatments did not affect feed intake, live weight gain, feed conversion or ending BW ($P > 0.05$). For Study 2, on d-21, OA were the largest, followed by CON, H2O2 and RACV ($P < 0.05$). OA consumed more feed than H2O2 and RACV birds, but the same amount as CON. Water intake was consistent for OA, CON and RACV, while H2O2 consumed the least ($P < 0.05$). On d-49, OA had higher BW than H2O2 and RACV, but the same as CON ($P < 0.05$). RACV and CON d-49 BW were the same and H2O2 had the lowest ending BW ($P < 0.05$). For both studies, on d-29 and d-50, samples were taken to determine the presence of *Salmonella* in feed, litter and water. An additive x location and an additive × sampling day interaction was observed for the presence of *Salmonella* ($P < 0.05$).

Key Words: antibiotic alternatives, organic broilers, *Salmonella*

347 Cecal microbial populations of young chicks fed several prebiotic-type compounds as determined by DGGE and quantitative PCR. C. M. Jacobs*, P. L. Utterback, and C. M. Parsons, *University of Illinois*, *Urbana*.

The objective of the current studies were to investigate the prebiotic effects of supplementing Grobiotic (GB) and Dairylac-80 (International Ingredient Corporation, St. Louis, MO), Temulose (Temple Inland, Diboll, TX), lactose, and Alternan (USDA, Peoria, IL) on cecal microbial populations in young chicks fed corn-SBM diets using DNA–based qualitative (denaturing gradient gel electrophoresis; DGGE) and quantitative (qPCR) techniques. In Experiment 1, 5% GB, 0.5% Temulose, and combinations thereof were fed for 3 or 7 d post–hatch. In Experiment 2, 5% GB, 1% lactose from Dairylac-80 or pure lactose were fed for 3, 7, or 21 d post–hatch. In Experiment 3, 1 or 2% Alternan was fed for 3, 7, or 21 d post–hatch. In Experiment 1, bacterial enumeration by qPCR did not detect any positive significant differences in bifidobacteria, lactobacilli, or *E. coli* populations when GB, Temulose, or combinations thereof were included in the diet for 3 or 7 d, but DGGE dendrograms and unrooted trees showed that replicates were clustered together by diet. In Experiment 2, at 3 and 7 d of age, there was an increase ($P < 0.10$) in bifidobacteria for all GB, Dairylac–80, and lactose treatments when compared with the basal diet treatments. At 21 d, 1% lactose decreased *E. coli* populations at every collection period. The DGGE indicated that replicates were clustered more by diet than age. In Experiment 3, the addition of Alternan had no positive effects on any selected microbial populations across all age periods. Replicates were clustered both by diet and age. When considering the effect of age for a single dietary treatment, there was a linear decrease ($P < 0.05$) for all selected microbial populations with increased age. Our results indicate that cecal microbial populations of young chicks can be affected by the addition of prebiotic–type compounds to the diet, but the changes in microbial populations as the birds age is not as clear.

Key Words: chick, denaturing gradient gel electrophoresis, polymerase chain reaction

348 Turkey response to the inclusion of a *Saccharomyces cerevisiae* fermentation product, Original XPC, in antibiotic free diets following a coccidia vaccination. D. M. Paiva*[1], C. L. Walk[1], R. Lehman[1], J. R. Sottosanti[1], C. F. Honaker[1], D. T. Moore[2], and A. P. McElroy[1], [1]*Virginia Polytechnic Institute and State University*, *Blacksburg,* [2]*Diamond V Mills, Inc.*, *Cedar Rapids, IA*.

Saccharomyces cerevisiae fermentation products are among feed additives with potential to support intestinal integrity and immune defense to improve intestinal health of commercial poultry. The objective of this study was to evaluate the effect of XPC (a commercially available fermentation product) supplementation on turkey performance to 63d during a mild intestinal challenge from a commercial live coccidia vaccine. Day old female, Hybrid Converter turkeys were obtained from a commercial hatchery, weighed and randomized (22poults/pen) into 8 treatment groups. The experiment was a 4 × 2 factorial design with 4 dietary treatments and 2 coccidia vaccination treatments (vaccinated and non-vaccinated). Vaccinated and non-vaccinated birds were given one of the 4 diets with different inclusion levels of XPC (no XPC = negative control; 0.0625% = 0.5X, 0.125% = 1X; 0.250 = 2X), and each dietary treatment was replicated by 18 pens (9 vaccinated and 9 non-

vaccinated). Body weight (BW) and feed intake were measured on d 0, 28, 42 and 63 and cumulatively (d0–63), and mortality was recorded daily. Adjusted feed conversion was calculated for each of these periods, corresponding to diet changes, and cumulatively. Birds fed with XPC had heavier ($P < 0.001$) BW than control fed birds at d28 and 42 and increased BW gain during pre-starter (d0–28) and starter (d28–42) feeding periods. Vaccinated birds were significantly heavier ($P < 0.004$) than non-vaccinated at d63 and had increased BW gain compared non-vaccinated birds during d42–63 ($P < 0.006$) and d0–63 ($P < 0.004$). Feed consumption was higher ($P < 0.05$) for birds fed diets containing XPC at 0.5X and 1X during d0–28. Feed conversion was only different during the d0 to 28 period with 2X inclusion of XPC resulting in the most efficient conversion. These results suggest that XPC was able to promote intestinal health and maintain turkey performance during mild challenge to the intestine from a live coccidia vaccine.

Key Words: fermentation product, coccidia vaccination, turkey

349 Effect of diet on equine gut microbiota. K. Daly*[1], C. J. Proudman[1], H. J. Flint[2], and S. P. Shirazi-Beechey[1], [1]*University of Liverpool*, *Liverpool, UK*, [2]*Rowett Institute of Nutrition and Health*, *Aberdeen, UK*.

The horse has evolved as a highly adapted hindgut fermenter, with a voluminous large intestine (LI) containing specialized microbial populations. Dietary plant fiber is fermented by intestinal microbiota to short chain fatty acids (SCFA) notably acetate, propionate and butyrate. SCFA, once absorbed, not only provide a significant proportion of horse's energy requirements, but are also important in regulating physiological processes essential for the maintenance of LI health. Today's horse, however, is fed diets supplemented with readily digestible hydrolysable carbohydrates (hCHO), generally in the form of grain, to provide further energy for the demands of work and performance. It is proposed that when horses are introduced abruptly to diets containing high levels of hCHO, a substantial proportion of starch reaches the LI. There it is fermented to metabolites which can cause drastic alterations in intestinal pH and composition of microbiota, disposing the horse to intestinal dysfunction e.g., colic. Using 16S rRNA oligonucleotide hybridization technology, we previously characterized and identified the major bacterial groups inhabiting the LI of horses maintained on pasture forage. Aims: to determine changes in microbiota and fermentation products measured in large intestinal content of i) 12 horses fed grain based diets and euthanized for conditions other than gastrointestinal disease and ii) 12 horses suffering from simple colonic obstruction and distension (SCOD). Results: In response to grain feeding and in disease, compared with grass-fed horses, the relative abundance of saccharolytic, lactate producing bacteria increased by up to 2-fold ($P < 0.05$), with a concomitant 2–4 fold ($P < 0.01$) decrease in the relative population abundance of acid intolerant cellulytic bacteria. Furthermore, there were significant increases in the intestinal concentration of lactic acid (up to 8-fold [$P < 0.01$]). Changes in both microbial population and fermentation products were exaggerated in horses suffering from SCOD. These alterations not only result in significant decline in SCFA, but also promote lactic acid and gas production, disposing the horse to intestinal dysfunction.

Key Words: horse, diet, gut microbiota

350 Spatial alternative splicing of Mucin 2 (*Muc2*) mRNA in chicken intestine. Z. Jiang*, C. Troche, A. C. Lossie, and T. J. Applegate, *Purdue University*, *West Lafayette, IN*.

Mucins are a large class of diverse, complex proteins that respond to their constantly changing intestinal environment by altering their production of specific protein isoforms. The complexity and diversity of gel-forming mucin isoforms within the gastrointestinal tract are largely regulated by its primary encoding gene, Mucin 2 (*Muc2*). We hypothesized that the protein diversity was generated by alternative splicing events, particularly within different regions of the intestine. Therefore, we isolated total RNA from 4 regions of the chicken intestinal mucosa (duodenum, jejunum, ileum and cecal tonsil; n = 4/each tissue) and performed RT-PCR across different domains of the *Muc2* gene on DNase treated RNA. A hypothetical chicken *Muc2* cDNA (XM_421035) localized the gene to Chr 5. Cross species comparisons indicated that the chicken gene shows 50 to 67% homology to zebrafish, cattle, mouse, chimpanzee and human. Based on this sequence, we designed 13 sets of primers to clone the chicken *Muc2* gene. These amplicons spanned bases 25–7961 of the 7968 bp predicted cDNA. Sequence data from these clones indicated a match with the predicted *Muc2* cDNA. PCR analysis demonstrated that all 13 amplicons were detected across the 4 intestinal tissues. Interestingly, primers that span exons 5 to 9 detected variably sized products. Ileal and cecal tonsil samples produced slightly smaller cDNA amplicons than duodenal and jejunal tissues. Further sequencing and correlation with *Muc2* protein would help understand the role of these tissue-specific alternatively spliced products.

Key Words: chicken, intestine, mucin

351 Differences in carbohydrate composition of barley varieties influence Salmonella transmission among pen mate weaned piglets. J. Bindelle[1], R. Pieper[2], J. K. Marshall[3], G. Malik*[3], B. R. Rossnagel[3], P. Leterme[4], and A. G. Van Kessel[3], [1]*University of Liege, Gembloux Agro-Bio Tech,*, *Liege, Wallonia, Belgium*, [2]*Freie Universitat*, *Berlin, Germany*, [3]*University of Saskatchewan*, *Saskatoon, SK, Canada*, [4]*Prairie Swine Centre Inc.*, *Saskatoon, SK, Canada*.

Indigestible carbohydrate (CHO) composition can vary markedly between barley varieties. They induce changes in intestinal ecophysiology and enhance growth of health-promoting bacteria. An experiment was undertaken to assess whether these changes could influence *Salmonella typhimurium* (ST) infection in pigs and transmission between penmates. A challenge study was undertaken using 84 recently weaned piglets divided in 12 pens, and fed one of the 4 experimental diets (3 pens/diet), according to the barley variety. Three hullless and one hulled varieties were chosen according to their differing CHO composition (amylose/amylopectin, β-glucan, and insoluble non-starch polysaccharides). After 14 d of adaptation, 2 pigs per pen (Trojan pigs, TrojP) were orally infected (8.0 log cfu/animal) with a low virulent, nalidixic acid and novobiocin resistant ST strain. The other animals were considered as Contact pigs (ConP) to assess ST transmission. Over 5 d following inoculation, pigs were monitored for detection of ST in the feces using plate counts. On d 6, 2 TrojP and 2 ConP per group were killed and intestinal samples as well as organ samples (liver, spleen, and lymph nodes) were analyzed for ST. The results showed that in TrojP, the cereal variety had no influence on ST fecal shedding over time and gastrointestinal tract (GIT) colonization. All pigs were positively tested for ST. Translocation of ST to lymph nodes was observed frequently but not to other organs. In ConP, compared with hulled barley, hulless barleys reduced the number of animals shedding ST ($P < 0.05$ for d 2) and the number of ST (cfu/g) in cecum on d 6 ($P < 0.01$). Although hulless barleys did not protect against colonization when directly challenged at a high oral dose, these barleys may be useful to reduce natural ST transmission among penmates.

Key Words: barley, pigs, Salmonella

352 Histomorphology and small intestinal sodium-dependent glucose transporter 1 gene expression in piglets fed phytic acid and phytase-supplemented diets. T. A. Woyengo*[1], J. C. Rodriguez-Lecompte[1], O. Adeola[2], and C. M. Nyachoti[1], [1]*University of Manitoba*, *Winnipeg, Manitoba, Canada*, [2]*Purdue University*, *West Lafayette, IN*.

An experiment was conducted to determine the effect of dietary phytic acid (PA) and phytase supplementation on small intestinal histomorphology and sodium-dependent glucose transporter 1 (SGLT1) gene expression in piglets. Twenty-four piglets with an average initial BW of 7.60 ± 0.73 kg (mean ± SD) were randomly assigned to 3 experimental diets to give 8 piglets per diet. The diets were a casein-cornstarch-based diet that was supplemented with 0, 2% PA (as sodium phytate), or 2% PA plus an *Escherichia coli*-derived phytase at 500 FTU/kg. The basal diet was formulated to meet NRC (1998) energy, amino acids, minerals and vitamins requirements for piglets. After 10 d of feeding, the piglets were killed for determining histomorphology and small intestinal SGLT1 gene expression. Phytic acid supplementation did not affect ($P > 0.05$) villous height (VH) and VH to crypt depth (CD) ratio, but decreased ($P < 0.05$) CD in the jejunum. Phytase supplementation did not affect ($P > 0.05$) VH, CD and VH to CD ratio. Phytic acid supplementation reduced SGLT1 gene expression in duodenum, jejunum and ileum by 1.1, 5.4 and 2.4 folds, respectively. Phytase supplementation increased SGLT1 gene expression in jejunum by 2.6 folds, but reduced the expression of the same in the duodenum and ileum by 2.0 and 4.0 folds, respectively. In conclusion, PA reduced the CD in the jejunum and the SGLT1 gene expression in the duodenum, jejunum and ileum, whereas phytase supplementation increased the expression of the SGLT1 in the jejunum. The reduced SGLT1 gene expression by PA implies that the latter reduces nutrient utilization in pigs partly through reduced expression of the SGLT1 that is involved in glucose and sodium absorption. The increased expression of the SGLT1 in jejunum by phytase supplementation implies that the latter alleviates the negative effects of PA partly through increased expression of the SGLT1.

Key Words: phytic acid, phytase, piglets

353 Effects of essential oils on *Clostridium perfringens* infections in broilers. T. Steiner*[1], F. van Immerseel[2], and R. Ducatelle[2], [1]*BIOMIN Holding GmbH*, *Herzogenburg, Austria*, [2]*Department of Pathology, Bacteriology and Avian Diseases, Ghent University*, *Merelbeke, Belgium*.

Clostridium perfringens-induced necrotic enteritis (NE) has become a major problem in broiler flocks. Application of essential oils in the drinking water was evaluated as potential alternative to reduce the incidence of NE. Mixed-sex Ross broilers were assigned to 3 dietary treatments (cages) with 30 birds per treatment: (1) Uninfected, untreated (Negative Control, NC), (2) Infected, untreated (Positive Control, PC), (3) PC + liquid phytogenic additive containing essential oils from oregano, anise, and citrus peel (Biomin P.E.P. sol) applied in the drinking water (60 mL/1000 L) from day 15-25. Birds were fed diets based on wheat, rye and soybean meal. From day 17 onwards, the diets contained 30% fishmeal as protein source. A Gumboro vaccine (Nobilis Gumboro D78, Intervet, Mechelen, Belgium) was applied in the drinking water at day 16 in all treatments. Furthermore, Treatments 2 and 3 were challenged orally three times a day with 4×10^8 CFU of *C. perfringens* strain 56 at days 17, 18, 19 and 20. At day 18 all birds were orally inoculated with a ten-fold dose of Paracox-5 (Schering-Plough Animal Health, Brussels, Belgium). At days 22, 23 and 24, 10 animals of each group were euthanized and intestinal lesions in the duodenum, jejunum and ileum were evaluated using a lesion score (ranging from 0, no gross lesions, to 6, severe necrosis typical of field cases). Lesion scores of 2 or more were classified as NE-positive. The data were analyzed with SPSS 16 software using the multivariate logistic regression method to compare the number of NE-positive animals in the test group with the number of NE-positive animals in the Positive Control group. Cage was the experimental unit. Birds in the NC had no intestinal lesions, whereas the PC had the highest percentage (58.6%) of birds with lesions. In comparison with the PC, the percentage of birds with lesions was reduced ($P < 0.05$) in Treatment 3 (27.6%). Lesions were found in the duodenum and jejunum, but not in the ileum, of birds in Treatments 2 and 3. In conclusion, application of essential oils in the drinking water has potential to prevent, at least in part, the development of NE infections in broilers.

Key Words: broilers, *Clostridium perfringens*, essential oils

Nonruminant Nutrition Symposium: Rethinking Equine Nutrition

354 Defining amino acid requirements in horses: Application of the indicator amino acid oxidation technique. K. L. Urschel*[1], R. J. Geor[2], and P. A. Harris[3], [1]*University of Kentucky*, *Lexington,* [2]*Michigan State University*, *East Lansing,* [3]*Waltham Centre for Pet Nutrition*, *Melton Mowbray, UK*.

Relatively little is known about the indispensable amino acid (AA) requirements of horses and how they are affected by physiological status. In the 2007 *Nutrient Requirements of Horses*, only lysine requirements are given and these requirements were not measured, but were extrapolated from the crude protein requirements. Because horses have a requirement for each indispensable AA rather than crude protein itself, it is important to know the individual AA requirements independent of crude protein. Most equine research has used either average daily gain or nitrogen retention to determine dietary AA adequacy; however, there are methodological drawbacks for each method. The indicator amino acid oxidation (IAAO) technique has been used extensively to determine AA requirements in pigs and humans and shows promise for use in horses. This method is based on the principle that indispensable AA are partitioned between protein synthesis and oxidation. The IAAO method measures the oxidation of an infused ^{13}C-labeled AA (the 'indicator') in response to graded levels of intake of another AA ('test' AA). As test AA intake increases from deficient to adequate, more protein synthesis can occur and less indicator is oxidized, until the requirement is met and indicator oxidation remains low and constant. The IAAO method has 2 key advantages: 1) it is sensitive, reducing the number of subjects required and 2) it requires only a short adaptation period to each level of AA intake and therefore each subject can be studied at each level of test AA intake over a short period. Work has begun in developing the IAAO method for use in horses: isotope infusion and breath sampling methodologies have been established, an isotopic method to measure total CO_2 production has been validated, and the 'indicator' infusion rate has been verified to result in measureable amounts of $^{13}CO_2$ in the exhaled breath samples. Using the IAAO to determine indispensable AA requirements in horses will allow for improved equine diet formulation to more closely meet the AA requirements and minimize the amount of excess dietary protein.

Key Words: amino acid requirements, equine, indicator amino acid oxidation

355 Current knowledge on the relative role of the equine small and large intestine in amino acid absorption. N. L. Trottier* and A. D. Woodward, *Michigan State University*, *East Lansing*.

The role of the small intestine as main site of amino acid absorption has been demonstrated using both in vivo and in vitro models of monogastric animals. There is limited information on the large intestine's contribution to the host N (nitrogen) homeostasis. Forage-fed equids rely on microbial fermentation of structural carbohydrates in the cecum and proximal large intestine; however, the accessibility of plant cell wall proteins to microbial proteases for amino acid availability and host absorption in the aborad gastrointestinal regions remain enigmatic. Knowledge of the small and large intestinal capacity for amino acid absorption would further our understanding of amino acid utilization in equids. Globally, the large intestine appears to significantly supply dietary N for absorption. Studies report larger contribution to total apparent N digestion from the large intestine compared with the small intestine. The relatively short time of passage through the small intestine parallels the lower digestive efficiency in that segment of the equine gastrointestinal tract, with digestive compensation mediated by post-cecal absorption. Earlier work demonstrated that protein metabolized by the equine cecum yields amino acids, urea, and ammonia; however, the relative role of these N products to total N absorption during large intestinal passage are largely unknown. Genes known to transport cationic and neutral amino acids across epithelial cells of other animal species are expressed in the equine large intestinal epithelium. These transporters may facilitate the absorption of microbial and dietary-derived amino acids across the epithelium of the large intestine. In conclusion, some evidence points to the large intestine as a site for N and amino acid absorption. Unless equids have a requirement for N, such evidence may mitigate the contradiction between the high estimates of maintenance protein requirement and the purported absence of large intestinal indispensable amino acid absorption in the solely forage-fed equid

Key Words: horse, intestine, amino acid

356 Importance of volatile fatty acid metabolism for horses. J. K. Suagee*, B. A. Corl, and R. J. Geor, *Virginia Polytechnic Institute and State University*, *Blacksburg*.

Horses evolved on sparse grasslands and have thus developed digestive mechanisms for extracting energy from energy-poor feeds. The upper portion of the equine digestive system is capable of digesting non-structural carbohydrates, such as starches and disaccharides to monosaccharides, while the cecum and large colon are sites for bacterial fermentation of structural carbohydrates. Thus, both diet-derived glucose and fermentation end products such as acetate, propionate, and butyrate are available to horses. The assumption that horses evolved on forages rich in structural carbohydrates, such as cellulose and hemicellulose, rather than non-structural carbohydrates, suggests an evolved capacity to meet energy requirements through volatile fatty acid metabolism. Horses primarily use acetate to synthesize fatty acids de novo in adipose tissue and lack the enzymatic pathway to covert glucose to acetate for fatty acid synthesis. The minimal capacity of the liver to synthesize lipids may indicate that the horse evolved to rely on hepatic gluconeogenesis. Estimates suggest that when fed a 100% forage diet, the horse can derive 50–60% of its glucose from propionate. Modern horse diets commonly consist of up to 50% grain-based supplemental feeds that are higher in non-structural carbohydrates. The effect of modern feeding practices on both hepatic gluconeogenesis and peripheral glucose metabolism is unknown. Future research should focus on determining how modern feeding practices alter volatile fatty acid production and metabolism. A further step would include investigating the effect of altered volatile fatty acid metabolism on the development of metabolic disorders that are associated with diets high in supplemental grain-based concentrates.

Key Words: acetate, propionate, horse

357 Glucose sensing and regulation of equine intestinal glucose transport. S. Shirazi-Beechey*, D. Arora, J. Dyer, and K. Daly, *University of Liverpool*, *Liverpool, UK*.

Glucose is transported across the luminal membrane of enterocytes by the sodium/glucose cotransporter 1, SGLT1. This also activates water absorption in the intestine. Regulation of SGLT1 is essential for the provision of glucose to the body and thus is important for maintenance of glucose homeostasis. The major aim of this talk is to report on recent progress made toward identifying mechanisms involved in regulation of equine intestinal glucose transport in response to a change in diet.

Cloning and sequencing the cDNA encoding equine SGLT1 and the determination of SGLT1 amino acid sequence allowed us to determine SGLT1 expression in equine small intestine. In the horse, glucose is transported mainly across the brush membrane of enterocytes by SGLT1. In horses maintained on pasture forage the highest rate of glucose transport was in proximal > mid with little in distal part of the small intestine. However, in horses fed controlled diets containing different ratios of hay and grain, SGLT1 expression is enhanced, with time, in response to increased dietary hydrolysable carbohydrate, not only in the proximal, but also in the distal small intestine. We have shown that sweet taste receptor, T1r2+T1r3 and its coupled G protein, gustducin, are expressed in enteroendocrine cells of the intestine of several species including the horse. Dietary sugars and artificial sweeteners act in the intestine, on the sweet taste receptor to elicit upregulation of SGLT1. Furthermore, knocking out either gustducin or T1r3 abolished the ability of mouse intestine to upregulate SGLT1 expression in response to increased dietary carbohydrate. Thus the equine intestinal sweet taste receptor has the potential to be used as a novel nutritional target to increase intestinal glucose and water absorption with the attendant promise of enhancing performance and overcoming the detrimental effects of post exercise dehydration.

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Key Words: SGLT1, equine, intestine

358 Blue-and-gold Macaw (*Ara ararauna*) postmortem semen collection. J. M. Silva[1], S. K. Cunha[1], C. D. Corcini[1], A. S. Varela Junior[2], A. P. N. Albano[1], A. L. S. Valente[1], and D. C. Bongalhardo*[1], [1]*Universidade Federal de Pelotas*, *Pelotas, RS, Brazil*, [2]*Universidade Federal de Rio Grande*, *Rio Grande, RS, Brazil*.

The blue-and-gold Macaw (*Ara ararauna*) is a Neotropical parrot from South America. It is rated as Least Concern by Bird Life International; however, there is a very heavy wild-caught trade of this species. In December 2008, one adult male was brought to the Wildlife Rehabilitation Center from the Federal University of Pelotas shortly after death. The main objective of this work was to perform a postmortem semen collection in this bird, aiming to recover sperm for cryopreservation. As a complement, testicular histology was observed to confirm that the macaw was sexually active. Necropsy was made approximately 3 h after death; at this time the testes, epididymis and deferent ducts were removed and placed in a Petri dish. Epididymis and deferent ducts were washed with Lakes diluent and the suspension was brought to the laboratory, where recovered sperm was evaluated by motility. Dry slides were made to observe sperm morphology, using 5 different stains: orcein, eosin, eosin-nigrosin, Giemsa, and Coomassie Blue. The testes were fixed in 10% buffered formalin; after 24 h they were dehydrated in crescent concentrations of alcohol, immersed in xylol at 100%, impregnated in Paraplast Xtra, and sliced (5 μm). The cuts were stained with Harris hematoxylin and eosin and observed in optical microscope. Few sperm were recovered from the epididimys and deferent ducts and motility was lower than 1%, therefore it was not possible to proceed with cryopreservation. The low motility could be attributed to the time elapsed between the death and the necropsy. Eosin was the only stain that allowed clear visualization of the sperm cell, which presented normal morphology. Histology of the testes showed intense seminiferous tubules activity; a multi stratified epithelium containing sperm in different stages of development could be observed, as well as polygonal Sertoli cells. The results show that the testis were fully functional and producing sperm with normal morphology. It was also demonstrated that it is possible to collect motile sperm from dead birds, however, to attempt cryopreservation, it is still necessary to acquire higher motility.

Key Words: *Ara ararauna*, postmortem semen collection, testis histology

359 To move or not to move? Gait analysis of the modern broiler and its implications. H. Paxton*, M. A. Daley, S. A. Corr, and J. R. Hutchinson, *Royal Veterinary College*, *Hatfield, Hertfordshire, UK*.

Ever since Darwin, it has been well recognized that artificial selection could bring about changes in animal behavior, physiology and morphology by the simple selection of human-desired traits. But what happens when these selection pressures begin to alter the locomotion of an animal and potentially result in an increase in musculoskeletal pathologies? The modern broiler has changed dramatically reaching its market weight faster and having an increased meat yield. Research indicates that these changes may predispose some of the broilers to leg pathologies which are a welfare concern. We therefore investigate whether the modern broiler and its 2 great-grandparent lines have adopted different locomotor strategies as a result of their altered morphology. We also investigate whether any changes might prevent these birds from walking economically or stably and perhaps predispose them to locomotor pathology. We collected force plate and kinematic data from 27 chickens (350 steps), including a commercial broiler strain and 2 great-grandparent lines (A and B) over a range of walking speeds, to quantify the 3D dynamics of the center of mass and determine how these birds modulate the force and mechanical work of locomotion. Walking speeds were slow (0.10 – 0.99 ms^{-1}) and ranges differed between groups with the fastest walking speeds recorded in the broiler population. There was greater variability in step width than step length, likely linked to increased mediolateral forces and control strategies for stability. We only found right-left limb asymmetries in the great-grandparent lines, with line B showing a decrease in step length with speed ($P = 0.01$) that is not commonly seen in ground birds. Based on current empirical models for cost, the differences in locomotor mechanics among lines suggest that Line B is likely to have a 10% higher cost of locomotion due to significantly higher stride frequencies ($P < 0.001$) and shorter step lengths. Thus selection for desirable traits in the broiler chicken lineage has carried along different gait characteristics that we have quantified for the first time.

Key Words: broiler chicken, locomotion, lameness

360 Effects of commercial in ovo injection of carbohydrates on broiler embryogenesis. W. Zhai*, R. Pulikanti, S. Womack, D. E. Rowe, and E. D. Peebles, *Mississippi State University*, *Mississippi State*.

The effects of in ovo injection of different carbohydrate solutions on hatch rate, hatch time, BW, body moisture, yolk sac weight, and yolk sac moisture of Ross × 708 broiler chicks, hatched from eggs laid by a 34-wk-old breeder flock, were investigated. Eggs containing live embryos were injected in the amnion on d 18.5 of incubation using an automated multiple-egg injector with 0.1, 0.4, 0.7, or 1.0 mL of commercial diluent or a carbohydrate dissolved in diluent. Commercial diluent containing 25% of the following carbohydrates were injected into eggs: glucose, fructose, sucrose, maltose, and dextrin. The results showed that no carbohydrate type or volume affected hatch time. Absolute and relative BW on hatch day were positively related to injection volume ($P < 0.0001$). However, hatch rate was negatively related to injection volume ($P < 0.0001$). To realize a 90% hatchability of fertilized eggs, injection volume could not exceed 0.7, 0.4, 0.4, 0.7, and 0.7 mL for glucose, fructose, sucrose, maltose, and dextrin, respectively. Yolk-free BW was negatively related to fructose and sucrose injection volume ($P < 0.004$), but was not related to diluent, glucose, maltose, and dextrin injection volume. Similarly, absolute and proportional yolk sac weights were positively related to fructose, sucrose, and dextrin injection volume ($P < 0.01$), but were not related to diluent, glucose, and maltose injection volume. Yolk sac moisture was positively related to injection volume for all injectables including diluent ($P < 0.03$). However, body moisture and yolk-free body moisture were not related to injection type or volume. In conclusion, the use of carbohydrates added to commercial diluent for the in ovo injection of broiler hatching eggs requires the use of appropriate volumes to promote growth and nutrient utilization without adversely affecting rate of hatch.

Key Words: BW, hatch rate, in ovo injection

361 The effect of egg weight loss on embryonic development in Chinese painted quail (*Coturnix chinensis*) exhibiting parthenogenesis. J. B. Wells, H. M. Parker*, A. S. Kiess, and C. D. McDaniel, *Mississippi State University*, *Mississippi State*.

Parthenogenesis, the development of an unfertilized egg, has been studied extensively in turkeys. Recently it has been revealed that

parthenogenesis occurs in the eggs of Chinese painted quail and the percentage of eggs exhibiting parthenogenesis is negatively correlated with egg production as well as clutch size. In broiler breeders it has been reported that the first egg of a sequence loses less moisture during incubation. Because the incidence of parthenogenesis is greater and egg weight loss is less in the first egg of a sequence, it is possible that parthenogenesis is also affected by egg moisture loss. Therefore, the objective of this study was to determine if a relationship exists between egg weight loss and parthenogenesis. In this experiment individual eggs were collected from 157 hens daily and labeled with hen number and date. Eggs were stored for 0 to 3 d at 20°C before incubation at 37°C. To determine egg weight loss, eggs were weighed on the day of collection and again after 10 d of incubation. Pearson's correlation coefficients were used to determine if relationships exist between egg weight loss and the percentage of eggs exhibiting parthenogenesis, parthenogen size, egg storage, and clutch position. The percentage of egg weight loss was negatively correlated with the incidence of parthenogenesis in eggs ($r = -0.56$; $P < 0.001$), parthenogen size($r = -0.49$; $P < 0.001$), and egg storage ($r = -0.24$; $P < 0.003$). However, the percentage of egg weight loss was positively correlated with average clutch position ($r = 0.32$; $P < 0.001$). In conclusion, it appears that eggshell quality possibly influences the incidence of parthenogenesis in Chinese Painted quail eggs because as the percentage of egg weight loss decreases, the incidence of parthenogenesis increases.

Key Words: parthenogenesis, moisture loss, clutch sequence position

362 Relationships of Ross × 708 broiler post-hatch development to embryonic temperature, incubation length, and eggshell water vapor conductance. R. Pulikanti, E. D. Peebles*, W. Zhai, A. Bello, C. N. Obi, and A. O. Sokale, *Mississippi State University*, *Mississippi State*.

To establish relationships between post-hatch broiler development, egg incubation length (IL), and eggshell water vapor conductance (G), Ross × 708 broiler hatching eggs were randomly set on 8 replicate tray levels of an incubator (20 eggs per replicate). On 10.5 d of incubation, transponders were implanted in the air cells of 4 embryonated eggs per replicate for determination of internal egg temperatures (embryo temperatures; IT) through d 18.5. External egg temperatures were determined using 2 water filled vials and 2 infertile eggs containing transponders per each replicate level. Hatch was monitored every 12 h between 18.5 and 21.5 d of incubation. The chicks were placed in corresponding replicate floor pens and grown through 49 d of age. On 28 and 48 d post-hatch, at least 2 chicks per pen were necropsied for determination of BW, and the relative weights and moisture contents of the liver, breast muscle, and left gastrocnemius muscle. Also, IL, G, relative G (RG), and the conductance constant (C) of each embryonated egg were determined. Mean IL, G, RG, and C were 20.7 d, 14.2 mg water/d × Torr, 24.6 mg water/d × Torr × 100 g egg weight, and 5.05. The IT was negatively correlated with relative chick BW and relative gastrocnemius muscle weight on d 28 post-hatch. However, IL was positively correlated with relative gastrocnemius muscle weight on d 28 but negatively correlated with gastrocnemius muscle moisture on d 48 post-hatch. Nevertheless, RG and C were negatively correlated with liver and breast muscle moisture contents on d 28 post-hatch. Correlations were considered significant at $P \leq 0.06$. Within physiological limits, RG was negatively associated with chick hydration status on d 28 post-hatch. The observed relationships were more pronounced initially during early post-hatch life and subsided as the chick reached market age.

Key Words: broiler, eggshell conductance, embryo temperature

363 NADH oxidase generated superoxide reduces nitric oxide availability in lungs of hypoxic broilers chickens. J. Bautista–Ortega*, E. A. Ellis, and C. A. Ruiz–Feria, *Texas A&M University*, *College Station*.

Xanthine (XO) and NADH oxidase (NOX) are important sources of superoxide in cardiovascular diseases including pulmonary hypertension syndrome (PHS). Previously we localized XO and NOX in the pulmonary artery endothelium of hypoxic broilers. Nitrotyrosine is a biomarker for peroxynitrite which is negatively correlated with the availability of nitric oxide (NO). Cytochemical localization of XO and NOX (reflectance units), and colloidal gold based immunocytochemical localization of nitrotyrosine (N of colloidal gold particles) were used to determine oxidative and nitrosative (reduced availability of NO) stress in lungs of broilers exposed to hypoxia (d 7 to d 36, simulated 3,000 m above sea level) and fed a control diet (CTL), or control plus arginine (ARG, 0.8% wt/wt), or CTL plus ARG and vitamins C (500 mg / L water) and E (200 IU / kg of feed) (AEC). Also, a group of normoxic broilers were fed the CTL diet (NOR). Nitrosative stress was also determined in hypoxic broilers with PHS and in clinically healthy ones. The XO activity was higher in NOR birds (586 ± 43) than in both AEC (456 ± 39) and ARG birds (394 ± 31), whereas CTL birds had the lowest XO activity (313 ± 27). The NOX activity or NO availability was not affected by dietary or hypoxia conditions in clinically healthy birds. Nevertheless, hypoxic birds that developed PHS had higher nitrotyrosine (145 ± 19) than hypoxic but clinically healthy birds (56 ± 11). Increased levels of superoxide generated by NOX may have resulted in decreased availability of NO as measured by nitrotyrosine. To our knowledge, this is the first time that XO and NOX activity has been semi–quantitatively determined in situ in lung samples of hypoxic broiler chickens. Supplementation with ARG and antioxidant vitamins C and E tended to produce NOX–derived superoxide levels similar to those in the normoxic chickens probably preserving NO in the system but significance was not reached probably due to limited number of birds. The dual role of XO, which produces superoxide and uric acid (antioxidant), may have buffered the effects of superoxides in clinically healthy birds.

Key Words: hypoxia, nitrotyrosine, pulmonary hypertension

364 Genistein effects on fatty liver syndrome induced by estrogen. L. M. Stevenson*, S. S. Oates, J. B. Hess, and W. D. Berry, *Auburn University*, *Auburn, AL*.

Soy phytoestrogens, such as genistein, have been demonstrated to have a protective effect against fatty liver syndrome in rats. A study was performed with old laying hens to determine if genistein had a protective effect against avian fatty liver syndrome induced by exogenous estrogen. Twenty-four 5 year-old laying hens were randomly selected and divided into 6 treatment groups. Each treatment group consisted of 4 hens. Genistein doses were given by a daily gavage for 14 d. The treatments were: Sham Control (gavage and injections of sesame oil), Estrogen Control (7.5 mg estrogen/kg body weight per dose), Genistein Control (20 mg genistein/kg body weight daily), Low Genistein (7.5 mg estrogen/kg body weight per dose and 10 mg genistein/kg body weight daily), Medium Genistein (7.5 mg estrogen/kg body weight per dose and 15 mg genistein/kg body weight daily), and High Genistein (7.5 mg estrogen/kg body weight per dose and 20 mg genistein/kg body weight daily). Estrogen doses were estrogen diproprionate and were given by injection in the subcutaneous tissue in the back of the neck 3 times during the experiment. All treatments were dissolved in sesame oil. Birds were weighed at placement and at the end of the study. There were no significant differences in body weights for any treatments at

placement ($P > 1.0$) or at the end of the study ($P > 0.6$). Blood samples were collected at placement and at the end of the study. Plasma genistein was analyzed by high performance liquid chromatography (HPLC). Levels of genistein in the plasma were significantly increased in birds on the genistein treatments ($P < 0.05$). Livers were removed, weighed, and samples were collected after the study. There were no significant differences in liver weights ($P > 0.5$) or livers as a percent of their final body ($P > 0.4$). Pictures were taken of all of the livers and visually scored to determine the degree of fatty liver. Birds in the Estrogen Control treatment had an increase in yellow coloring of the liver as compared with the other treatments.

Key Words: genistein, estrogen, liver

365 Gene expression of thyroid hormone regulating elements in reproductively photosensitive and photorefractory turkey hens. S. W. Kang*, S. Kosonsiriluk, and M. E. El Halawani, *University of Minnesota*, *St. Paul*.

Thyroid hormones are important in the reproductive neuroendocrine response to changing photoperiod in birds. Regulation of thyroid hormone homeostasis in the brain is mainly determined by thyroid hormone transporter (transthyretin (TTR)), type II iodothyronine deiodinase (Dio2), type III iodothyronine deiodinase (Dio3) and thyrotropin-releasing hormone (TRH). TTR plays a key role in transporting thyroid hormones into the brain via the choroid plexus (CP). Tuberal hypothalamus (TuH) is a well known site in the brain where Dio2 is involved in converting thyroxin (T4) into triiodothyronine (T3). In this study, to gain insights into seasonal photoperiodic mechanism(s) that govern reproductive photoresponsiveness and photorefractoriness of turkey hens, we investigated gene expression of thyroid hormone regulating elements (i.e., TTR, Dio2, Dio3, and TRH) in the brain of photosensitive and photorefractory hens using real-time PCR. The expression of each gene was determined in microdissected brain areas from reproductively inactive short day photosensitive hens (SD), long day photostimulated photosensitive hens (LD), and long day photorefractory hens (RF) at 2 circadian time points (CT14, CT19). In TuH of LD, Dio2 was significantly greater (2.8 fold, $P < 0.01$) and Dio3 was repressed (42%, $P < 0.05$) when compared with that of SD. In LD, TTR was 2.5 fold greater relative to that in SD ($P < 0.01$). And, TTR expression was downregulated (3.5 fold, $P < 0.01$) in long day RF relative to LD. Also, TTR was greater (45%, $P < 0.05$) during the photosensitive phase (CT14) than during the dark phase (CT19). CP Dio2 was significantly higher (2.1 fold, $P < 0.01$) in LD compared with that of SD and RF. TRH in the paraventricular nucleus was 2.8 fold greater in LD compared with that of RF ($P < 0.01$), and the levels in RF were 22% ($P < 0.05$) lower when compared with SD. In summary, Dio2 in CP as well as TuH appears to be an important gene involved in the expression of photorefractoriness. TTR in CP might be a significant thyroid hormone transporter involved in photoperiodic response of turkey hens.
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Key Words: transthyretin, turkey reproduction, deiodinase 2

366 Identification of a nonclassical glucocorticoid responsive region of the growth hormone gene during chick embryonic development. K. A. Heuck-Knubel* and T. E. Porter, *Department of Animal & Avian Sciences, University of Maryland*, *College Park.*

Growth hormone (GH) affects growth and contributes to a lean phenotype in broiler chickens; however, exogenous GH has little effect on post-hatch growth. Elucidation of the regulation of the GH gene could result in alternative approaches for maximizing growth in broilers. GH secretion occurs naturally between embryonic day (e) 14 and e16, concomitantly with a rise in adrenal corticosterone (CORT) secretion. Treatment of chicken embryonic pituitary (CEP) cells with CORT induces GH secretion prematurely. Inspection of the regulatory region of the GH gene reveals no glucocorticoid (GC) response element (GRE). Pretreatment of e11 cells with a protein synthesis inhibitor, CHX, resulted in blockage of the CORT-induced increase in GH mRNA. This leads to the hypothesis that a GC-responsive intermediary protein is necessary for the CORT induced increase in GH. Characterization of the upstream region of the GH gene may identify such a protein. −1727/+48 bp of the GH gene was cloned into a luciferase reporter plasmid and transfected into e11 CEP cells. Treatment with 100 nM CORT increased luciferase activity 10-fold (n = 3; $P < 0.05$). Truncation of this construct to −954 abolished activity. Thirteen additional constructs were tested, revealing an inhibitory region from −1467 to −1430 and a GC-responsive region (GCRR) from −1045 to −954 ($P < 0.05$; n = 3). Other constructs showed that the GCRR is position-, orientation-, and context-dependent. Potential transcription factor motifs in the GCRR include ETS1, ELK4, and a GC-binding region (GBR). Mutation of the ETS1 site or the GBR in the −1045/+48 reporter resulted in a loss of Luciferase activity. Nuclear proteins bind to a GCRR probe in a CORT-regulated manner in gel shift assays, and unlabeled competitor can compete off binding. In a single experiment, an ELK4 antibody (ab) did not result in a supershift, but an ETS1 ab abolished protein binding to the probe. The chicken GH gene is GC responsive and contains a putative ETS1 and GBR site at −1017 to −985. Investigation of protein binding to the GCRR is underway using gel shift assays and chromatin immunoprecipitation.

Key Words: luciferase, corticosterone, pituitary

367 Detection and expression of the glucocorticoid receptor in the laying hen's oviduct. L. A. Bola*, D. V. Arbona, and J. B. Hoffman, *North Carolina State University*, *Raleigh*.

The hen's oviduct is critical in the process of egg formation and ovipositioning. Specifically, the components of the oviduct including the infundibulum, magnum, isthmus, uterus/shell-gland, and vagina are responsible for both interior egg quality as well as exterior shell quality. Due to the sensitivity of the oviduct during hormonal and cellular changes that occur during the formation of the egg, stress susceptibility may have a significant impact on egg quality and formation. Specifically regulation of hormonal action on the oviduct is subject to paracrine modulation by steroids such as glucocorticoids. The presence of glucocorticoid receptors (GR) in the oviduct that bind corticosterone, the avian glucocorticoid, may be an indicator of oviductal tissue sensitivity to stress. The expression of GR was characterized in the oviducts of 6 Leghorns at 27 weeks of age. Tissue samples were removed from the infundibulum, isthmus, magnum, uterus/shell-gland, and vagina from each hen by manual dissection. Subsequently, RNA extraction and real-time RT-PCR analyses were performed. Our results showed expression of the GR in each of the tested regions of the oviduct tissue. These results suggest that corticosteroids may directly act on the oviduct to influence the process of egg formation and overall egg quality.

Key Words: glucocorticoid receptor, oviduct, egg quality

368 Detection and expression of glucocorticoid receptors in the germinal disc (GD) and non-germinal disc (NGD) regions of the laying hen's hierarchical ovarian follicles. J. B. Hoffman*, D. V. Arbona, and L. A. Bola, *North Carolina State University*, *Raleigh*.

The influence of corticosterones on fertilization and developmental events post-fertilization has yet to be fully characterized in the laying hen. Because the left adrenal gland is embedded in the ovary, it is possible that corticosterones may act through a paracrine mechanism to influence fertilization, sex-ratio distributions, and embryological development. However, paracrine mediation by corticosterones is dependent upon the presence of glucocorticoid receptors (GR) in the germinal disc (GD) region of the F1 hierarchical follicle where fertilization occurs. Additionally, differences in expression of GR in the GD versus the non-germinal disc region (NGD) which is not involved in the process of fertilization may further elucidate the degree to which corticosterones are involved in regulating these processes. In this study, the expression of GR was characterized in the granulosa tissue of the GD and NGD from the F1-F4 hierarchical follicles of 6 Leghorns at 32 weeks of age. Tissue samples (3 cm x 3 cm) were removed from the GD and NGD by manual dissection. Subsequently, RNA extraction and real-time RT-PCR analyses were performed. Our results showed expression of the GR in the GD and NGD regions of the F1-F4 hierarchical follicles suggesting that corticosterone may influence the process of fertilization and post-fertilization events.

Key Words: germinal disc, glucocorticoid receptor, fertilization

369 Molecular cloning and characterization of chicken and zebrafish prostaglandin receptors. A. H. Y. Kwok*, Y. Wang, and F. C. Leung, *The University of Hong Kong*.

Prostaglandin E2 (PGE2) and F2α (PGF2α) are autocrine/paracrine mediators responsible for regulation of vital physiological processes, ranging from systemic effects such as fever generation and ACTH-related stress response, to tissue-localized effects such as inflammation, vascular homeostasis and reproduction. Four receptor subtypes have been identified for PGE2, namely prostaglandin E receptor subtypes 1 (EP1), EP2, EP3 and EP4, and prostaglandin F receptor (FP) for PGF2α. Though the receptors were extensively studied in mammals, little is known about their functionality and expression in non-mammalian vertebrate species. Complementing our previous study on chicken EP2 (cEP2), cEP3, cEP4 and cFP (including cFPa and a novel middle-truncated isoform, cFPb) in which full-length cDNAs were first cloned and preliminarily characterized, in the present study, we furthered our investigation, first, by quantitative real-time PCR, the relative expression of cFPa and cFPb were detected in 12 adult chicken tissues and hen oviduct, wherein both isoforms were found to be widely expressed. Interestingly, the putative functional ortholog cFPa was expressed in abundance in testis, in contrast, only minimal signal of cFPb was detected; an inverse expression ratio was observed in ovary. As EP1 appears to be absent in chicken (neither found in genome database nor detected by degenerate primers designed), we proceeded to examine whether EP1 was present in other lower vertebrates, such as fish. Three full-length EP1 cDNAs were identified from zebrafish (Danio rerio), they were named zEP1a, zEP1b and zEP1-like (zEP1-L) respectively, based on their corresponding sequence identities to mammalian EP1 orthologs (from 38% to 42%). By semiquantitative reverse transcription (RT-) PCR, zEP1a and zEP1b were found in all 9 adult tissues examined, while zEP1-L was detected only in brain and kidney. Subsequent functional assays for the cloned receptors are under way, which, in combination with the above results, would help to elucidate the physiological roles of PGE2 and PGF2α and their receptors in target tissues of non-mammalian vertebrate.

Key Words: chicken, prostaglandins, prostaglandin receptors

370 Effect of seminal plasma progesterone on sperm hole penetration in White Leghorns. E. M. Anderson* and K. J. Navara, *University of Georgia*, *Athens*.

While there has been significant interest in identifying the hormonal contributions passed on with gametes by female birds, the hormone content of fluids contributed during reproduction by the male remains relatively unstudied. We aimed to characterize the hormone content, and the potential function of those hormones, in avian seminal plasma. First, we measured the concentrations of 5 hormones within seminal plasma collected from White Leghorn roosters, including progesterone (P4), testosterone (T), dihydrotestosterone (DHT), estrogen (E) and corticosterone (B). P4 levels were higher in seminal plasma compared with other hormones analyzed, ranging from 0 to 14.8 ng/ml (all other levels were <1.1ng/ml). Given this relatively high concentration of seminal plasma progesterone, we then attempted to determine how progesterone in seminal plasma may function in fertility. White Leghorn hens were assigned to 2 treatment groups: progesterone-treated or control (n = 24 hens per treatment). Semen was collected via abdominal massage from 24 White Leghorn roosters. Each semen sample was divided into 2 equal volumes, one treated with progesterone (0.4 ng/50 μL) and the other with a control of diluent and artificially inseminated into each treatment group of hens. Eggs were collected 2 d after insemination. A perivitelline layer sperm hole assay, a method that can be used as a predictive measure of fertility, was performed for each egg and the number of sperm holes was counted under a microscope. The effects of treatment were then analyzed and the number of sperm holes were significantly less in the progesterone treated group compared with the control on the second day after insemination ($P = 0.0307$). These results suggest that progesterone has a detrimental effect on the ability of sperm to penetrate the IPVL, and that males that deposit more progesterone into seminal plasma may have a decreased capability to fertilize an egg.

Key Words: seminal plasma, progesterone, white leghorn

371 *Salmonella* recovery following air chilling for matched neck-skin and whole carcass sampling methodologies. R. J. Buhr*, N. A. Cox, J. A. Cason, L. L. Rigsby, and D. V. Bourassa, *USDA-ARS Russell Research Center*, *Athens, GA*.

The prevalence and serogroups of *Salmonella* recovered following air chilling were determined for both enriched neck skin and matching enriched whole carcass samples. Commercially processed and eviscerated carcasses were air chilled to 4°C before removing the neck skin (8.3 g) and stomaching in 83 mL buffered peptone water. The remaining carcass was subjected to whole carcass enrichment in 500 mL buffered peptone water. Both neck skins and whole carcasses were incubated at 37°C for 24 h before aliquots were transferred to selective enrichment broths (RV and TT) and incubated at 37°C for 24 h. Following incubation, BGS and MLIA plates were streaked and incubated at 37°C for 24 h. Three typical colonies were individually stabbed into TSI and LIA slants and incubated at 37°C for 24 h. For neck skin samples, 14/18 were Salmonella-positive with 5 identified as serogroup C1, 8 serogroup C3, and 2 serogroup E. For whole carcasses 16/18 carcasses were Salmonella-positive with 1 identified as serogroup B, 6 serogroup C1, 9 serogroup C3, and 2 serogroup E. Two *Salmonella* serogroups were detected from one neck skin (C3/E) sample and 2 *Salmonella* serogroups were detected from 2 non-matched carcasses (C1/C3 and C3/E). All 4 of the Salmonella-negative neck skin samples had Salmonella-positive matching whole carcasses and the 2 Salmonella-negative whole carcasses had Salmonella-positive matching neck skin samples. Selecting 3 individual colonies, versus only one, from BGS and MLIA plates resulted in 2 additional Salmonella-positive neck skin samples (C1) and 2 additional Salmonella-positive carcasses (C1 and C3). In this study, individual neck skin enrichment (78%) and whole carcass enrichment (89%) sampling methodologies were comparable in the prevalence detection of *Salmonella* from matched air-chilled carcasses.

Key Words: *Salmonella* serogroups, whole carcass enrichment, neck skin enrichment

372 Effect of ultrasonication and phosphate level during marination on numbers of *Salmonella* and *Escherichia coli* on broiler breast meat. D. P. Smith*, *Poultry Science Dept., North Carolina State University*, *Raleigh*.

Four trials were conducted to determine the effect of ultrasonic treatment and phosphate level during marination on numbers of *Salmonella* and *Escherichia (E.) coli*. In each trial 2 whole boneless, skinless chicken breasts were obtained from a retail store and split into paired fillets. One fillet from each pair was assigned to marination either with or without ultrasonication for 20 min. Trials 1 and 2 marination solution contained 91% water, 6% NaCl, and 3% sodium tripolyphosphate (STP); for Trials 3 and 4 the solution consisted of 91% water, 6% STP, and 3% NaCl. Ten min before marination fillets were inoculated with 1.0 mL of a culture containing nalidixic acid-resistant strains of *Salmonella* Typhimurium, Enteritidis, *heidelberg*, and *montevideo* (mean count of 7.1 $\log_{10}$), and an *E. coli* strain (mean count of 6.1 $\log_{10}$). After marination fillets were shaken for 1 min in a 50 mL rinse of 1% BPW. Serial dilutions were plated onto BGA with sulfapyridine with 200 ppm nalidixic acid and incubated at 37°C for 24 h, and onto *E. coli*/coliform Petrifilm and incubated at 35°C for 24 h. Post-treatment marination solutions were sampled and average *Salmonella* counts of 1.7 $\log_{10}$ were recovered; no *E. coli* were recovered. Bacterial counts were transformed to $\log_{10}$ CFU/ml, data main effects analyzed by ANOVA, and mean differences due to treatment analyzed by *t* test. There were no significant ($P < 0.05$) differences due to ultrasonication for either *Salmonella* (mean count 4.6 $\log_{10}$ CFU) or *E. coli* (mean count of 2.8 $\log_{10}$ CFU). Higher STP significantly reduced *Salmonella* numbers (from 4.7 to 4.5 $\log_{10}$ CFU) but had no effect on *E. coli*. The reduction of *Salmonella* numbers was small and would have limited usefulness in practical application. Ultrasonic treatment during marination was not effective for reducing numbers of *Salmonella* and *E. coli* on broiler breast meat.

Key Words: broiler breast meat, ultrasonic marination, *Salmonella*

373 The enrichment of breast and thigh meat in broilers for DHA using supplemental DHA. M. K. Manangi*, B. Wuelling, J. Hux, S. Carter, and M. Vazquez-Anon, *Novus International, Inc.*, *St. Charles, MO*.

A 44-d experiment was conducted to evaluate the enrichment levels of DHA (docosahexaenoic acid) in broiler breast and thigh meat along with various other tissues using supplemental source of DHA (DHA GOLD) in a corn-SBM based diet. A total of 540 Ross-708 male broiler chicks were raised in floor pens up to d 23 of age using starter and grower diets. On d 23, 432 birds were assigned to 3 treatments with 12 pens/treatment and 12 birds/pen under completely randomized block design. The 3 treatments were: 1) 0% DHA GOLD; 2) 1% DHA GOLD; 3) 1.5% DHA GOLD supplementation. DHA GOLD was supplemented as 'on-top' addition from d 23 to 44. DHA was quantified in various tissues at d 37 and only for breast meat at d 44. D 37 data indicates significant ($P < 0.05$) increase in DHA content due to supplemental DHA for breast and thigh meat and skin, liver, and fat pad. D 44 breast meat data also indicates a significant ($P < 0.05$) increase in DHA content. Supplementing broilers diets with 0, 1, and 1.5% DHA GOLD on top for 14 d (d 23 - 37) resulted in 17, 26 and 34 mg of DHA/100g of breast muscle; 17, 32, and 43 mg of DHA/100 g of thigh muscle; 20, 160, and 274 mg of DHA/100g of breast skin; 27, 119, and 253 mg of DHA/100 g of thigh skin; 4, 80, and 160 mg of DHA/100 g of liver; and 13, 179, and 289 mg of DHA/100 g of fat pad, respectively. Supplementing broilers with diets containing 0, 1, and 1.5% DHA GOLD on top for the last 21 d (d 23 - 44) resulted in 13, 35, and 54mg of DHA/100g of breast muscle, respectively. Data also indicates that supplementing up to 1.5% of DHA GOLD on top in the broiler diets does not affect ($P > 0.05$) weight gain and F:G. In summary, supplemental DHA GOLD can be used to enrich broiler meat with levels of DHA to satisfy recommended daily allowance. Further increase in enrichment was possible by extended period of dietary DHA inclusion. DHA GOLD is a dried whole cell algae product, derived from *Schizochytrium sp*, contains a minimum of 18% DHA by weight.
DHA GOLD is a registered trademark of Martek Biosciences Corporation, USA.

Key Words: broiler, DHA

374 Effect of feeding hatchery waste meal processed by different techniques on egg quality and productive performance of laying hens. A. Mahmud*[1], Saima[1], M. A. Jabbar[1], A. W. Sahoota[1], Z. Ali[2], and M. Z. U. Khan[1], [1]*University of Veterinary & Animal Sciences*, *Lahore, Pakistan*, [2]*Big Feeds (Pvt) Ltd.*, *Lahore, Pakistan*.

The present experiment was conducted in 2 phases. In the first phase, hatchery waste (HW) was subjected to the following processing techniques; cooking, autoclaving and extrusion to prepare hatchery waste

meal (HWM). Prepared HWM was chemically analyzed. In the second phase, an optimum inclusion level for each type of processed HWM was determined in layer diets. For this purpose, 3 hundred White Leghorn hens were randomly distributed to 10 dietary treatments. A negative control diet was prepared without HWM, while 9 experimental diets contained 4, 8 or 12% of cooked, autoclaved or extruded HWM, respectively. Completely randomized design was used and statistical analyses were carried out with SAS version 9.1 using Duncan multiple range test for mean comparisons at 5% probability. Results showed that maximum egg production was achieved with 4% HWM processed by autoclaving. Processing of HW with extrusion significantly reduced egg production and a more pronounced decrease was found with 12% of extruded HWM. Egg mass and feed conversion followed the same trend observed for egg production. Average egg weight due to different treatments fell within a very narrow range and showed no difference ($P > 0.05$) among treatments. Shell, yolk and albumen weights, as a percentage of egg weight, were not significantly affected with the use of different levels and processing of HWM. Maximum values for albumen height as well as Haugh units were obtained by feeding the 4% autoclaved HWM. Other egg quality parameters like shell thickness, yolk index and color were independent of the dietary treatments. The findings of this study suggest that autoclaving of hatchery waste is better than extrusion or cooking techniques and 4% of autoclaved HWM may be included in layer rations to get more production than diets without HWM. Nevertheless, layer diets up to 8% HWM could be used to feed the laying hens to maintain reasonably good production without detrimental effects on egg quality.

Key Words: hatchery wastes, processing, layers

375 Effect of feeding flaxseed and two types of antioxidants on quality parameters of omega-3 enriched eggs during storage. Z. Hayat*[1,2], G. Cherian[3], T. N. Pasha[2], F. M. Khattak[2], and M. A. Jabbar[2], [1]*University College of Agriculture, University of Sargodha, Sargodha-40100, Pakistan*, [2]*University of Veterinary and Animal Sciences, Lahore-54000, Pakistan*, [3]*Department of Animal Sciences, Oregon State University, Corvallis*.

Inclusion of flaxseed to enhance omega-3 content of eggs is well documented. However, increasing omega-3 fatty acids perpetuates the extent of fatty acid unsaturation, leading to oxidative damage of yolk lipids and reduction in egg quality. This phenomenon is aggravated during storage, and needs suitable strategies to combat deterioration of egg quality. Currently, a limited number of antioxidants are available that poses major challenge for the feed industry to use them efficiently. Therefore, the aim of present study was to examine the effect of 2 types of antioxidants and storage on quality parameters of eggs enriched with omega-3 fatty acids. ISA brown layer pullets were fed corn-soybean meal-based diet with no added antioxidants (Control) or 10% flax seed and 2 types of antioxidants (α-tocopherols, butylated hydroxytoluene, [BHT] at 0, 50, 100, 150 IU or mg/kg). A total of 384 eggs (48/diet) were collected and stored at 4°C for 60 d. On d 0, 20, 40, and 60 of storage, 2 eggs from each replicate (totaling 12 eggs per treatment) were selected randomly. Egg quality parameters such as egg weight, yolk weight, yolk color, albumen weight, albumen height, shell weight, shell thickness and Haugh unit were measured. Storage over 20 d affected all the parameters except egg weight, shell weight and shell thickness ($P < 0.05$). Supplementation of antioxidants at higher levels (150 IU or mg/kg) was found to be effective in reducing the drop in egg quality. This may be at the expense of antioxidants as storage led to over 50% reduction in egg tocopherols content ($P < 0.05$). The interaction of storage with diet was not significant on all egg quality parameters tested ($P > 0.05$). Egg weight, shell thickness and shell weight as percentage of total egg weight were not affected by diet or storage ($P > 0.05$). These data demonstrate that added antioxidant supplementation may be needed in improving the quality parameters during storage in eggs from hens fed flaxseed.

Key Words: flaxseed, antioxidants, egg quality

376 Quality of shell eggs stored under modified atmosphere packaging. T Yalamanchili*, C. Z. Alvarado, L. D. Thompson, and C. J. Brooks, *Texas Tech University*, *Lubbock*.

The processing of shell eggs involves collecting of eggs and transporting them to a packaging plant where they are cleaned, sorted and packaged. However, the cooling capacity at the farm, storage, and the transportation trucks as well as time to the retail outlet can decrease egg quality. The objective of this experiment was to determine the effect of a modified atmosphere packaging (MAP) on the quality of USDA Quality grade AA shell eggs placed in a Master bag (Cryovac 33cm × 55.88cm) and stored at 4°C. Shell eggs were subjected to one of the 2 packaging treatments: (1) control–air; (2) 20% CO_2 and 80% N_2. Packaged eggs were stored for 28 d in the master bag at 4 ± 1°C. A total of 5760 eggs were used in 2 experiments, with 2 trials and 5 replications each. Five master bags were used for analyses on 1, 7, 14, 21, and 30d. In Experiment 2, and the packages were allowed to sit at 4 ± 1°C for 24h before testing for quality attributes. Analyses included albumen pH, Haugh units, yolk index, color (hard cooked and raw), foam ability, foam stability and TBARS. The data were analyzed by ANOVA in a 2 (packaging treatment) × 5 (time points) × 2 (trial) factorial design. In both the experiments, pH of the albumen of the eggs stored in MAP was lower than the eggs stored in air. The albumen of the raw eggs stored in MAP was lighter than those stored in air. However, in both the experiments, the albumen of the raw eggs stored in MAP were more yellow than the eggs stored in air. The hard cooked albumen of the eggs stored in MAP showed increased brightness and intensity in color. The yolk of the eggs stored in MAP maintained a more vivid and lighter yellow color. The carbon dioxide present in the MAP lowered the pH of the egg and thus may have prevented the green ring formation. Thus, packaging eggs in a MAP master bag was effective in reducing egg deterioration and loss of some functional quality during storage at refrigerated temperatures.

Key Words: shell eggs, packaging, quality

377 Evaluation of fatty acids and proteins in eggs from cage and range laying hens. L. K. Kerth*[1], P. A. Curtis[1], K. R. Willian[2], C. R. Kerth[1], and K. E. Anderson[3], [1]*Auburn University, Auburn, AL,* [2]*Tuskegee University, Tuskegee, AL,* [3]*North Carolina State University, Raleigh*.

Consumer trends and new legislation have furthered the transition of caged layers to range. However, little research has evaluated the impact that these environmental rearing changes will cause to the egg itself. This study was designed to compare what changes occur in the egg when layers are raised on a range system versus traditional cage system. In the 37th North Carolina Layer Performance and Management Test Hy-Line Brown hens were used in both the range environment and the cage. This strain was selected because it is the current brown egg strain used in the US. Hens were reared according to what environment they were going into and all other rearing husbandry was identical. On a quarterly basis, eggs were gathered from layers at 17 to 82 wk of age. Once collected eggs were pooled into 2 replicates and functional and proximate analyses were conducted in duplicate on each pooled set. Remaining egg samples were stored for further testing. Initial findings found that angel food cake volume was significantly higher ($P < 0.05$)

for caged eggs when compared with range. However, that difference could not be attributed to the ph and percent fat of the albumen as neither was different ($P > 0.05$). Upon further investigation it was discovered that the percentage of solids and protein were higher ($P < 0.05$) in range eggs. When the functional properties of the yolk were evaluated range eggs had a stronger ($P < 0.05$) emulsion in both fresh and stored mayonnaise. Conversely, there were no differences ($P > 0.05$) in pH, percentage of solids, fat or protein in the yolk from cage or range eggs. The frozen samples were tested for fatty acid methyl ester profiles on the yolk samples and SDS-PAGE on the albumen samples to identify and quantify fatty acids and proteins. The amount of saturated and omega-3 fatty acids present in the yolk, were highest ($P < 0.05$) in the last sampling period. Saturated fatty acids were also found to be higher ($P < 0.05$) in eggs from caged birds as opposed to a range birds.

Key Words: eggs, fatty acids, proteins

378 Intermittent feeding strategies of ractopamine hydrochloride on growth performance and carcass characteristics of feedlot steers. M. G. Dib*[1], G. E. Erickson[1], T. J. Klopfenstein[1], J. R. Benton[1], W. A. Griffin[1], J. J. Sindt[2], and W. T. Choat[2], [1]*University of Nebraska*, *Lincoln,* [2]*Elanco Animal Health*, *Greenfield, IN*.

The objective of this experiment was to evaluate intermittent feeding of ractopamine hydrochloride (OPT) on growth performance and carcass characteristics. Crossbred steers (n = 320; initial BW = 480 + 12 kg) were used in a randomized complete block design with 4 treatments, 8 pens/treatment, and 2 weight blocks. Treatments consisted of no OPT (NEGCON), OPT fed continuously during the last 35 d prior slaughter (POSCON), OPT fed for 7 d followed by 4 d of withdrawal (4-dINT) and OPT fed for 7 d followed by 7 d of withdrawal (7-dINT). All treatments receiving OPT (POSCON, 4-dINT and 7-dINT) received OPT for a total of 35 d but on different days. Before the experiment, each steer was weighed on 2 consecutive days after feed restriction (decrease of 1 kg/d of DM) for 3 d in an attempt to minimize variation due to gut fill. Pens of animals were weighed weekly, with a 4% shrink, throughout the 63 d of the experiment before slaughter. Steers were slaughtered on the same day after 165 d on feed, and 63 d of treatment. Data were analyzed using a mixed model analysis with treatment and block included in the model as fixed variables and pen as the experimental unit. Final BW increased ($P < 0.04$) by 6 kg for steers fed OPT compared with NEGCON when measured on a live basis. Final BW on a carcass-adjusted basis and HCW were not impacted by treatment ($P > 0.18$). Feed intake was 0.3 kg greater ($P < 0.05$) for 7-dINT compared with the other treatments. Gain based on live BW was greater for OPT compared with NEGCON, which tended ($P = 0.09$) to increase G:F for steers fed OPT compared with NEGCON. Carcass performance or traits were not affected ($P > 0.18$) by feeding OPT compared with NEGCON except for calculated USDA Yield grade. No differences were observed for ADG, G:F, or carcass traits between POSCON, 4-dINT, and 7-dINT in this study. Further research may be necessary to determine the response to re-stimulation of β-receptors in cattle.

Key Words: beef cattle, performance, ractopamine hydrochloride

379 Effectiveness of ractopamine when fed as a top dress in beef steers. K. L. Neuhold*[1], P. T. Grubb[1], J. J. Wagner[1], T. E. Engle[1], R. K. Peel[1], and A. L. Schroeder[2], [1]*Colorado State University*, *Fort Collins,* [2]*Elanco Animal Health*, *Greenfield, IN*.

A clinical trial was conducted to investigate the effectiveness of ractopamine (RAC) as a top dress (TD) pellet during the final 42 d of feeding. Crossbred yearling steers (n = 144) were selected for the study. Steers were housed in 9 animals per pen with 8 pens per treatment. Treatments consisted of a steam-flaked corn based feedlot diet plus 0.9 kg per animal per d of TD containing 1) no RAC (Control) or 2) 400 mg/animal/d of RAC (400-RAC). Steers were fed 3 times daily. Top dress was applied evenly over the top of the total mixed ration immediately after the second feeding. Initial steer weights (526.8 kg) were similar ($P > 0.94$) between treatments. Final steer weight ($P < 0.03$) and average daily gain ($P < 0.02$) were greater for 400-RAC when compared with control (615.8 vs 605.2 ± 6.3 kg and 2.1 vs 1.86 ± 0.13 kg/day, respectively). Steers consuming 400-RAC had lower daily DMI ($P < 0.04$) compared with control (10.9 vs 11.4 ± 0.32 kg/animal/day). Gain to feed ratio was greater ($P < 0.001$) in steers fed 400-RAC (0.194 vs 0.164 ± 0.46). Dressing percentages ($P > 0.96$) were similar across treatments resulting in greater hot carcass weights ($P < 0.002$) for 400-RAC supplemented steers (373.5 vs 367.4 ± 2.3 kg). There were no differences between treatment groups for 12th rib fat depth ($P > 0.54$) and KPH ($P > 0.69$). Steers receiving 400-RAC had increased ($P < 0.007$) longissimus muscle area than controls (96.39 vs 91.03 ± 0.19 cm^2). Longissimus muscle area expressed per unit hot carcass weight was greater ($P < 0.04$) for 400-Rac steers compared with control steers indicating that RAC increased carcass muscling. Yield grades tended ($P < 0.19$) to be lower RAC-400 steers compared with controls (2.34 vs 2.52 ± 0.08). No differences in marbling score or carcass quality grade were observed between treatments. These data indicate that feeding RAC in a TD application for the final 42 d of the finishing period will increase rate of gain, final weight, hot carcass weight and gain to feed ratio while maintaining carcass quality.

Key Words: steers, ractopamine, top dress

380 Effects of prepartum rumen-protected choline supplementation on performance of beef cows and calves. L. A. Pacheco*[1], J. R. Jaeger[2], L. R. Hibbard[1], M. J. Macek[1], N. A. Sproul[1], G. J. Eckerle[1], E. A. Bailey[1], J. W. Bolte[2], and K. C. Olson[1], [1]*Kansas State University*, *Manhattan,* [2]*Western Kansas Agricultural Research Center*, *Hays*.

The objective of our study was to evaluate the effect of prepartum ruminally-protected choline (RPC) supplementation on cow and calf performance. Angus crossbred cows and heifers (n = 403; average initial weight = 533.2 ± 4.0 kg) grazing native range were blocked by weight and parity and assigned randomly to 1 of 2 treatments: a 40% CP soy-corn supplement (CON) or a 40% CP soy-corn supplement containing RPC. Treatments were applied during a 60 d period that immediately preceded the earliest predicted calving date; each cow was fed 2.38 kg/hd/d of CON or RPC 6 × per week. The feeding rate of choline averaged 4.5 g/cow/d. Body weight, BCS, and ultrasonically measured longissimus muscle characteristics of cows and BW of calves were recorded at intervals from January to October. Changes in cow BW, BCS, backfat thickness, and intramuscular fat between the outset of the trial and pregnancy diagnosis were similar ($P \geq 0.25$) between treatments. Cows fed RPC tended to lose more ($P = 0.10$) longissimus muscle depth between the outset of the trial and pregnancy diagnosis. Conversely, BW of cows fed RPC tended to be greater ($P = 0.07$) at pregnancy diagnosis than that of cows fed CON. Calf BW at birth, at pregnancy diagnosis, and at weaning were not different ($P \geq 0.39$) between treatments; however, ADG from pregnancy diagnosis to weaning tended ($P = 0.06$) to be greater for calves of RPC-fed dams than for calves of CON-fed dams. Within parity class, timed-AI pregnancy and overall pregnancy were not affected ($P \geq 0.14$) by treatment. Under the conditions of our study, prepartum RPC supplementation had minimal effects on performance of beef cows and calves.

Key Words: beef cows, choline, supplementation

381 Evaluation of ractopamine fed in a top dress feed on growth and standard carcass characteristics of crossbred cattle. A. L. Schroeder*[1], T. H. TerHune[2], M. Edmonds[3], R. P. Lemenager[4], S. L. Lake[4], F. K. Mckeith[5], and J. J. Wagner[6], [1]*Elanco Animal Health*, *Greenfield, IN*, [2]*HMS Veterinary Development*, *Tulare, CA*, [3]*Johnson Research*, *Parma, ID*, [4]*Purdue University*, *West Lafayette, IN,* [5]*University of Illinois*, *Urbana*, [6]*SECRC-Colorado State University*, *Lamar*.

Ractopamine (RAC) was originally approved for feeding continuously to cattle during the last 28 to 42 d of the finishing period. Growth per-

formance and standard carcass characteristic effects of feeding RAC one time daily at: 1) 0 mg or 2) 400 mg/h/d (RAC400) in a top dress (TD) feed during the last 42 d was evaluated in 560 steers at 4 sites. A randomized complete block design was used at each site. Eight replicates (blocks) per site resulted in 32 experimental units (8–10 steers/pen, depending on location) per treatment. Cattle were fed either 2 or 3 times daily with RAC TD fed on top of existing feed in the bunk after the first or second feeding (depending on feeding frequency) in 0.45 or 0.9 kg of TD feed per head per day. Initial weights were similar ($P \geq 0.72$) between treatments. Final weight ($P \leq 0.02$) and average daily gain ($P \leq 0.006$) was increased for the RAC400 treatment compared with control (613.0 vs. 603.3 ± 9.75 kg and 1.91 vs. 1.68 ± 0.19 kg per day, respectively). Dry matter intake (DMI) was not different ($P \geq 0.15$) between treatments (11.21 for control and 10.96 ± 0.20 kg for RAC400, respectively). Gain to feed ratio was greater ($P \leq 0.006$) and DMI to gain ratio was improved ($P \leq 0.02$) for RAC400 compared with control animals (0.174 vs. 0.150 ± 0.016) and 5.28 vs. 6.03 ± 0.15, respectively). Dressing percentages were similar ($P \geq 0.78$) resulting in heavier hot carcass weights ($P \leq 0.008$) for the RAC400 treatment compared with controls (366.8 vs. 360.4 ± 13.4 kg). No differences existed in 12th rib fat ($P \geq 0.30$) and KPH ($P \geq 0.58$). RAC400 supplemented animals had larger longissimus muscle area ($P < 0.008$) than controls (91.1 vs. 87.3 ± 2.89 cm^2, respectively). Yield grade was improved ($P < 0.02$) for RAC400 carcasses compared with control carcasses (2.47 vs. 2.66 ± 0.13, respectively). Marbling score and quality grades were similar ($P \geq 0.10$) between treatments. The data demonstrate RAC fed in a TD feed for the last 42 d of the finishing period will increase average daily gain, live weight, HCW, LM area and yield grade without adversely affecting marbling score and carcass quality.

Key Words: cattle, top dress, ractopamine

382 Ractopamine hydrochloride did not affect growth or fermentation of ruminal bacteria in pure culture. C. E. Walker*, J. M. Heidenreich, and J. S. Drouillard, *Kansas State University*, *Manhattan.*

Catecholamines have been observed to enhance pure culture bacterial growth in vitro. In this research, effects of the synthetic catecholamine ractopamine hydrochloride (RAC) on bacterial growth were evaluated in vitro. Representative strains of bacterial species commonly found in the rumens of high-concentrate fed cattle, particularly species involved in proteolysis, were evaluated. Pure cultures of *Butyrivibrio fibrisolvens*, *Clostridium aminophilum*, *Clostridium sticklandii*, *Fusobacterium necrophorum*, *Megasphaera elsdenii*, *Prevotella ruminicola*, *Selenomonas ruminantium*, and *Streptococcus bovis* were obtained from the American Type Culture Collection. Cultures were grown in Hobson M2 media and incubated at 39°C. Treatments were 0 mg (Control) or 2.26 mg RAC/L added to culture tubes immediately before inoculation with bacterial cultures. Bacterial growth was evaluated as changes in optical density at 650 nm using a spectrophotometer. Change in pH and redox potential for each tube were determined after incubation was complete. Cultures were then centrifuged and the resulting pellet was dried at 105°C to determine impact of RAC on bacterial cell yield. To measure the impact of RAC on fermentation, concentrations of VFA and lactate were analyzed using gas chromatography, and ammonia and α-amino N were analyzed colorimetrically by an auto analyzer. The Mixed models procedure of SAS was used with fixed effects of RAC, bacterial strain, and time to assess changes in optical density. A mixed model including effects of RAC and strain was used to evaluate effects on fermentative end products. RAC did not affect pure culture growth, culture pH, redox potential, or bacterial cell yield ($P > 0.10$). Additionally, RAC did not affect concentrations of VFA, lactate, ammonia, or amino acid in vitro ($P > 0.10$). Growth or fermentative end products of pure cultures containing select strains of ruminal bacteria were not affected by the presence of ractopamine hydrochloride.

Key Words: ractopamine hydrochloride, ruminal bacteria, fermentation

383 Accelerated step-up regimen with 44 mg/kg monensin. C. E. Walker*, G.L Parsons, K. A. Miller, L. K. Thompson, J. J. Higgins, and J. S. Drouillard, *Kansas State University*, *Manhattan*.

Crossbred steers (n = 720; initial BW = 453 kg) were used to evaluate effects of monensin concentration and step-up regimen on feedlot performance and carcass traits in a randomized complete block experiment with a 2 × 2 factorial treatment arrangement. Factor 1 consisted of 33 or 44 mg/kg monensin (MON) fed for the entire 153 d trial; and factor 2 was length of the step-up period (10 or 21 d). Cattle from wheat pastures were received into the feedlot and fed chopped hay and salt for 2 wk. On d 1 of the study, cattle were stratified by BW and allotted to pens of 15 cattle each, with 12 pens/treatment. Starting d 1, a 3-diet (60, 77, and 93% concentrate) step-up system was used in which cattle were fed ad libitum 60% concentrate am (0900 h) and pm (1300 h) for step 1; 60% concentrate am and 77% concentrate pm for step 2; 77% concentrate am/pm for step 3; 77% concentrate am and 93% concentrate pm for step 4; and 94% concentrate am/pm for the final finishing diet. Diet changes were implemented on d 6, 11, 16, and 21 for the traditional regimen, and on d 4, 6, 8, and 10 for the accelerated regimen. BW were determined on d 0, 50, and before shipping to a commercial abattoir on d 153. There were no interactions between level of MON and step-up regimen ($P > 0.10$) and no effects of step-up regimen on performance or carcass traits ($P > 0.10$), but steers on the accelerated regimen consumed less roughage ($P < 0.05$). Increasing MON from 33 to 44 mg/kg decreased DMI during the first 50 d ($P < 0.01$) and the entire 153-d study period ($P < 0.01$), and improved gain efficiency by 8% for the first 50 d ($P < 0.10$) and by 3% for the 153-d trial ($P < 0.05$). Yield grades were lower for steers fed 44 mg/kg MON compared with steers fed 33 mg/kg MON ($P < 0.05$), but other carcass traits were not affected ($P > 0.10$). Steers can be transitioned to high-concentrate diets in 10 d without compromising performance, and less roughage is used. Steers fed 44 mg/kg MON were more efficient than steers fed 33 mg/kg MON.

Key Words: step-up, monensin, roughage

384 Effects of Zilmax on blood metabolites in finishing cattle. C. L. Van Bibber*, G. L. Parsans, K. A. Miller, L. K. Thompson, and J. S. Drouillard, *Kansas State University*, *Manhattan*.

Effects of Zilmax (Z) on blood metabolites and carcass traits were evaluated in crossbred finishing steers (n = 18) that were stratified by BW and randomly assigned, within strata (block), to control (C) or Z treatments. Cattle were fed once daily ad libitum in individual feeding pens (9 pens/treatment). Z was fed 23 d and withdrawn 3 d before harvest. Blood samples and measures of BW were taken on d 0, 7, 14, and 21. Metabolites were analyzed as repeated measures using Proc Mixed, with fixed effects of treatment, day, and treatment × day, and random effects of block and block × treatment. Performance and carcass traits were analyzed with treatment as fixed effect, and block and block × treatment as random effects. Concentrations of β-hydroxybutyrate (BHB), glucose, and lactate were determined in whole blood, and NEFA, urea nitrogen (PUN), and long-chain fatty acids (LCFA) were analyzed in plasma. Adipose tissue samples were analyzed for LCFA profiles. Feeding Z decreased DMI by 8% ($P < 0.10$), but did not impact BW gain or efficiency ($P > 0.10$). Feeding Z resulted in greater HCW and LM

area ($P < 0.10$), numerically decreased marbling score and yield grade, but did not influence other carcass traits ($P > 0.10$). Z increased plasma concentrations of elaidic, vaccenic, and docosapentaenoic acids ($P < 0.10$), but adipose tissue concentrations of LCFA were unaffected ($P > 0.10$), suggesting no preferential oxidation of specific fatty acids. Blood metabolites for d 0 and 21 of the study are shown in the table.

Table 1. Effects of Zilmax on Blood Metabolites

Item, mM	C d0	Z d0	C d21	Zd21	SEM
Glucose‡	3.32	3.39	3.48	3.09	0.24
Lactate	2.83	2.80	2.16	1.54	0.48
NEFA	126	175	140	174	36
BHB	0,01	0.08	0.02	0.06	0.83
PUN† ‡	4.15	3.74	4.44	3.26	0.24

The symbols † and ‡ denote effects of Z and Z × d interaction, respectively ($P < 0.10$).

Key Words: zilpaterol hydrochloride, plasma urea nitrogen, glucose

385 Intake and digestion of cotton co-product and distillers grain blocks fed as a cattle hay replacement. G. M. Hill* and D. J. Renney, *University of Georgia*, *Tifton*.

A new compressed block product (CPM, 0.34% S; A. G. Daniel Co., Eastman, GA) that contained cotton gin trash (59%), distillers dried grains with solubles (DDG, 0.66% S), wheat middlings, a molasses product and minerals, was formulated to replace hay in cow diets. Brangus and Angus crossbred steers (n = 30; age 2 yr; initial BW 453.6 ± 33.9 kg) selected to mimic beef cow intake, were ranked by BW, randomly assigned to treatments, and individually-fed diets for 18 d. Supplements (SUP) were fed with or without free-choice coarsely ground hay (H; Tifton 85; DM, CP, NDF, TDN, %: 87, 9.3, 77, 52). Treatments were: hay only (HAY); H with whole cottonseed (WCS) fed at 0.5% BW daily (HWCS), H with DDG (HDG); H with CPM (HCPM); or free-choice CPM (CPMFC). The DM, CP, NDF, crude fat, TDN (% DM), respectively, were: WCS, 91.4, 23.4, 53.5, 18.1, 71; DDG, 86.7, 31.6, 31.7, 82; CPM, 89.3, 16.4, 56.6, 5.2, 48. Chromic oxide was fed (10 g/steer, d 9 to d 18), and fecal samples (11/steer, d 14 to d 18) were analyzed to determine apparent digestion. Hay DMI was highest (Table 1; $P < 0.01$) for HAY, HWCS, and HDG, and lowest for HCPM. Steers had more than double total DMI for HCPM and CPMFC ($P < 0.01$) compared with other treatments. The OM digestibility was highest ($P < 0.02$) for HCPM, and CP digestibility was highest ($P < 0.01$) for HCPM, intermediate for HWCS, HDG, and CPMFC, and lowest for HAY. Digestibility of ADF and NDF were highest for HAY ($P < 0.01$); but NDF digestibility was lowest for CPMFC ($P < 0.01$), and similar for HWCS, HDG, and HCPM. The CPM treatments demonstrated adequate OM digestibility, but feeding CPM increased DMI compared with traditional cow wintering diets.

Table 1.

Item	HAY	HWCS	HDG	HCPM	CPMFC	SE	P <
Hay DMI, kg	6.68	5.30	5.15	1.98	0.00	0.23	0.01
SUP DMI, kg	0.00	1.88	1.49	13.09	15.61		
Total DMI, kg	6.77	7.20	6.67	15.51	15.64	0.37	0.01
Apparent digestion, %							
OM	70.58	69.13	70.29	74.03	72.25	1.00	0.02
CP	63.66	69.78	70.84	73.33	71.15	1.06	0.01
ADF	69.91	57.91	57.55	61.68	57.81	1.41	0.01
NDF	70.66	66.57	66.89	65.70	62.66	1.32	0.01

Key Words: steer, cottonseed, digestion

386 Late gestation supplementation of beef cows: Effects on cow and calf performance. D. W. Bohnert*[1], R. Mills[1], L. A. Stalker[3], A. Nyman[1], and S. J. Falck[2], [1]*Oregon State University*, *Burns*, [2]*ARS-USDA*, *Burns, OR*, [3]*University of Nebraska*, *North Platte*.

We conducted a 2-yr study to evaluate the influence of cow BCS and dried distillers grains (DDGS) supplementation during late gestation on cow and calf productivity. The experimental design was a 2 × 2 factorial; 2 BCS (4 or 6) and supplemented or not supplemented. Approximately 12.7 kg/cow of low quality meadow hay (6.4% CP) was provided each day and supplemented cows received 1.81 kg/cow of DDGS every Monday and Wednesday and 2.72 kg/cow on Friday. On each supplementation day, supplemented cows were gathered and sorted into pens based on their respective blocking structure. After completing consumption of their allocated supplement, cows were returned to a common pasture. Performance data and binomial data were analyzed as a randomized complete block using PROC MIXED and PROC GLIMMIX in SAS, respectively. Calf birth weight was greater with BCS 6 cows compared with BCS 4 ($P = 0.002$) and for supplemented compared with unsupplemented cows ($P = 0.05$). In addition, weaning weight was greater for BCS 6 compared with BCS 4 ($P = 0.05$) and calf weaning weight and ADG to weaning were greater for the offspring of supplemented compared with unsupplemented cows ($P \leq 0.02$). We noted no differences in post-weaning calf performance or carcass characteristics ($P > 0.10$). However, BCS 6 cows had approximately 10% more live calves at birth and at weaning ($P < 0.001$) compared with BCS 4 cows. Also, pregnancy rate was 91% for BCS 6 compared with 79% for BCS 4 cows ($P = 0.005$). Supplementation during late gestation resulted in an estimated net return of $7/cow if calves were sold at weaning compared with not supplementing. More importantly, because of additional weaned calves, the estimated net return for BCS 6 cows at weaning was $71/cow more than BCS 4. Likewise, with retained ownership, BCS 6 cows yielded a net return of $130/animal more than BCS 4 cows. This research demonstrates the potential consequences of not maintaining cows in good BCS (>5) at calving; greater calf losses, less weaned calves, decreased pregnancy rate, and lower economic return.

Key Words: supplementation, fetal programming, protein

387 Effect of forage energy intake and supplementation on gene expression of adipose tissue in growing beef cattle. P. A. Lancaster*, E. D. Sharman, G. W. Horn, C. R. Krehbiel, and U. DeSilva, *Oklahoma Agricultural Experiment Station*, *Stillwater*.

Additional benefit to the stocker cattle production phase could be realized by influencing adipose tissue development before finishing. Previous research has indicated that nutritional management can affect fat deposition in growing cattle. Our objective was to evaluate forage energy intake and type of fermentation on gene expression of adipose tissue in growing steers. Angus steer calves (n = 68; 258 ± 29 kg BW) were randomly allotted by BW to 4 treatments: (1) 1.02 kg•hd^{-1}•d^{-1} of a 40% CP supplement (CON) to meet their DIP requirement while grazing dormant native range; (2) CON plus corn-based supplement at 1% BW (CORN) while grazing dormant native range; (3) grazing wheat pasture at a high stocking rate to achieve a low ADG (LGWP); and (4) grazing wheat pasture at a low stocking rate to achieve a high ADG (HGWP). Supplements were fed individually 5 d per week. Following winter grazing, 3 steers per treatment were harvested and subcutaneous (SC), perirenal (PR), and intramuscular (IM) adipose tissue collected. Total RNA was extracted and gene expression determined using qRT-PCR. Performance and carcass data are presented in a companion abstract (Sharman et al., 2010). There were no treatment × adipose tissue interactions for any genes evaluated indicating that each

adipose tissue responded similarly to the treatments. mRNA expression of genes involved in triglyceride synthesis (glycerol-3-phosphate dehydrogenase, fatty acid synthase, and diacylglycerol acyltransferase 2) and glucose utilization [ATP citrate lyase (ACLYS) and NADPH malate dehydrogenase (MDH)] were greater ($P < 0.05$) for HGWP and LGWP compared with CON and CORN. ACLYS mRNA expression was greater in SC and PR compared with IM, and MDH mRNA expression was greater in PR compared with SC and IM. Further analyses will evaluate genes related to adipogenesis. These data indicate that greater propionate type of fermentation increased triglyceride synthesis and glucose/lactate utilization for fatty acid synthesis, and SC and PR had increased glucose/lactate utilization compared with IM irrespective of forage energy intake or type of fermentation.

Key Words: adipose tissue, gene expression, stocker cattle

388 Angus and Simmental calves exhibit differential trace mineral metabolism. S. L. Hansen*, E. L. Richter, and M. E. Drewnoski, *Iowa State University*, *Ames*.

To examine the effects of cattle breed on the clearance rate of an injectible mineral 10 Angus and 10 Simmental calves were blocked by breed and initial BW (332 ± 33 kg) and injected with either Multimin90 (MIN) or sterilized saline (CON) at a dose of 1 mL/45 kg BW. The Multimin90 contained 60 mg Zn/mL (as Zn disodium EDTA), 10 mg Mn/mL (as Mn disodium EDTA), 15 mg Cu/mL (as Cu disodium EDTA), and 5 mg Se/mL (as sodium selenite). Calves were weight matched and treatment was balanced within pens (2 head per pen). Calves received a corn-silage based diet and Mn, Cu, Zn, and Se were supplemented at NRC recommended levels. Jugular blood for plasma mineral analysis was collected immediately before injection and at 8 and 10 h post injection, and on d 1, 8 and 15 post injection. Liver biopsies for mineral analysis were collected 3 d before injection and on d 1, 8 and 15 post injection. Plasma concentrations of Mn and Se were greater ($P < 0.001$) at 8 and 10 h and d 1 post injection in MIN calves compared with CON calves. Plasma Se remained elevated ($P < 0.05$) through d 8 in MIN calves vs. CON calves. Regardless of treatment, Simmental calves exhibited lower ($P = 0.05$) plasma Cu at 10 h post injection and tended ($P = 0.07$) to have greater plasma Mn on d 1 compared with Angus calves. Plasma concentrations of Cu, Zn and Mn did not differ due to treatment by d 8. Liver concentrations of Cu and Se were greater ($P < 0.01$) in MIN calves compared with CON calves on d 1, 8 and 15 post injection. Liver Zn concentrations were greater ($P < 0.01$) on d 1 in MIN calves versus CON calves. Liver Mn concentrations were greater ($P < 0.05$) on d 8 in MIN calves compared with CON calves, but did not differ among treatments on d 1 or 15 post injection. Interestingly, Simmental calves exhibited greater ($P < 0.01$) liver Mn concentrations on d 15 compared with Angus calves, regardless of treatment. In summary, these data suggest that Angus cattle clear Mn from the body at a faster rate than Simmental cattle, which may have implications on supplementation strategies.

Key Words: cattle, mineral, breed

389 Effects of polyunsaturated fatty acid (PUFA) supplementation on performance and acute-phase response of transported beef steers. R. F. Cooke*[1], A. B. Scarpa[1], F. M. Nery[1], F. N. T. Cooke[1], P. Moriel[2], B. W. Hess[2], R. R. Mills[3], and D. W. Bohnert[1], [1]*Oregon State University*, *Burns,* [2]*University of Wyoming*, *Laramie,* [3]*Oregon State University*, *Pendleton*.

The objective was to compare ADG, DMI, and acute-phase response of steers supplemented or not with PUFA for 30 d before shipping to the feedlot. Seventy-two Angus steers weaned at 7 mo of age (d −55) were stratified by BW on d −30 of the study, and randomly allocated to 18 drylot pens (4 steers/pen). Pens were assigned to receive a grain-based supplement (avg. 1.4 kg/steer/d) without (CO) or with 0.15 kg/steer/d of a PUFA source (PF; Megalac-R, Church and Dwight, Princeton, NJ) or a saturated fatty acid source (SF; Megalac, Church and Dwight). Treatment intakes were formulated to be iso-caloric, iso-nitrogenous, and offered daily from d −30 to d 0. Mixed alfalfa-grass hay was offered in amounts to ensure ad libitum access during the same period. On d 0, steers were loaded onto a commercial livestock trailer and transported for approximately 350 km over a 6 h period. However, steers remained in the truck for a total of 24 h before unloaded into a commercial feedlot (d 1), where steers were maintained in a single pen, managed similarly, and received a diet not containing PF or SF. Forage DMI was evaluated daily from d −30 to d −1. Shrunk BW was collected on d −33 and 1 for ADG calculation. Blood samples were collected on d 0, 1, and 3, and analyzed for plasma concentrations of interleukin 1 and 6, tumor necrosis factor (TNF)-α, haptoglobin, ceruloplasmin, cortisol, and fatty acids. No treatment effects were detected for ADG ($P = 0.54$) or F:G ($P = 0.56$). During the study, DMI was often reduced for PF steers compared with CO and SF (treatment × day interaction; $P < 0.01$). Concentrations of PUFA were greater in PF steers compared with CO and SF before and after transportation (treatment × day interaction $P < 0.01$). Following transportation, concentration of TNF-α increased for CO, did not change for SF, but decreased for PF steers (treatment × day interaction, $P < 0.01$). In conclusion, PUFA supplementation during preconditioning had detrimental effects on DMI, but did not impair ADG and reduced plasma concentrations of TNF-α following transportation and feedlot entry.

Key Words: polyunsaturated fatty acids, transportation, beef steers

390 Effect of feeding polyphenols from pomegranate extract on health, growth, nutrient digestion, and immunocompetence of calves. M. C. Perdomo*[1], R. A. Oliveira[1], C. D. Narciso[1], R. S. Bisinotto[1], M. A. Ballou[2], M. Dreher[3], and J. E. P. Santos[1], [1]*University of Florida*, *Gainesville,* [2]*Texas Tech University*, *Lubbock,* [3]*POM Wondersull*, *Los Angeles, CA*.

Objectives were to evaluate the effects of feeding pomegranate extract (POMx) rich in polyphenols on performance, health, nutrient digestion, and immunocompetence of calves. Holstein calves (n = 67), at 2 ± 1 d of age were randomly assigned to 0 (control), 5 (POMx5), or 10 g/d (POMx10) of POMx containing 16.9% gallic acid equivalent. Calves received colostrum in the first 24 h, pasteurized milk thereafter until d 61, and grain was fed ad libitum for the first 70 d of age. Calves were housed in individual hutches and grain intake, attitude and fecal scores, incidence and duration of health disorders, and health treatments cost were evaluated. Body weight (BW) was measured at 2, 30 and 70 d of age. Concentrations of glucose and 3-hydroxybutyrate (BHBA) were measured in plasma. Nutrient digestion was measured using total fecal collection. Neutrophil phagocytic and killing activities and antibody response to ovalbumin were measured. Cytokine production by peripheral blood mononuclear cells was measured. Feeding POMx had no effect on intake or BW gain in the first 30 d of age, but grain intake and BW gain reduced ($P < 0.05$) with increasing addition of POMx after d 30, which resulted in calves that were 1.8 and 4.3 kg lighter at 70 d of age for POMx5 and POMx10, respectively, compared with controls. Feeding POMx did not influence DM, organic matter or starch digestibility, but it reduced ($P < 0.01$) protein and tended ($P = 0.06$) to affect fat digestion. Plasma concentrations of glucose and BHBA, attitude and fecal scores, rectal temperature, incidence of fever, health treatment cost, neutrophil phagocytic and killing activities did not differ among treatments. Feeding POMx increased ($P < 0.05$) interferon-γ, interleukin-4, and IgG to ovalbumin vaccination. These results suggest that feeding POMx top dressed onto the grain suppresses grain intake and digestibility of protein. Nevertheless, POMx enhanced mitogen-induced cytokine production and response to vaccination which might benefit immune competence of calves and potentially health.

Key Words: calf, polyphenols, pomegranate

391 Effect of high-protein milk replacer followed by high-protein starter on transcript profiles in ruminal tissue of Holstein bull calves. A. Naeem*, J. K. Drackley, J. Stamey, S. L. Rodriguez-Zas, R. E. Everts, H. A. Lewin, and J. J. Loor, *University of Illinois*, *Urbana*.

The calf must be adapted to its nutrition from milk or milk replacer to make the metabolic, nutritional, and behavioral changes to become a functional ruminant in a period of 6 to 8 wk after birth. Objective of this study was to evaluate ruminal epithelium transcriptomics in response to high-protein/low-fat milk replacer followed by high-protein starter for 10 wk. From 3 through 42 d of life, male Holstein calves were fed reconstituted control milk replacer (20% CP, 20% fat; 0.567 kg solids/calf) or a high-protein/low-fat milk replacer (28.5% CP, 15% fat; at ca. 2% of body weight). All calves were weaned on d 43. Calves in the control group were then fed a control starter containing 16% CP through d 70 of life. In contrast, calves in the high-protein/low-fat group were fed a starter containing 22% CP through d 70 of life. Groups of calves in control and high-protein/low-fat treatments were harvested after 43 (wk 5) and 71 d (wk 10) of feeding. Ruminal epithelium samples harvested from 5 animals in each group at each time point were used for transcript profiling using a 13,257 bovine oligonucleotide (70-mers) array. Preliminary ANOVA of wk 10 data revealed 75 differentially expressed genes (DEG, $P < 0.01$) due to diet. Among DEG, the most enriched biological functions were cellular process (n = 34) and regulation of biological process (n = 17). In addition, genes with a 2-fold change between treatments were related to physiological processes including protein degradation (e.g., PGA3, pepsinogen 3, group I A) and growth (e.g., RDH10, retinol dehydrogenase 10). Preliminary results show that feeding a high-protein/low-fat milk replacer followed by a high-protein starter caused alterations in ruminal epithelium gene expression profiles.

Key Words: transcriptomics, development, metabolism

392 Field evaluation of the effects of free-access feeding of acidified milk replacer on the growth performance of dairy replacement heifers and veal calves. C. G. Todd*[1], K. E. Leslie[1], S. T. Millman[2], T. J. DeVries[3], N. G. Anderson[4], and J. M. Sargeant[1], [1]*Department of Population Medicine, University of Guelph*, *Guelph, Ontario, Canada*, [2]*Veterinary Diagnostic and Production Animal Medicine, Biomedical Sciences, Iowa State University*, *Ames,* [3]*Department of Animal and Poultry Science, University of Guelph, Kemptville Campus*, *Kemptville, Ontario, Canada*, [4]*Ontario Ministry of Agriculture, Food and Rural Affairs*, *Elora, Ontario, Canada*.

The objective of this research was to determine the effects of free-access feeding of acidified milk replacer on pre and post-weaning growth of Holstein replacement heifers and veal calves. The study was conducted at a commercial dairy operation in central Ontario. Heifer calves were reared as replacement animals and male calves were marketed as grain-fed veal. Calves (n = 495) were randomly assigned at birth to 1 of 2 milk feeding programs: free-access (ad libitum) feeding of acidified milk replacer (ACID, n = 250) or conventional (3 L fed twice daily) feeding of milk replacer (CONV, n = 245). Calves were fed milk replacer containing 24% crude protein and 18% fat. Formic acid was used to acidify the milk replacer for the ACID treatment. The target pH for acidified milk replacer was between 4.0 and 4.5. Calves were gradually weaned from milk replacer at approximately 6 weeks of age (mean ± SD: 41.1 ± 7.7 d of age). Body weight, hip width, hip height, body length and heart girth were measured at birth and weaning. A post-weaning body weight measurement was also collected for each calf (mean ± SD for heifer calves: 283.3 ± 57.2 d of age; mean ± SD for veal calves: 235.0 ± 25.1 d of age). There was no difference between the ACID and CONV calves for any of the measurements collected at birth. The ACID calves had significantly higher pre-weaning body weight gain compared with the CONV calves (28.2 vs. 21.2 kg, SE = 0.9, $P < 0.05$), as well as greater change in hip width (3.6 vs. 2.5 cm, SE = 0.1, $P < 0.05$), hip height (8.5 vs. 7.0 cm, SE = 0.4, $P < 0.05$), body length (11.9 vs. 9.5 cm, SE = 0.7, $P < 0.05$) and heart girth (12.4 vs. 9.8 cm, SE = 0.4, $P < 0.05$). The ACID and CONV calves did not differ for post-weaning weight gain (heifer calves: 224.7 vs. 226.8 kg, SE = 6.0, $P > 0.05$, respectively; veal calves: 257.1 vs. 257.2, SE = 2.0, $P > 0.05$, respectively). These results indicate that free-access feeding of acidified milk replacer supports improved body weight gain and structural growth during the pre-weaning period, but does not affect post-weaning weight gain.

Key Words: milk replacer, free-access feeding, acidification

393 Comparison of raw colostrum, colostrum replacer, and pasteurized colostrum on IgG, growth, and health of dairy calves. C.

L. Wilson* and L. E. Davis Rincker, *Eastern Kentucky University*, *Richmond*.

Colostrum consumption is key to the health and survival of dairy calves. However, feeding raw colostrum can spread disease from dam to calf. Pasteurized colostrum and colostrum replacer can be used when disease spread is a concern. A direct comparison between pasteurized colostrum and colostrum replacer is lacking. The primary objective was to determine serum immunoglobulin G (IgG) concentration of calves fed colostrum replacer (CR, 150 g globulin protein/dose), pasteurized colostrum (PC), and raw colostrum (RC). Other objectives were to evaluate intake, growth, feed efficiency, and health of calves. Male and female dairy calves born at Eastern Kentucky University Stateland Dairy Center were randomly assigned to 1 of 3 treatments (n = 11/trt): RC, PC, or CR and fed their respective treatment twice (1.89 L/feeding) on d 1 of life. Calvings were monitored so that calves did not suckle the dam. High quality (green) colostrum, as measured by a colostrometer, was pooled for the RC and PC treatment. Blood was collected before colostrum feeding and again between 46 and 60 h for analysis of serum IgG. Calves were raised similarly after 1 d of age and data was collected until weaning at 7 wk of age. Statistical analysis used the GLM procedure of SAS. Calves fed RC or PC had greater concentrations of serum IgG than CR ($P < 0.01$), but no difference existed between RC and PC. Average fecal scores and rectal temperatures taken daily during the first 2 wk of age were not different. Total intake of starter and milk replacer, initial and final growth parameters, feed efficiency, and average daily gain were not different. No major health challenges were noted in these calves. It is possible that if CR calves had been exposed to major illneses, health and growth parameters may have been compromised due to low immunity. Results indicate that if properly pasteurized, PC does not compromise immunity, health or growth parameters.

Key Words: colostrum, calf, immunoglobulin

394 Effect of the ingredients on acid binding capacity and ph of calves starter ration. Y. Tu*[1], Q. Y. Diao[1], S. S. Feng[2], Y. Zhou[1], and Q. Yun[1], [1]*Feed Research Institute of Chinese Academy of Agricultural Sciences*, *Beijing, China*, [2]*Beijing University of Agriculture*, *Beijing, China*.

This experiment was conducted to study on the effects of the ingredients and its acid binding capacity (ABC) or pH on the ABC or pH of calves starter ration. Nine feed raw ingredients (5–7 samples each) including corn, wheat bran, soybean meal, whey powder, $CaHPO_4$, limestone, salt, mineral premix and vitamin premix, which were ordinarily used in the northern China, were mixed with calves starter rations based on $L_{27}(3^{13})$ orthogonal test table. The ABC and pH of the ingredients and starter rations were determined, and then multiple regression method was used to analyze the data. The results showed that, 1) the ABC of limestone was highest (2040.00), while that of salt was lowest (0.40). The order of ABC from high to low was soybean meal, wheat bran, corn in plant feed ingredients, which were 47.82 ± 4.51, 27.31 ± 3.47, 7.11 ± 0.54, respectively; 2) The pH of minerals were alkaline, and that of corn, wheat bran and soybean meal were 5.79 ± 0.23, 5.65 ± 0.20 and 5.92 ± 0.11, respectively; 3) All the ingredients had significant effect on the ABC and pH of starter ration ($P < 0.05$). 4) When the ABC of starters was Y_1(mmol/100 g), pH of starters were Y_2(mmol/100 g), and the proportions in starter and ABC of soybean meal, wheat bran, whey powder, $CaHPO_4$, limestone, salt, vitamin premix, corn were X_1-X_8 (%) and a_1-a_8(mmol/100 g), respectively, the regression equation $Y = f(a_iX_i)$ was: $Y_1 = 1.0944a_1X_1+0.4817a_2X_2+ 1.2354a_3X_3-0.1568a_4X_4+ 0.1136a_5X_5+ 62.5969a_6X_6+ 60.2618a_7X_7+ 0.9150a_8X_8$($S_{Y.X}$ = 1.85603,R^2 = 0.9945, $P < 0.0001$); $Y_2 = 1.0792b_1X_1+ 0.9830b_2X_2+ 0.7687b_3X_3+ 1.0101b_4X_4+ 0.8997b_5X_5-0.3266b_6X_6- 27.0485b_7X_7+ 1.0142b_8X_8$($S_{Y.X}$ = 0.05691, R^2 = 0.9999, $P < 0.0001$). These results indicate that in the range of the experiment design, the suitable content of ingredients in calves starter ration were: soybean meal ≤20%, wheat bran 0–10%, whey powder ≤20%, CaHPO4 ≤2%, limestone ≤2%, salt 0–1.0%, vitamin premix 0–0.04%. There were significant multiple linear correlation between the ABC or pH of calves starter ration and content, ABC or pH of ingredients.

Key Words: calves starter ration, acid-binding capacity and pH, mathematical model

395 Study on in vitro evaluation of acidifier and its effect on growth in calves fed milk replacer. Y. Tu*, Y. Zhou, Q. Yun, Y. Q. Fu, and Q. Y. Diao, *Feed Research Institute of Chinese Academy of Agricultural Sciences*, *Beijing, China*.

This experiment was conducted to study on the in vitro evaluation method of acidifiers in calves milk replacer, and then validated the effect of the acidifier in calves using feeding trials. In the in vitro test, antibacterial activity in vitro (Y1), pH of 1% acidifier solution (Y2), buffering capacity of 1% acidifier solution (Y3), volume of acidifier solution to reduce the pH of milk replacer solution from 6.3 to 5.0 (Y4) and buffering capacity of milk replacer solution added acidifier (Y5) were chosen as the indices to evaluate the effect of the tested acids including formic acid, acetic acid, citric acid, fumaric acid, lactic acid and hydrochloric acid. Eighteen and 12 healthy neonatal Chinese Holstein male calves were assigned randomly to Treatment A1, A2, A3 in trial A and Treatment B1, B2 in trial B, respectively, and each treatment had 6 calves. The pH of milk replacer solution were reduced by hydrochloric acid from 6.3 to 5.5 or 5.0 in Treatment A1 or A2, respectively, and was reduced by formic acid from 6.3 to 5.0 in Treatment B2. Body weight, feed efficiency and the incidence of diarrhea were determined. The results indicated that, in the in vitro test, Y1 were highest when hydrochloric acid (95.12%) or formic acid (94.19%) was used, Y2 was lowest in hydrochloric acid solution, Y3 was best in hydrochloric acid solution, Y4 was least when formic acid solution used, and Y5 was best in acetic acid solution. So formic acid and hydrochloric acid were selected to be the acidifier in calf milk replacer. In the feed trails, comparing with that in Treatment A1, ADG improved 5.2% and 12.1% in Treatment A2 and A3. The incidence of diarrhea was 9.7% in Treatment A3, which decreased by 29.7% comparing with the 13.8% in Treatment A1. ADG of calves was significantly higher in Treatment B2 than that in Treatment B1 ($P < 0.05$), the incidence of diarrhea decreased by 37.5% in Treatment B2 (16.2%) than that in Treatment B1 (25.9%). It is concluded that, the growth performance of calves may be improved by using hydrochloric acid or formic acid as acidifier in milk replacer, and the in vitro evaluation method of acidifier was viable.

Key Words: calf milk replacer, acidifier, in vitro evaluation

396 Simulated straw bedding intake and effect of high and low cereal grain starters on rumen development of neonatal Holstein calves. W. B. Fokkink*[1], T. M. Hill[1], H. G. Bateman II[1], J. M. Aldrich[1], R. L. Schlotterbeck[1], and A. F. Kertz[2], [1]*Nurture Calf Research, Provimi North America*, *Lewisburg, OH,* [2]*ANDHIL, LLC*, *St. Louis, MO*.

Our hypothesis was that simulated straw bedding intake would be minor and that calves fed a texturized high cereal grain starter (TEX) would have greater rumen papillae development than calves fed a fine particle, pelleted, low cereal grain starter (PEL). Male Holstein calves (initially 45 ± 1.1 kg BW, 2 d of age; 4 calves/treatment) were fed TEX or PEL and long-stem wheat straw over a 56-d trial. Starter TEX contained

37% whole corn, 25% whole oats, 35% supplement pellets (containing 68% soybean meal, 16% wheat middlings, and 16% other ingredients) and 3% molasses. Starter PEL contained 43% dried distillers grains, 26% wheat middlings, 15% soybean hulls, 10% fine rolled corn, and 6% other ingredients. Starters contained equal concentrations of CP (20% DM basis), Ca, P, and salt. Calves were fed a 27% CP, 17% fat milk replacer at 0.66 kg DM daily and weaned at 35 d. Calves were fed wheat straw, starter, and water ad libitum and housed in individual pens with geotextile fabric over rock as flooring with no bedding. After sacrifice on d 56, gastro intestinal tracts were divided at the pyloric sphincter (stomach and intestine sections) and weighed. Rumen wall and rumen papillae samples were measured. Data were analyzed as a completely randomized design. Straw intake averaged 7 g/calf daily or 0.8% of total intake, and did not differ by starter type. Calves fed TEX had greater final BW and greater ADG than calves fed PEL. Empty stomach weight was greater for calves fed TEX. Intestine and digesta weights were lower and stomach and intestine plus digesta weights were lower for calves fed TEX vs. PEL. Rumen papillae length was greater for calves fed TEX vs. PEL. Feeding a texturized high cereal grain diet developed rumen papillae better and contributed to less stomach, intestine, and digesta as a percent of BW than feeding a fine particle, pelleted low cereal grain diet.

Key Words: calf, rumen, starters

397 Growth and health of calves pre- and post-weaning fed milk replacers with differing levels of neomycin sulfate and oxytetracycline. N. B. Litherland*[1], B. Ziegler[2], D. Schimek[2], D. Carlson[3], D. Ziegler[4], M. L. Raeth-Knight[1], G. G. Golombeski[1], H. Chester-Jones[4], and J. G. Linn[1], [1]*University of Minnesota*, *St Paul,* [2]*Hubbard Feeds Inc.*, *Mankato, MN,* [3]*Milk Products Inc.*, *Chilton, WI,* [4]*University of Minnesota Southern Research and Outreach Center*, *Waseca*.

New regulations for the use of medicated milk replacers (MR) containing neomycin sulfate (NEO) and oxytetracycline (OXY) have resulted in a need to explore the effects of amount and duration of antibiotic feeding on calf growth and health. Previous work by our group showed removal of antibiotics from MR at 14 d reduced growth compared with feeding antibiotics through 42 d. The aims of this study were to evaluate growth and health of calves fed MR containing varying amounts of antibiotics for 0, 14, 26, or 42 d. Holstein heifer calves (n = 100, 2 to 4 d of age) were assigned randomly to 1 of 4 MR programs. All calves were fed 20% CP, 20% fat MR at 0.57 kg/d (as-fed powder weight) from d 1–35 and 0.28 kg/d from d 36–42. Four different antibiotic amounts and durations were included in the above MR to yield 4 treatments; TRT1 - 400 g NEO/200 g OXY per ton of MR on d 1–42; TRT2 - 0 g NEO/0g OXY per ton of MR on d 1–42; TRT3 - 1600 g NT/1600 g OXY per ton of MR on d 1–14; TRT4 - 1600 g NEO/1600 g OXY per ton of MR on d 1–14 and d 16- 28. Calves were fed MR twice daily from d 1–35, and once daily from d 36–42. An 18% CP (as-fed) texturized calf starter was offered free choice along with water throughout the study. Calves were housed in individual pens within a naturally ventilated barn. Average daily gain and total body weight gain was lower ($P < 0.05$) for TRT2 when compared with TRT1 and TRT4. Total starter intake and total dry matter intake was lower ($P < 0.05$) for TRT 2 compared with TRT1 and TRT 4 through 42 d of age. Dry matter required for gain was higher ($P < 0.05$) for TRT2 compared with all other treatments. Fecal scores were not different and averaged 1.3 across treatments. Scouring days (fecal score of 4) were significantly higher ($P < 0.05$) for TRT 2 compared with TRT 4 through d 42. Calves fed increasing amounts and duration of NT and OT grew more efficiently, ate more starter, and had fewer days scouring than calves fed no antibiotics. The future of antibiotic use in calf MR is unclear. Non-medicated MR additives that promote growth and health should be explored.

Key Words: dairy calf, neomycin sulfate, oxytetracycline

398 Meta-analysis for designing an empirical model to predict growth of neonatal Holstein calves through eight weeks of age. H. G. Bateman II*[1], T. M. Hill[1], J. M. Aldrich[1], R. L. Schlotterbeck[1], and J. L. Firkins[2], [1]*Nurture Research Center, Provimi North America*, *Lewisburg, OH,* [2]*The Ohio State University*, *Columbus*.

A data set was constructed from individual animal means gathered in the Nurture Research Center (a curtain-sided, naturally ventilated nursery) and used in a meta-analysis to parameterize an empirical model predicting growth measures. This data set contained 993 observations from 20 research trials in all seasons. Growth measures gathered included average daily gain (ADG) pre-weaning, post-weaning, and through 8 weeks of age. Independent variables gathered included: age at weaning (WEAN), total starter intake (SI), total milk replacer intake (MRI), milk replacer CP % (MRCP) and fat % (MRfat) contents, number of days with abnormal fecal scores (AFS), average environmental temperature pre-weaning (temp-pre), post-weaning (temp-post), and through 8 weeks of age (temp-all), minimum (mintemp) and maximum (maxtemp) during the entire 8 weeks, BW at d 0 (BW0), and initial serum protein concentration (SERP). Additionally the interactions of SI, MRI, and MRCP and MRfat were considered for the model. Backward elimination multiple regressions were conducted using a mixed model with a random effect of trial. Terms least probable to differ from zero were removed sequentially from the model except that when interactions terms appeared in the model their constituent terms remained regardless of level of significance. When all terms were significant at $P < 0.05$ variance inflation factor (VIF) was calculated. If VIF was greater than 100 the term with the lowest probability of being different from zero was removed until the VIF was 100 or less. The final model for total ADG indicated that increasing SI or MRI improves calf growth. Also increasing MRCP increased growth but increasing MRfat depressed growth due to the interactions among SI, MRI, and MRfat. Growth of neonatal dairy calves appears more controlled by nutrient intake and their interactions than surrogates for health status of the calves (AFS and SERP) or environmental temperature.

Key Words: calf, growth, meta analysis

399 Effect of different fiber sources on performance and feed intake of Holstein calves. L. Castells*[1], A. Bach[1,2], and M. Terré[1], [1]*Department of Ruminant Production, IRTA*, *Caldes de Montbui, Spain*, [2]*ICREA*, *Barcelona, Spain*.

The objective of this study was to evaluate the effect of different fiber sources on performance and feed intake of Holstein calves. Sixty Holstein male calves (initial BW = 43.9 ± 5.86 kg) were randomly assigned to one of 3 different dietary treatments that consisted on a common starter plus alfalfa hay (A), rye-grass (R), and no access to forage (C). All calves were offered 2 L of milk replacer (MR) at 12.5% DM twice daily via a bottle until 50 d of age, and then only one daily dose of 2 L of MR at 12.5% DM during the week before weaning (57 d of age). Starter, MR, and forage intakes were recorded daily and BW was recorded weekly. Calves were individually housed using wood shavings as bedding material. Intake data were transformed using square root to achieve a normal distribution and were analyzed using a mixed-effects model with repeated measures that included initial BW as a covariate, and dietary treatment, week of study and their 2-way interaction as fixed effects, and the animal as a random effect. Starter

intake tended to be greater ($P = 0.05$) in R (1.2 ± 0.03 kg/d) than in A calves (0.9 ± 0.03 kg/d), but no differences were observed between C calves (1.0 ± 0.03 kg/d) and the other 2 treatments. Forage intake was greater ($P < 0.05$) in A (144 ± 0.26 g/d) than in R calves (59 ± 0.26 g/d) . Total dry matter intake (DMI) tended to be greater ($P = 0.10$) in R (1.7 ± 0.03 kg/d) than in C (1.4 ± 0.03 kg/d) and A calves (1.5 ± 0.03 kg/d). No differences were observed among treatments on ADG and feed efficiency. Offering forages to calves does not compromise total DMI, and it may foster consumption of starter, especially when the forage offered is rye-grass.

Key Words: forage, calves, performance

400 Effect of housing and management on dairy calves less than two months of age. T. M. Hill*, H. G. Bateman II, J. M. Aldrich, R. L. Schlotterbeck, D. L. Carr, and A. B. Chestnut, *Nurture Research Center, Provimi North America*, *Lewisburg, OH*.

Housing (hutches, naturally ventilated nursery), bedding (straw, sand), and summer cooling with fans were management conditions evaluated in 3 trials. Holstein calves (42 ± 2 kg BW) initially 2 to 4 d of age were managed at the Nurture Research Center in southwest Ohio. Calves were fed milk replacer (27% CP, 17% fat fed at 0.657 kg DM per calf daily), starter (20% CP DM, textured, fed free-choice), and water (free-choice). Measurements were for 56 d. In Trial 1, 28 calves per treatment were bedded with straw and housed either in poly hutches or wire mesh nursery pens. This trial was conducted from September to March. The average temperature was 8°C and ranged from −17 to 31°C. In Trial 2, 16 calves per treatment were managed in wire mesh nursery pens bedded with straw, in nursery pens bedded with sand, or in poly hutches bedded with sand. This trial was conducted from May to September. The average temperature was 21°C and ranged from 7 to 33°C. In Trial 3, 26 calves per treatment were housed in wire mesh nursery pens and bedded with straw with or without supplemental cooling with fans between 8AM and 5 p.m. This trial was conducted from May to September. The average temperature was 22°C and ranged from 8 to 34°C. Data were analyzed by trial as completely randomized block designs with calf as the experimental unit. Differences were declared at $P < 0.05$. In Trial 1, daily gain of calves in nursery pens was 7% greater than that of calves in hutches. In Trial 2, daily gain and starter intake of calves in the nursery with straw bedding were greater and scouring was less than calves bedded with sand in the nursery or hutches. In Trial 3, daily gain, feed efficiency, and hip width change were greater and breaths per minute were less for calves cooled with fans than calves that were not cooled. Straw bedding was preferred to sand, nursery pens were preferred to hutches, and summer daytime cooling with fans was preferred to no cooling.

Key Words: bedding, temperature, cooling

401 The effect of oral supplementation of selenium on passive transfer of immunoglobulins in dairy calves. B. Nelson*[1], S. M. Godden[2], B. W. McBride[1], T. F. Duffield[1], and K. E. Leslie[1], [1]*Department of Population Medicine, University of Guelph*, *Guelph, ON, Canada*, [2]*Department of Veterinary Population Medicine, University of Minnesota*, *St. Paul*.

The objective of this study was to evaluate the effects of oral selenium supplementation by the addition of sodium selenite to colostrum or colostrum replacer, on the success of passive transfer of immunoglobulin G (IgG) and on whole blood selenium status. During the summer of 2008, a total of 122 Holstein calves were enrolled at the Transition Management Facility, Emerald, Wisconsin. Calves were randomly assigned to receive either colostrum from their dam, or a commercially available colostrum replacer product. Calves were further randomized to receive selenium (sodium selenite) or placebo added to their respective colostrum treatments, at a concentration of 3 ppm. Blood samples were collected from every calf at birth, before feeding of colostrum, and again 24 h following feeding of colostrum. Whole blood samples were analyzed for selenium concentration using a fluorometric method. Serum samples were analyzed for IgG concentration using a radial-immunodiffusion assay. Statistical analysis was conducted using linear regression techniques in STATA. Calves that received colostrum or colostrum replacer with selenium had significantly increased whole blood selenium concentrations compared with placebo calves (μg/mL: 0.31; 0.22 ; $P < 0.001$). Calves fed colostrum from their dam had significantly higher serum IgG concentrations 24 h following colostrum feeding than calves fed the colostrum replacer product (g/L: 35.95; 17.6 ; $P < 0.001$). There were no significant differences in serum IgG at 24 h between calves fed maternal colostrum with or without selenium supplementation and calves fed colostrum replacer with or without selenium supplementation (g/L; 36.02, 35.87; 18.72, 16.58, respectively). From the results of this study, selenium supplementation of colostrum or colostrum replacer for improvement of passive transfer of IgG is not warranted.

Key Words: selenium, colostrum, passive transfer

402 Effects of endophyte-infected fescue seed on physiological parameters of mature female meat goats. A. R. Boyer*[1], T. L. Mays[1], G. W. Webb[1], M. A. Brown[2], and E. L. Walker[1], [1]*Missouri State University*, *Springfield,* [2]*USDA Grazinglands Research Center*, *El Reno, OK.*

The objectives of the study were to determine if consumption of endophyte-infected (E+) fescue seed would affect thermoregulation and DMI in mature female goats. During a 4 wk study, a total of 18 goats (Boer type) were assigned to treatments (n = 6 per treatment); endophyte-free KY-31 (E-), endophyte-free STF-43 (E43-), or E+ seed. Goats were fed a ration consisting of a 2:1:1 ratio of alfalfa pellets, a commercial sweet feed, and 1 of 3 types of fescue seed. All goats were fed 2% of BW, and orts were collected and weighed daily on a DM basis. At the initiation of the study, age and BCS were recorded. Temperature loggers designed for intravaginal insertion were used and temperature (T) collected. Average temperatures for 0400, 1000, 1600, 2200 h were recorded. Urine, blood, and BW were collected weekly. Ergovaline levels in the urine increased after 1 wk on treatment ($P \leq 0.03$). Dry matter intake was affected by age ($P \leq 0.01$). A treatment × week interaction ($P \leq 0.05$) occurred in wk 1 of the study, with E43- having greater DMI than E-, and E+ being intermediate. Seed intake was affected ($P \leq 0.02$) in E+ throughout the study and in E- wk 1 and 4 of study. Treatment ($P \leq 0.03$), treatment × week ($P \leq 0.01$), and age ($P \leq 0.007$) also had an effect on seed intake for E+ and E- treatments. Intake of alfalfa pellets and sweet feed did not differ ($P \leq 0.56$) among treatments. No difference in ADG among treatments ($P \leq 0.22$) occurred. A date affect on T occurred at 1600 h ($P \leq 0.002$) in E- and E43- treatments and at 2200 h ($P \leq 0.0003$) in E- and E+ treatments. At 0400 h, E43- maintained a greater T than other treatment groups ($P \leq 0.03$). At 1000 h, there was a treatment × week interaction ($P \leq 0.01$) and E43-maintained a greater ($P \leq 0.06$) T than the other treatments. Treatment affected DMI, seed intake, T, and urine concentrations of ergovaline. However, goats may handle ergovaline differently than other species and more research is required to evaluate these potential differences.

Key Words: endophyte, goat, intake

403 The effects of protein supplement on leptin concentrations in lambs and meat goat kids grazing bermudagrass pastures in central Oklahoma. E. L. Walker*[1], S. A. Nusz[2], D. H. Keisler[3], and M. A. Brown[4], [1]*Missouri State University*, *Springfield,* [2]*Redlands Community College*, *El Reno, OK,* [3]*University of Missouri*, *Columbia,* [4]*USDA Grazinglangs Research Center*, *El Reno, OK*.

Lambs and kids weaned and pastured on bermudagrass (BG; *Cynodon dactylon*) may not receive enough protein to reach maximal growth during mid to late summer when protein in BG declines. Leptin is an adipocyte-derived hormone that increases as body condition increases and is involved in body temperature regulation. Our objective was to determine the affects of protein supplementation on leptin status in lambs and meat goat kids grazing on summer BG pastures. In 2007, 10 Boer type (BT) and 13 Spanish × Savanna (ST) kids (start bw = 14 ± 5 kg) and 23 Katahdin (KK), 14 Katahdin × Suffolk (KS), 14 Suffolk × Katahdin (SK), and 21 Suffolk (SS) lambs (start bw = 30 ± 5 kg; start age for sheep and goats = 100 ± 10 d) were used. In 2008, 27 BT and 28 ST kids (start bw = 18.8 ± 0.6 kg) and 11 KK, 15 KS, 21 SK, and 25 SS lambs (start bw = 25.8 ± 0.7 kg; start age for sheep and goats = 100 ± 5 d) were used. Animals were allotted by weight, breed, and gender to one of 2 treatments: 1.22 ha of BG with no protein supplement (NP; n = 2) or with 21% molasses-based protein blocks (PT, n = 2). Animals were weighed and blood samples collected every 2 weeks. Data were analyzed using proc mixed as a split plot design and the analysis included the fixed affects of treatment, species, breed nested within species, gender, and all possible interactions. In 2007, serum concentrations of leptin did not differ by treatment ($P = 0.94$) or between species ($P = 0.60$) or gender ($P = 0.29$). There was a breed within species interaction ($P = 0.01$). Serum leptin values tended to decline from June to August ($P = 0.10$). In 2008, serum leptin tended to be greater in PT than NP animals ($P = 0.08$) and greater in kids than lambs ($P \leq 0.001$). No breed within species interaction was observed ($P = 0.49$) nor did gender affect serum leptin ($P = 0.33$). There was a strong association between date and serum leptin concentrations ($P \leq 0.001$) and there was a breed by date within species interaction ($P = 0.009$). In both trials, serum leptin values declined from June to August as forage quality decreased throughout the summer.

Key Words: kids, lambs, leptin

404 Factors affecting birth, 60-day, and weaning body weights of commercial meat goat kids born in two different seasons. K. Andries* and E. Sherrow, *Kentucky State University*, *Frankfort*.

Little information is available on the impact of season of kidding on growth and performance of meat goat kids. However, seasonal market trends have many producers kidding in the late fall and winter. Because of this, a study was designed to evaluate kid performance using 2 kidding seasons. The objectives of the study were to evaluate kid growth from birth to weaning by comparing birth, 60 d, and weaning BW; rate of gain to weaning; and kid survival to weaning in 2 alternative kidding seasons. Five hundred and 40 3 Boer sired commercial meat goat kids born in either fall (October, November, and December) or spring (March, April, and May) of 2005 through 2007 were available for this study. Data collected included, birth type; sex; and birth, 60 d, and weaning weight. Data was analyzed using Proc Mixed in SAS. Season of birth had a significant effect on birth and weaning weight, and ADG between 60 d and weaning. Birth type was significant for all traits except ADG between 60 d and weaning. Single born kids were heavier at birth than twin or triplet born kids (3.91, 3.47, 3.20 kg, respectively). Spring born kids were lighter than fall born kids at birth and weaning (3.37 vs. 3.68 kg for birth and 16.86 vs. 18.09 kg for weaning, respectively). Fall born kids gained faster between 60 d and weaning (170 vs. 130 g/d, respectively). The interaction between year and birth type was significant for birth weight and the sex by birth type interaction was significant for 60 d weight and ADG to 60 d. Season of birth did not have an effect ($P = 0.105$) on survival to weaning, however type of birth was significant ($P < 0.001$) for survival. Single born kids were more likely to survive to weaning than all other birth types. Twin born kids were second most likely to survive and triplet and quadruples were similar in survival to weaning. This project indicates that season of birth and birth type have an effect on performance for meat goat kids.

Key Words: meat goat, preweaning growth, season of birth

405 Relationship between body measurements and milk yield and a method to predict the milk production of Saanen goats. S. Dikmen*, A. Orman, H. Üstüner, and M. M. Ogan, *University of Uludag*, *Bursa, Turkey*.

Type traits are functional traits in dairy goats and have an indirect effect on production. Because of moderate to high heritability of these traits, they are valuable tool in breeding program of dairy cattle. In dairy cattle these measurements are used for prediction of some production traits. Despite the wide use of evaluations for type in goats, little is known about the association between body conformation and production traits. The objective of this study was to investigate the relationship between body measurements and milk yield in Turkish Saanen goats and to develop a method to predict the lactation milk yield. A total of 40 goats were used for this study. Body condition score (BCS), live weight (LW) and a total of 24 body measurements were recorded 7 d after birth. Milk yield was recorded fortnightly and 60, 90, 120, 150, 180, 210, 240 d and lactation milk yield (LM) were estimated using these records. Lactation milk yield was 689.8 ± 38.0 kg in 298.1 ± 2.3 d. The effects of birth month (February or March), birth type (single or twin), BCS, LW (kg), age (month), parity, DIM (day) and all interactions were investigated using PROC MIXED of SAS. The correlations between body measurements and milk yield were also determined. The effects of BCS ($P < 0.05$), LW ($P < 0.01$) and DIM ($P = 0.08$) on LM were found significant and these effects were determined as a base model for regression analysis. Afterward, LM corrected for age and stepwise regression analysis was used for identifying the most reliable model which has the highest determination coefficient degree ($r^2 = 0.45$) on age corrected LM (CLM) of Saanen goats. The prediction model of CLM was determined as; CLM = −460.5 + (−379.6 × BCS) + (51.9 × Chest depth) + (−21 × Abdomen depth) + (29.9 × Abdomen width) + (31.7 × Shoulder joint - tuber coxae angle) ($P < 0.001$). Based on these results, this equation could be used to predict the CLM of Saanen goats. However, more data are needed to increase the reliability of the model.

Key Words: milk yield, prediction, Saanen

406 Effects of prepubertal growth rate of dairy ewe lambs on their subsequent lamb and milk production. D. L. Thomas* and Y. M. Berger, *University of Wisconsin-Madison*, *Madison*.

A study was conducted at the Spooner Ag Research Station of UW-Madison with 252 dairy ewe lambs born from 2004 to 06 to determine if ad libitum feed intake during the prepubertal period would be detrimental to their subsequent production. The lambs were of East Friesian and/or Lacaune breeding. They were raised on milk replacer and a high concentrate ad libitum diet until 30 d of age. At 50 d of age, they were randomly assigned to 1 of 2 growth treatments: full (F) or restricted (R) feed. Both treatment groups were fed a 13% CP grain mix of whole shelled corn and a high protein pellet in straw-bedded pens. Full treatment lambs received as much of the grain mix as they could consume, and R lambs received ~70% of the average per head intake of the F lambs. Treatments continued for ~100 d until lambs were ~5 mo of age. Ewe lambs were mated to lamb first at ~1 yr of age, and lamb and milk production was recorded through 2008. At the end of the treatment period, R lambs were 6.5 kg lighter ($P < 0.05$) than F lambs. However, R lambs had greater ($P < 0.05$) ADG from the end of the treatment period to their first mating and from their first mating to their first lambing and were slightly heavier ($P < 0.10$) than F ewes at first lambing. Ewe fertility and litter size were very similar between the F and R ewes when lambing at 1 yr of age and at older ages. Lactation traits (lactation length; yield of milk, protein and fat; and % protein and fat) were not significantly different between treatments, but mean values were actually slightly higher for F ewes compared with R ewes for all lactation traits (e.g., +9.2 kg for lactation milk yield). There were no differences between treatments for the proportion of ewes remaining in the flock on June 30, 2009 or the average age at which ewes left the flock. The results of this study indicate no detrimental effects of ad libitum prepubertal feeding of dairy ewe lambs to 5 mo of age.

Key Words: lactation, prepubertal, sheep

407 Milk production and lamb growth of hair sheep weaned at 63 or 90 d of age in an accelerated lambing system in the tropics. R. W. Godfrey* and K. Facison, *University of the Virgin Islands*, *St Croix*.

This study was designed to evaluate the impact of weaning age on lamb and ewe productivity in an accelerated lambing system. During a fall and summer lambing, St. Croix White ewes (n = 19 and 22) and lambs (n = 30 and 34), and Dorper × St Croix White ewes (n = 18 and 27) and lambs (n = 31 and 39) were used. Lambs were assigned to be weaned at 63 (CTRL; n = 70) or 90 d of age (LATE; n = 64) based on breed, sex and litter size. In the summer 8 ewes/group were evaluated for milk production at 28, 63, 76 and 90 d postpartum (PP) using oxytocin and 4 h lamb removal. After weaning lambs were fed concentrate (2% BW/d) and grazed guinea grass. Ewes grazed guinea grass at all times. Weights were analyzed using breed and weaning age as main effects. Milk production was analyzed using breed, days PP and weaning age in a repeated measures model. Season was not significant for any trait so data were pooled. Ewe weight at breeding before the first lambing was the same ($P > 0.10$) as at the subsequent breeding (40.9 ± 1.1 vs. 41.9 ± 1.1 kg, respectively). At the start of the subsequent breeding 43% of LATE and 10% of CTRL ewes were nursing lambs ($P < 0.0004$). Pregnancy rate at the subsequent breeding, determined by ultrasound, was not different ($P > 0.10$) between LATE and CTRL ewes (97.4 vs. 97.8%, respectively). At weaning LATE lambs were heavier ($P < 0.0001$) than CTRL lambs (14.5 ± 0.4 vs. 11.2 ± 0.4 kg, respectively). There was no breed x weaning age interaction. At 90 d of age LATE and CTRL lambs had similar ($P > 0.10$) weights (14.5 ± 0.4 vs. 13.9 ± 0.4 kg, respectively). Milk production on d 63 was not different between breed or weaning age ($P > 0.10$). By d 76 and 90 milk production of LATE ewes had decreased to 84 ($P < 0.07$) and 66% ($P < 0.0002$) of d 28 levels. Weaning at 90 d of age can be done in an accelerated lambing system with no detrimental effect on ewe productivity. Late weaning led to a decrease in the amount of time that lambs received high cost, imported feed without a reduction in their growth. There is potential to have a positive impact on the economics of producing hair sheep in the tropics.

Key Words: hair sheep, weaning, milk production

408 Economic impacts of ram mating behavior. L. K. Gardiner*, B. S. Rashford, J. P. Hewlett, and B. M. Alexander, *University of Wyoming*, *Laramie*.

Little is known about producers' perceptions of ram performance and ranch-level economic impacts of improved ram management. This research combines a survey of Wyoming sheep producers and a partial budget analysis to better understand producers' perceptions and the economic consequences of ram performance. We used a modified Dillman sampling design with a stratified random sample based on flock size to collect survey data on Wyoming sheep producers. Five strata were defined according to the number of bred ewes owned: small operations (<30 ewes), small to medium (30–49 ewes), medium (50–99 ewes), medium to large (100–299 ewes), and large operations (>300 ewes). The National Agricultural Statistics Service administered the survey to assure a statistically valid stratified sample. The survey′s respondents represent approximately 40% of Wyoming sheep producers. The number of responses from each stratum is consistent with the actual distribution of sheep operations in Wyoming. Current ram management practices

and opinions about the importance of ram performance are included in the survey. Analysis of the data shows the majority of producers believe breeding competence is critical to flock productivity (56% of respondents strongly agree) and testing ram performance is important for profitability (45% of respondents strongly agree). Survey data suggests that producers may not be integrating beliefs into management. For example, 77% of the respondents listed age and not libido as the primary reason for culling rams. Less than 10% of respondents listed ram libido as an important criteria for ram selection. Budget analysis indicated smaller high-performing ram batteries may increase profits. Profit increases are sensitive to the cost of identifying ram performance, operation type, and the flow of genetic characteristics. Our results suggest a need for producer education and research concerning the economic impacts of ram performance.

Key Words: sheep, economics, libido

POSTER PRESENTATIONS

Animal Behavior and Well-Being: Swine and Poultry

T1 Recognition of maternal amniotic fluid by pre-weaning piglets. J. Figueroa*, D. Solà-Oriol, R. Davín, J. F. Pérez, and X. Manteca, *Universitat Autònoma de Barcelona*, *Bellaterra, Barcelona, Spain.*

Pigs have a very developed olfactory system that allows them to recognize cues from the environment within the first days after farrowing. Amniotic fluid is a cue that piglets use to recognize their own mother and guide them to this key resource post-natally. The aim of this study was to estimate if sucking piglets of different ages have the ability to discriminate between their own mother's amniotic fluids versus an alien one. Forty male/female pigs from 10 litters (4 piglets/litter) were used to test their attraction for 3 olfactory stimuli (triple-choice feeding test) using a Triple-U-Testing Arena (TUTA), located in an isolated room on d 4, 14 and 21 after farrowing. Olfactory tested cues included strips impregnated with their own maternal amniotic fluid (MAF), alien amniotic fluid (AAF) and water in the middle as a control. The position of MAF and AAF were rotated in each test. Piglets were tested in litter-pairs to avoid fear and distractive behaviors. Each test lasted 7 min, during which, the time spent by piglets in nasal contact with each strip was measured by direct observation. Data were analyzed using the GLM procedure of SAS. Latency time accounted to more than 6 min of the 7 min test. Older piglets became increasingly agitated, looking for alternative routes to escape and they also had more play and exploring behaviors at the TUTA. Piglets showed preferential responses toward MAF at d 4 (10.32 s/couple) and 14 (2.57 s/couple) as compared with AAF (4.75, $P < 0.01$ and 0.98, $P < 0.05$ s/couple) and water (0, $P < 0.01$ and 0.54, $P < 0.01$ s/couple). No differences were observed at d 21. These results show that piglets are able to discriminate between their mother′s amniotic fluid and amniotic fluid from other sows during their first weeks of life. This attraction might keep piglets protected near to the sow and also teach them to follow cues of maternal pregnancy feeding. Attraction for amniotic fluid begins to disappear as piglet needs and motivation changes with age.

Key Words: amniotic fluid, piglets, preference

T2 The effect of colostrum supplementation on piglets′ body temperature recovery and lactation performance. R. Muns*, J. L. Ruiz de la Torre, P. S. Agostini, X. Manteca, and J. Gasa, *SNiBA, Departament Ciència Animal i dels Aliments, Universitat Autònoma de Barcelona*, *Barcelona, Spain*.

The objective of this paper was to evaluate the effect of helping piglets′ colostrum intake on lactation performance. Fifteen Danbred sows from a commercial farm were distributed to 3 treatment groups based on BW, parity and back fat thickness 4 d before farrowing. After farrowing piglets with less than 1.250 kg BW (n = 56) were treated (T1: no intervention, n = 24; T-2: administration of manually milked sow's colostum (10 mL/animal), n = 18; T-3: single doses of a commercial product (Calostrene/ANIVET) fed on d 0, n = 14). All piglets (n = 172) were weighted on farrowing day (d 0), d 1 and d 21 of lactation; rectal temperature was measured at birth and d 1. Piglet mortality was also recorded. Data of treated piglets were analyzed using the GLM procedure of SAS with piglet being the experimental unit. Piglet′s initial BW did not differ statistically among groups (mean value of 1.028 g/piglet, $P = 0.9$). T2 piglets tended to show higher BW gain after 24h of birth than T1 piglets (78.7 vs. 44.9g ± 62.63; $P = 0.08$). Piglets rectal temperature at 24h of life was higher for T2 and T3 compared with T1 (38.8 and 39.1 vs. 38.2°C ± 0.73; $P < 0.05$). Compared with T1 (3.624g), treated piglets total weight gain from d 0 to d 21 were 8.5 and 14.9% numerically higher for T2 and T3, respectively ($P = 0.3$); meanwhile corresponding values for all piglets improved by 6.1% and 9.7% for T2 and T3, respectively, over a 4.158 g/piglet for T1 ($P = 0.3$). Although T-2 had the lowest numerical mortality (when considering all the piglets) during lactation compared with T-1 and T-3 (7.9 vs. 10.6 and 9.6%; $P = 0.9$) it did not differ statistically among groups. These results show the importance of guaranteeing the colostrum intake by small piglets during the first hours of life enhancing its body temperature recovery and tending to improve its weight gain during the first 24h of live.

Key Words: piglet, colostrum, body temperature

T3 Comparison of pig restraint and sampling methods on blood lactate concentration. B. Buzzard*[1], L. N. Edwards[1], R. D. Goodband[1], D. B. Anderson[2], T. E. Engle[2], and T. Grandin[2], [1]*Kansas State University*, *Manhattan,* [2]*Colorado State University*, *Fort Collins*.

The objective of the study was to examine the effects of restraint and blood sampling method on blood lactate concentration (LAC) in pigs. Restraint methods were snaring or restraint with sorting boards. Blood was sampled from 120 pigs (58 barrows, 62 gilts) at approximately 165 d of age (126.1 ± 2.9 kg) over 2 consecutive days. Each day, 30 pigs were sampled per method. All pigs were housed in one barn and pigs in adjacent pens were not sampled simultaneously. Snaring consisted of a trained handler snaring each pig while blood was collected via jugular venipuncture (approx. 7 mL). Restraint with sorting boards consisted of a trained handler restraining each pig with 2 sorting boards and the side of the pen to form a 3-sided barrier reducing pig movement. The distal ear vein was pricked with a 20-gauge needle to obtain several drops of blood for LAC analysis. LAC was measured using a hand-held lactate analyzer. The duration of restraint and a behavior score (1–4, 1 = no vocalization or movement and 4 = constant movement, vocalization and struggle) for each pig were recorded during sampling. LAC was compared between the 2 sampling methods and duration of restraint was used as a covariate in the analysis. Results indicated that pigs that were snared had greater ($P = 0.04$) LAC than pigs that were restrained using the sorting board method, 2.4 ± 0.1 and 2.1 ± 0.1 m*M* respectively. Both measurements of LAC were considerably lower than baseline LAC reported in published literature. There was a positive correlation (r = 0.42, $P = 0.001$) between duration and LAC for pigs that were restrained by snaring; the longer the restraint duration, the greater the LAC. Positive correlations were observed between duration and behavior score (r = 0.41, $P = 0.001$), duration and LAC (r = 0.64, $P < 0.001$) and behavior score and LAC (r = 0.26, $P = 0.05$) in pigs restrained with sorting boards. In the boarded group, longer durations and higher behavior scores were related to increased LAC. Restraint duration should be kept at a minimum when both methods are used.

The sorting board sampling method is a potential technique to use when sampling small quantities of blood in pigs.

Key Words: lactate, restraint, pig

T4 The effect of alleyway width on gestating sow welfare in a free-access stall system. L. A. Mack*[1], M. F. Elischer[1], S. D. Eicher[2], A. K. Johnson[3], D. C. Lay, Jr.[2], B. T. Richert[1], and E. A. Pajor[4], [1]*Purdue University*, *West Lafayette, IN*, [2]*LBRU, USDA-ARS*, *West Lafayette, IN*, [3]*Iowa State University*, *Ames*, [4]*University of Calgary*, *Calgary, AB, Canada*.

Free-access stalls allow sows to choose the protection of a stall or use of a shared alleyway. This study investigated the effect of alleyway width on production and physiological variables in gestating sows. At ~33 d of gestation, 21 sows (n = 168) were equally assigned to 1 of 3 pens that had 7 free-access stalls. Each pen had a shared alleyway of 0.91, 2.13, or 3.05 m wide. Sows were moved to farrowing ~5 d before expected farrowing date. Back fat (BF), BW, BCS, and lameness (LM) were measured on d 35, 65, and 101. Sows' body lesions were scored weekly. Blood samples were collected on d 30, 66, and 100. Data were analyzed in SAS using a mixed model with a post-hoc Tukey adjustment. Although similar basally, overall BF was greater in 0.91 m sows than 2.13 m sows ($P < 0.05$) and increased in all groups over time ($P < 0.05$). Sow BW increased over time ($P < 0.0001$) but did not differ by treatment. BCS showed no overall treatment or time differences, but on d 35 0.91 m sows had a higher BCS than 3.05 m sows ($P < 0.05$). Lameness increased slightly in 2.13 and 3.05 m sows immediately after mixing and decreased afterward in 3.05 m sows ($P < 0.05$). Upper body lesions increased immediately after mixing and then decreased in all treatments ($P < 0.0001$). Lower body lesions showed no differences by treatment or time. Cortisol increased after mixing and then decreased ($P < 0.01$), but no treatment differences were observed. Neutrophil percentage was greater ($P < 0.05$) and the neutrophil: lymphocyte ratio tended to be greater ($P < 0.08$) in 0.91 m sows than the 3.05 m sows. No other leukocyte populations differed by time or treatment. Overall, the 3 alleyway widths were similar, but 0.91 m sows had greater back fat implying decreased activity and musculation due to space restrictions. The sows in 0.91 m alleyway also showed increased neutrophil percentage suggesting a slightly greater stress level.

Key Words: sow housing, welfare, stress

T5 A comparison of two farrowing environments on piglet performance. A. R. Hanson*, P. M. Walker, and J. P. Holt, *Illinois State University*, *Normal*.

Traditional farrowing stalls have been designed to maximize piglet survival, with minimal concern regarding sow welfare. Standard litter data (birth weight, number born alive, etc.) from farm records were evaluated in an observation study utilizing a 200 sow (Chester White cross and Landrace cross) operation over a 6 y period (1449 litters) to compare 2 stall types, free stalls with movable sides (F), or traditional, fixed bow-bar stalls (B), on piglet performance and welfare. The F stalls were closed (in a straight position) ~1d before expected date of parturition and opened up to a triangular shape at ~3d post farrowing giving sows the ability to turnaround. Sows were placed into stalls 3–7 d before their expected date of parturition (n = 740 for B and 709 for F) and fed the same diet. Data were statistically analyzed, assuming a completely randomized design, using SPSS ANOVA procedures with year, season and room used as covariates and stall type as the independent variable. Sow parity was known for a limited number of litters (351), so a separate test was conducted using year, season, room, and parity group (PG) as covariates. When data were analyzed with PG excluded, there were differences favoring the B stall for birth performance and weaning performance ($P < 0.05$). Adjusted weaning weight was greater ($P < 0.05$) in B stalls compared with F stalls (mean = 61.22 ± 10.8 kg and 57.429 ± 11.56 kg, respectively). Number of pigs crushed was not impacted by any independent variable in this study (mean = 1.03 ± 1.24 and 1.01 ± 1.48 pigs/litter for B and F stalls, respectively). Data analysis suggested that larger sows may have been allotted to B stalls due to the difficulty for them to turnaround in F stalls successfully. Therefore, PG was included as a covariate to account for sow size, assuming that larger sows were multiple parity sows. Consequently, differences between the stalls became nonsignificant ($P > 0.05$). These results indicate that success in farrowing stalls may be affected by an interaction between sow size and stall design. Stalls which offer increased sow movement can be used without negative effects on piglet performance.

Key Words: farrowing stall, sow housing

T6 Behavior of Duroc pigs on sudangrass (*Sorghum bicolor*) pastures. S. Pietrosemoli*[1,2], J. C. Guevara[2], A. Lobo[3], J. Cardona[3], W. Maradiaga[3], and J. T. Green[4,2], [1]*Animal Science Department, North Carolina State University*, *Raleigh,* [2]*Alternative Swine Research and Extension Project*, *Raleigh, NC*, [3]*Universidad Nacional de Agricultura*, *Catacamas, Olancho, Honduras*, [4]*Crop Science Department, North Carolina State University*, *Raleigh.*

To evaluate the effect of weekly movement of shade and drinking structures on pig behavior, 72 Duroc pigs (castrated males and females; 32 and 97 kg initial and final live weight, respectively) were used during 5 weeks (July - August 2009) at the Center for Environmental Farming System (CEFS) in Goldsboro, NC. Twelve pigs were randomized to each of 6 sudangrass 0.16 ha paddocks (135 m^2 /pig), and were managed under 2 different strategies: Stationary (S) or Mobile (M) shade and drinking structures, in M shade and drinkers were moved on a weekly basis. Animals were kept under a continuous grazing system, with ad libitum access to a concentrated feed (16% PC) and water. Pig behavior was registered by one trained observer through direct observation (12 min/paddock) of the activity of the animals from outside the paddock twice a week, 5 times/day: 8:00 and 10:00 a.m. and 12:00, 2:00 and 4:00 p.m. Animals activities were categorized as eating, drinking, lying/resting, walking, grazing and rooting, and were expressed as percent. The experimental design was a completely randomized block, with 3 field replicates. Data was square root (x+1) transformed before performing ANOVA through PROC GLM of SAS v9.1. Pigs spent most of their time lying/resting (65.8 ± 2.1%, eating 8.64 ± 0.9%, drinking 3.02 ± 0.4%, walking 14.69 ± 1.5% grazing 5.49 ± 0.9% and rooting 2.4 ± 0.4%). Shade and drinkers movement strategies did not show an effect in any of the animal activities. The time of the day influenced animal behavior ($P < 0.05$), pigs being more active in the morning, as can be observed from lying/resting pattern 8:00 a.m.: 39.5%; 10:00 a.m.: 47.1%; 12:00 p.m.: 86.9%; 2:00 p.m.: 87.3% and 4:00 p.m.: 68.2%. In conclusion, these results suggest that pigs are more active during the cooler time of the day and that movement of shade and drinking structures had no effect on pig behavior.

Key Words: outdoor pigs, behavior, sudangrass

T7 Effects of postnatal serotonin agonism on fear response and memory. R. L. Dennis* and H. W. Cheng, *Livestock Behavior Research Unit, USDA-ARS*, *West Lafayette, IN*.

The neurotransmitter serotonin (5-HT) acts as a neurogenic compound in the developing brain. Early administration of a 5-HT agonist alters

the development of serotonergic circuitry, altering behaviors mediated by 5-HT signaling, such as memory, fear and aggression. The present study was designed to investigate the effects of early 5-HT agonism on later behaviors. White leghorn chicks were given an injection of 5-MT (5-HT agonist) at 2.5mg/kg (low dose), 10mg/kg (high dose) or saline (control) on day of hatch and a second dose 24 h later. Chicks (n = 13/treatment) were tested for fear response and memory at 2 wks of age. Chicks were subjected to a social isolation fear test for 20 min, time to first vocalization, number of vocalizations, time to first leap and number of leaps were recorded. ANOVA using SAS proc mixed revealed that chicks injected with low dose of 5-HT agonist had significantly shorter latency to time of first vocalization and a greater number of vocalizations compared with control birds ($P < 0.05$). Chicks treated with the high dose of 5-HT agonist tended to exhibit the same pattern of behavioral change ($P < 0.10$). No difference was found in latency to or frequency of leaps. In a memory test, chicks were placed in a running wheel and presented with an imprinted object (white box with a red light) and a novel object (blue box with a white light). The distance traveled in the wheel toward each object was measured. Analysis of variance results revealed that chicks from all groups traveled a similar distance toward a familiar object. However, control chicks walked the least toward a novel object, low dose chicks tended to walk further toward a novel object ($P < 0.10$), and high dose chicks walked significantly farther for a novel object ($P < 0.05$). No difference was found between treatments in a tonic immobility fear test ($P > 0.05$). Body weight and fluctuating asymmetry of the shank, and shank absolute length and width did not differ among treatments ($P > 0.05$). Our data show that later behaviors including fear and memory can be altered by early alteration of the 5-HT system without altering growth development, such as body weight, leg size and bilateral symmetry.

Key Words: serotonin, postnatal, behavior

T8 Influence of increasing-dim and bright, and split-dark-bright lighting on broiler mobility and stress. R. J. Lien*, J. B. Hess, and S. F. Bilgili, *Auburn University*, *Auburn, AL*.

The objectives were to determine lighting and strain effects on mobility and stress responses for tray pack (TP) and breast yield (BY) broilers exposed to programs meeting either US or EU lighting guidelines. Forty males were placed by strain in each of 2 1.5 by 3.7 m pens in 12 light controlled rooms. An increasing-dim (ID) treatment (23L:1D, 1–7 d; 12L:12D, 8–14 d; 14L:10d, 15–21 d; 17L:7D, 22–28 d; 20L:4D; 29–35 d; 23L:1D; 36–48 d; 2 FC to 7 d and 0.25 thereafter) was provided in 4 rooms. An increasing-bright (IB) treatment (23L:1D, 1–7 d; 12L:12D, 8–14 d; 14L:10D, 15–21 d; 16L:8D, 22–28 d; 18L:6D, 29–45 d; 23L:1D, 46–48 d; 2 FC throughout) was provided in 4 rooms. A split-dark-bright (SDB) treatment (16L:4D:2L:2D and 2 FC) was provided in 4 rooms. Sitting or standing on 15 cm high raised platforms (decking), the ability to climb onto raised platforms to feed, tonic immobility (TI), and heterophil:lymphocyte ratios (H:L) were determined at approximately 3 and 6 wk. Gait scores and latency to lie durations were determined during wk 7. Data were analyzed by GLM of SAS with a statistical significance level of $P < 0.1$. At 3 wk, decking was greatest in IB treatment (11.0%), least in SDB (6.7%), and intermediate in ID (8.7%)($P = 0.03$). Decking was greater in the TP (11.5%) than BY (6.7%) strain at 6 wk ($P = 0.001$). Feeding on raised platforms was greater in the TP (1.67) than BY strain (1.34) at 3 wk ($P = 0.004$). TI was greater in the ID (267 s) and IB (283 s) than the SDB treatment (201 s) at 6 wk ($P = 0.09$), and nearly greater in the TP (194 s) than BY (128 s) strain at 3 wk ($P = 0.13$). At 3 wk, H:L was greatest in the IB treatment (0.52), least in SDB (0.40), and intermediate in ID (0.43)($P = 0.06$). Gait scores and latency to lie durations were not affected ($P > 0.1$) by treatment or strain. In this study, lighting treatments and broiler strains inconsistently affected measures of mobility and physiological or psychological stress.

Key Words: broiler, lighting, stress

T9 The use of lidocaine as an analgesic to study immediate pain associated with hot blade beak trimming in 1- and 10-day old White Leghorn chicks. M. Cho*[1], K. Schwean-Lardner[1], A. Livingston[2], and H. L. Classen[1], [1]*Department of Animal and Poultry Science, University of Saskatchewan*, *Saskatoon, Saskatchewan, Canada*, [2]*Department of Veterinary Biomedical Sciences, University of Saskatchewan*, *Saskatoon, Saskatchewan, Canada*.

Hot blade (HB) beak trimming (BT) is commonly used by the poultry industry to reduce feather pecking and cannibalism. As there is a poor understanding of pain immediately post HB trimming, research was conducted using lidocaine as an analgesic and behavioral observation as an indicator of a pain response to BT. An initial study used behavioral observation and the known analgesic effects of lidocaine to select 0.4 mL of 0.02% lidocaine with epinephrine (LE) as an effective dose for 1-d old chicks. Based on 1-d old chick results and body weight, 0.4 mL of 0.04% LE was set as a suitable dose for 10-d old chicks. Trials with 1- and 10-d old chicks compared the effect of LE with BT (removal of 1/3 of beak), saline with BT, BT with needle insertion, no BT with needle insertion and LE without BT on bird behavior for 135 min post HB trimming. Leghorn chicks (40 1-d, 30 10-d) were assigned to treatment groups and 1 chick per treatment was assigned to each of 8 and 6 replications, respectively. Behavior was analyzed using the SAS GLM procedure and a priori contrasts to evaluate the effects of liquid injection, LE injection and BT on chick behavior (% of time; $P \leq 0.10$). Less walking behavior was seen in 1- (2.2 vs. 3.8%) and 10- (2.1 vs. 3.6%) d old chicks with liquid injection. LE injection to BT chicks did not affect behavior in contrast to those trimmed with either saline injection or needle insertion indicating that pain is not associated with the period immediately post treatment in 1- and 10-d old chicks. However, BT decreased standing (16 vs. 21%) and feed pecking (6.3 vs. 9.4%) and increased resting (66 vs. 59%) behavior in 10-d old chicks in comparison to untrimmed chicks suggesting that physical trauma other than pain impacts chick behavior. In conclusion, these results suggest a painless phase post HB trimming at 1- and 10-d of age but that trimming continues to affect behavior in comparison to untrimmed birds.

Key Words: poultry welfare, pain, feather pecking

T10 Comparison of an enriched and barren environment on welfare related fear behaviors of commercial laying hens. C. J. Davis*, H. Taira, M. M. Beck, and P. A. Skewes, *Clemson University*, *Clemson, SC*.

In response to the debate over laying hen welfare, this study was conducted to determine the effects of housing environment on 2 welfare related fear behaviors of commercial laying hens. Emergence test [EM] and tonic immobility test [TI]) were used to determine the fearfulness of the laying hens. Nine hundred day-old Leghorn chicks were randomly assigned to either a floor pen environment or a commercial cage housing environment. The cage chicks were housed in 20 commercial battery brooder cages (25 per cage) up until 4 weeks of age and then moved to 39 battery grower cages (10 per cage). At 16 weeks of age, the pullets were moved into 39 commercial layer cages (8 per cage) for the remainder of the experiment. The floor pen birds were continuously housed in 14 individual floor pens (28 per pen) enriched with perches, dust baths, and nest boxes. Behavioral assessments were conducted at wk 17, 21, 25, 29

and 33. Both behavioral assessments were conducted on 10 hens from the cage environment and 10 hens from the pen environment. Cages and pens were selected randomly. The latency to emerge from a box was recorded in the EM and the latency to recover from tonic immobility was recorded during TI. Comparison of environmental treatments with a 2 sample *t*-test showed a shorter mean EM and TI duration in birds housed in the enriched environment ($P < 0.001$). The mean emergence duration for cage birds was 320.6 ± 30.0 s compared with 155.9 ± 30.0 s for floor pen birds. The mean tonic immobility duration for cage birds was 384.3 ± 35.8 compared with 212.2 ± 35.1 for pen birds. In addition to the overall treatment difference, there were significant differences at specific sample times. Although previously it was found that the effect of rearing environment was not consistent with fear responses for chicks and pullets, it appears that the housing environment had a consistent effect on fear response for the adult laying hens. In this study, hens from the enriched environment showed less fear than those from the barren environment.

Key Words: tonic immobility, emergence test, laying hen welfare

T11 The behavior of Japanese quail fed diets supplemented with passionflower. J. D. T. Silva, F. H. Hada, R. H. Marques, R. A. Gravena, V. K. Silva, S. A. Queiroz, and V. M. B. Moraes*, *São Paulo State University*, *Jaboticabal, SP, Brazil*.

This study evaluated the effect of passionflower (*Passiflora alata*), phytotherapic properties with anxiolytic and sedative, on the diet on the behavior of Japanese quail in the reproductive phase. Twenty-four female and 8 male 35-d-old birds were mated in a completely randomized design consisting of 2 treatments (0 and 500 mg passionflower/kg feed) with 4 replicates of 4 birds (3 female:1 male) for 120 d. During the observation period, a 4 camera CCTV surveillance system was mounted in the roof of the facility, that recorded the behavior of quails. The behavioral parameters (eating, drinking, feather preening, comfort movement, avoid and escape, aggressiveness, crouching) were tabulated over 5-h time spans made every 14 d, for a total of 6 observation periods for each cage. The assessment of focal bird behavior was accomplished by marking the birds with non-toxic paint. The inclusion of passionflower in the diet of the breeding quail increased consumatory behaviors of birds in time spent by eating (from 25.92 to 27.19%), drinking (from 13.45 to 17.26%), feather preening (from 9.10 to 14.95%), comfort movement (from 13.02 to 17.08%) and crouching (from 7.35 to 14.46%) ($P < 0.0001$). Expressions of avoid and escape (from 14.08 to 6.20%) and aggression (from 17.07 to 2.85%) were reduced ($P < 0.0001$). It was concluded that passionflower enhances the positive expression of behaviors related to the welfare of Japanese quail during breeding.

Table 1. Average percent time spent by birds on behaviors as affected by diets supplemented with and without passionflower

Passionflower (mg)	Eating	Drinking	Feather preening	Comfort movement	Avoid and escape	Aggressiveness	Crouching
0	25.92 [b]	13.45 [b]	9.10 [b]	13.02 [b]	14.08 [a]	17.07 [a]	7.35 [b]
500	27.19 [a]	17.26 [a]	14.95 [a]	17.08 [a]	6.20 [b]	2.85 [b]	14.46 [a]
P	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001
CV (%)	1.88	4.01	6.47	1.24	7.26	5.38	15.25

Means followed by same letter in column do not differ by Fisher's test ($P \leq 0.05$).

Key Words: behavior, *Coturnix coturnix japonica*, welfare

T12 Strain differences among six varieties of fowl in two fear tests. G. S. Archer* and J. A. Mench, *University of California, Davis*.

Fear tests are often used to assess the well-being of chickens. It is important to examine how genetics may affect behavioral responses during fear testing. We conducted 2 fear tests to examine the responses to induction of tonic immobility (TI) test and inversion after catching (INV), on 6 different varieties of fowl: red Junglefowl (JF, n = 17), red Junglefowl/Rhode Island Red crosses (JFC, n = 20); 3 different single-comb White Leghorn (SCWL) varieties (HyLine CV20, n = 20, a commercial egg layer; UCD-03, n = 20, an inbred line of MHC recombinants; Mono-PNU, n = 20, which lacks the MHC II receptor), and featherless chickens (FL, n = 20, derived from multiple crosses). Data were analyzed using GLM or Kruskal-Wallis. JF and FC required more inductions ($P < 0.05$) than CV20 and Mono-PNU during TI. The UCD-03 also required more ($P < 0.05$) inductions than Mono-PNU. Latency to first head movement during TI was longer ($P < 0.05$) in CV20 (54.3 s) than in all other varieties (15.8 s). Latency to right was longer ($P < 0.05$) in CV20 (301 s) and Mono-PNU (517 s) than JF (112 s) and FL (225 s) varieties. UCD-03 had a shorter ($P < 0.05$) duration of wing flapping (3.9 s) and fewer total flaps (15.9) than all other varieties during INV (9.4 s, 55.2 flaps). UCD-03 (3 flaps/sec) and Mono-PNU (3.6 flaps/sec) wing flapped less intensely ($P < 0.05$) than all other varieties (5.9 flaps/sec) except JFC (5.2 flaps/sec), while FL flapped (6.8 flaps/sec) more intensely ($P < 0.05$) than all varieties except JF. Factor analysis revealed that there were 2 factor loadings for each variety but that the variables measured loaded differently for each variety. These results demonstrate that different varieties of fowl react differently during different fear tests and different types of fear responses predominate in different varieties.

Key Words: fear, chicken, genetics

T13 Behavior expression of testosterone treated cockerels in response to social grouping. S. S. Askari Rankouhi*, M. A. Karimi Torshizi, R. Vaez Torshizi, A. Niknam, and A. Maghsoudi, *Tarbiat Modares University*, *Tehran, Iran*.

For many years it is demonstrated that testosterone hormone increase sex secondary
characters and also, enhance aggressive behavior of animals. The objectives of this study were evaluation of sex secondary character expression in testosterone injected birds as affected by un-injected pen-mates' behavior. Total of 60 1-d-old male broilers (Arian - Iranian Hybrid) were divided into two identical groups (30 birds per group). Chicks of the first group received 25 mg of testosterone enanthate by intramuscular injection. Birds of the second group were injected by sterile physiological serum and were considered as control group. A week post injection, a third experimental group was formed by mixing 10 birds form each of the two initial groups, therefore the three final experimental groups were un-injected control, testosterone injected and blend of injected and un-injected birds. The length of neck feathers, size of comb (mm) and attack toward wood stick or hand (number of attacks per minute) were evaluated at days 21 and 42 of age. The testosterone injection caused significant differences in all measured variables compared to control un-injected birds at 21 days of age ($P < 0.05$). Interestingly, at 42 days of age the effects of testosterone on measured variables were influenced by the composition of pen-mate individuals. The testosterone induced changes on above mentioned sex secondary characters were rapidly restored in those injected birds which had un-injected pen-mates, while testosterone induced sex secondary

characters stayed unchanged in all-injected birds group ($P < 0.05$). The results of the present study showed the impact of social behavior of pen-mates on the expression of physiological and behavioral changes induced by testosterone injection in cockerels.

Key Words: testosterone, cockerels, social behavior

T14 Results from the Washington State bovine viral diarrhea virus voluntary control project. J. R. Wenz*, D. A. Moore, H. L. Neibergs, and J. S. Neibergs, *Washington State University*, *Pullman*.

Control of bovine viral diarrhea virus (BVDV) in beef cow-calf herds has been predicated on the identification and removal of persistently infected (PI) animals. Calves are born PI following exposure to BVDV during approximately 40 to 140 d of gestation and are the primary source of BVDV in the herd. The purpose of the BVDV voluntary control project was to educate producers, facilitate herd ear notch testing and implementation of control measures. From January 2008 to December 2009, 12 producer meetings were held at county and state beef producer meetings and a brochure detailing the project was mailed to 1700 members of the Washington Cattlemen's Association. Sixty herds from 18 counties enrolled and completed testing. Ear notch samples were screened by PCR on pools of up to 36 and PI positive samples were identified by a positive commercial antigen capture ELISA test. All PI animals were ELISA positive on 2 ear notch samples collected 2 to 3 weeks apart. Of the 60 herds tested 13.3% had at least one PI. Prevalence of PI animals was 0.81% (80/9881). For calves tested, 0.092% (79/8624) were PI and 1/1257 (0.08%) other cattle (yearlings, bulls, open cows) tested were PI. Only 2/79 (2.5%) dams of PI calves were PI. Two herds contributed 87% of the PI calves. In one herd 12.7% of 213 calves were PI and 52% of 83 calves were PI in the other. Excluding these 2 herds resulted in a PI calf prevalence of 0.12%. The herd prevalence was higher than previous reports from the US and may have been due to enrollment bias (suspected BVD in herd, subsidized testing). The prevalence of PI in calves, excluding the high prevalence herds, was similar to previous reports. A yearling PI was identified, highlighting the importance of testing all animals that may contact pregnant cows in the herd. Except for the herd with 52% PI calves, all PI animals were immediately removed from the herd. Three PI positive herds screened the subsequent year's calf crop and no PI calves were found. Low enrolment in the project suggests cow-calf producers in the state did not perceive sufficient risk posed by BVDV to warrant the cost of whole herd testing.

Key Words: BVDV, persistent infection, beef

T15 Effects of source and level of energy on the immune competence and response to an infectious bovine rhinotracheitis virus (IBRV) challenge in cattle. L. R. Schwertner*[1], L. E. Hulbert[1,2], J. A. Carroll[2], M. L. Galyean[1], and M. A. Ballou[1], [1]*Department of Animal and Food Sciences, Texas Tech University*, *Lubbock,* [2]*Livestock Issues Research Unit, USDA–ARS*, *Lubbock, TX.*

Objectives were to evaluate how dietary energy level and source affect immune competence and response to an IBRV challenge in cattle. Forty–8 crossbred beef steers were stratified by BW within 2 periods and randomized to 1 of 3 dietary treatments (8 steers/treatment within period). Treatments were: a 70% concentrate diet fed ad libitum (70AL); a 30% concentrate diet fed ad libitum (30AL); and 70% concentrate diet restricted to the NEg intake of 30AL (70RES). Ex vivo immune competences were evaluated after treatments were applied for 28 d, after which cattle were moved into individual pens (d 28 to 40) and intranasally challenged with IBRV on d 30. On d 34, all cattle were offered a 50% concentrate diet ad libitum until d 50. Both energy source ($P < 0.02$) and level ($P < 0.04$) affected peripheral blood mononuclear cell synthesis of tumor necrosis factor-α (TNF- α), with cell culture supernatant concentrations averaging 2,264, 1,887, and 1,241 pg/mL for 70AL, 70RES, and 30AL, respectively. Neither whole blood killing of *Mannheimia hemolytica* nor neutrophil oxidative burst in response to *M. hemolytica* were affected by treatments. Rectal temperature following IBRV peaked 3 d post challenge and returned to baseline by d 6, but it was not affected by treatment. After switching cattle to the 50% concentrate diet on d 4 after the IBRV challenge, there were no differences in DMI while the cattle were individually penned. When cattle were group–penned 10 d after the IBRV challenge, the 70RES cattle had greater DMI ($P < 0.04$). Following the IBRV challenge, serum glucose concentrations did not differ among treatments; however, the 70AL cattle had greater blood urea N concentrations ($P < 0.01$). There was a treatment × time interaction ($P < 0.01$) for NEFA; such that cattle fed the 70AL had elevated NEFA on d 3 and 5 after IBRV. Data indicate that cattle fed higher energy diets and to an extent a higher percentage of concentrates had a more pronounced pro-inflammatory response, but other aspects of innate immune competence were not influenced by level or source of energy.

Key Words: bovine, dietary concentrate, immune

T16 The effects of dam parity and antibiotics on immune parameters and gastrointestinal bacterial diversity in weanling pigs. E. E. Hinkle*, H. Tran, J. W. Bundy, R. Moreno, P. S. Miller, J. Walter, and T. E. Burkey, *University of Nebraska*, *Lincoln*.

The progeny of first parity (P1) dams may have reduced growth performance compared with the progeny derived from mature dams (≥P2). A 42-d experiment was conducted to evaluate the effect of dam parity and antibiotics on immune parameters and the gastrointestinal (GIT) microbiota among progeny derived from P1 or P4 dams. Weaned pigs (n = 96, 6.02 ± 0.07 kg) initially derived from P1 or P4 dams were allotted to 2 dietary treatments: control (CTL) or antibiotic (50 g/ton Mecadox; AB). This created a 2 × 2 factorial with the following treatments: 1) P1, CTL; 2) P1, AB; 3) P4, CTL; and 4) P4, AB (6 pigs/pen, 4 pens/trt). Blood samples were collected on d 0 and weekly thereafter for quantification of serum immunoglobulin (Ig) G and A via porcine specific ELISA. There was no effect of parity or AB, or their interaction ($P > 0.05$) for IgG concentrations; however, a parity × AB interaction ($P < 0.05$) was observed for circulating IgA where P1 pigs had decreased serum IgA concentrations when fed AB, while P4 pigs had greater serum IgA concentrations when fed AB. The fecal microbiota at d 7 and 42 was characterized by denaturing gradient gel electrophoresis. Bionumerics software was used to calculate similarity and diversity indices. The similarity index represents the percentage of the microbial fingerprint that is similar within a group (P1 vs. P4). The diversity indices (Shannon′s and Simpson′s) of the gut microbiota can be inferred from DGGE fingerprints by using Shannon′s and Simpson′s indices. A greater Shannon′s index signifies a more diverse microbial population, while a lower Simpson′s index indicates a greater microbial diversity. No differences were observed in bacterial population similarity on d 7 or 42. Significant differences (Shannon′s, $P = 0.03$; Simpson′s, $P = 0.09$) in bacterial species diversity were observed on d 7 and 42 among progeny derived from P1 compared with P4 dams, while AB administration had no effect. The results obtained in our study suggest that immune parameters and gastrointestinal bacteria may be affected by dam parity.

Key Words: bacterial diversity, dam parity, immunoglobulins

T17 Serum IgG concentrations and performance, incidence of diseases, and risk of death in pre-weaned Holstein calves. M. C. Perdomo* and J. E. P. Santos, *University of Florida*, *Gainesville*.

Holstein calves, 782 females and 200 males, housed in individual hutches received 5.7 L of frozen-thawed colostrum in the first 24 h of life. From d 1 to 21 of age, calves were fed 1.9 L of pasteurized whole milk 3 times daily, and twice daily thereafter until 60 d of age, when they were weaned. Calves were fed grain ad libitum, and amounts offered and refused were measured daily during the first 70 d of age. Body weights (BW) were measured on d 1, 30 and 70 of age. Blood was sampled 48 h after colostrum feeding and serum was analyzed for concentrations of total immunoglobulin (Ig) G using a single-radial immunodiffusion assay. Rectal temperature was taken daily in the first 10 d of age, and again at every diagnosis of disease. Feces were scored daily for detection of diarrhea. Respiratory disease was evaluated based on respiration rate, nasal discharge, and coughing reflex. Duration of disease events and treatment costs were measured. Hazard of death was analyzed using the Cox′s proportional model using IgG and gender as predictors for survival. Failure of passive transfer (PT; IgG < 1.5 g/dL) was used as predictor of grain intake, BW, grain conversion into BW, and treatment cost. Rate of death decreased ($P < 0.01$) 29% for every 1 g/dL increase in serum IgG concentration (hazard rate = 0.71, 95% CI = 0.56–0.90). Calves with failure (IgG < 1.5 g/dL) or adequate (IgG > 1.5 g/dL) PT had, respectively, 11.9 and 5.7% mortality ($P < 0.02$), and 45.2 and 35.9% more than 1 disease event ($P < 0.05$). Disease treatment costs ($/calf) were 6.05 and 4.90 for failure and adequate PT ($P = 0.08$). For calves with failure and adequate PT, BW gain in the first 30 d (295 vs. 330 g/d, $P = 0.02$) and BW at d 60 (73.4 vs. 75.5 kg; $P = 0.05$) differed; however, failure of PT did not influence ($P > 0.10$) BW gain from 30 to 60 d (693 vs. 666 g/d), grain dry matter intake in the first 30 d (104 vs. 107 g/d) or from 30 to 60 d (901 vs. 914 g/d), or efficiency of conversion of grain into BW. Improving IgG absorption decreased the risk of mortality and treatment costs, and improved weaning weight, but it did not influence grain intake or feed conversion.

Key Words: calf, health, IgG

T18 Effects of live and killed *Mycoplasma gallisepticum* vaccines prior to an F-strain *Mycoplasma gallisepticum* overlay on the reproductive and digestive organ characteristics of commercial layers. R. Jacob*[1], E. D. Peebles[1], J. D. Purswell[2], and S. L. Branton[2], [1]*Mississippi State University*, *Mississippi State,* [2]*USDA-ARS, Poultry Research Unit*, *Mississippi State, MS*.

The effects of prelay vaccinations of ts-11 strain *Mycoplasma gallisepticum* (MG), MG-Bacterin, or their combination, when overlaid with F strain MG (FMG) post-peak production, on the digestive and reproductive organ characteristics of commercial layers were investigated. A total of 160 Single Comb White Leghorn layer hens were used. In each of 16 isolation units (pens), 10 birds were housed, with 4 replicate units in each of 4 treatments. The following treatments were utilized at 10 wk of age (woa): 1) Control (no vaccinations); 2) ts-11 strain MG, (Mycoplasma Gallisepticum Vaccine); 3) MG-Bacterin (MG-Bac); and 4) ts-11 strain MG /MG-Bacterin combination. At 45 woa, the birds in 2 replicate pens were challenged with a 99th passage of FMG, increasing the number of treatments to 8. A completely randomized experimental design was used. PCR tests using choanal swab samples confirmed the presence of MG in vaccinated birds and its absence in non-vaccinated birds. Necropsies were performed at the end of the trial (58 woa), using 2 birds per replicate pen (4 birds per treatment). Parameters examined included BW; liver, ovary, oviduct and small intestine weights; ovarian follicular hierarchy; and the lengths and weights of the components of the oviduct and small intestine. Results indicated that there were no significant treatment differences ($P > 0.05$) for any of the parameters investigated. Mean relative oviduct weight in control birds with and without FMG and birds given the combinatorial treatment with and without FMG were 4.18, 4.00, 4.00, 4.23% (SEM = 0.24), respectively. In conclusion, the individual or combinatorial use of ts-11 strain MG vaccine and MG-Bacterin, when administered during prelay, are effective in preventing possible adverse effects on the reproductive and digestive organs in response to a post-peak production challenge of FMG.

Key Words: layers, *Mycoplasma gallisepticum*, vaccine

T19 Discovery of differentially expressed microRNAs in porcine reproductive and respiratory syndrome (PRRS) virus infected alveolar macrophages. J. A. Hicks, N. Trakooljul, and H. C. Liu*, *North Carolina State University*, *Raleigh*.

Porcine reproductive and respiratory syndrome (PRRS) has a major impact on the swine industry. PRRS is characterized by abortions in pregnant sows and respiratory disease, particularly in young pigs. The causative agent is the arterivirus, porcine reproductive and respiratory syndrome virus (PRRSV). Determination of alterations in host gene expression upon PRRSV infection will provide a better understanding of the pathogenesis of the virus. It is now well-established that small RNAs are an important class of gene regulators. MicroRNA (miRNA, ~22nt) is a family of small RNAs that post-transcriptionally regulate gene expression. Studies have found that viral infections induce changes in the expression of miRNAs of infected host cells. These miRNAs often target genes associated with the immune response. The goal of the present study is to determine changes in host miRNA expression during PRRSV infection. Alveolar macrophages (SAMs) were isolated from seven 8-wk-old pigs. SAMs were maintained for 24hrs in RPMI 1640 with 10% FBS and then infected with PRRSV strain VR-2332 at an m.o.i. = 10. Infected and uninfected SAMs were collected at 24 or 48 h p.i. MiRNA expression analysis was carried out using the miRScript RT-PCR system. Over 40 miRNAs were found to be differentially expressed at either 24 h or 48 h p.i. upon PRRSV infection compared with non-infected cells. The expression of these miRNAs is dynamic, as some miRNAs are altered early (24hrs p.i.) while other miRNAs are differently expressed late (48hrs p.i.) upon infection. Among these are known immune miRNAs, including miR-146a and members of the miR-17–92 cistron, as well as miRNAs which have not previously been associated with viral infections, such as miR-130b and miR-342–3p. Target prediction and subsequent validation via luciferase assay of selected miRNAs suggest that these miRNAs target not only immune genes but also genes associated with intracellular signaling and trafficking. Our data indicates that miRNAs play a role(s) during PRRSV infection by affecting gene expression associated with PRRSV pathogenesis.

Key Words: PRRSV, microRNA, gene regulation

T20 Development of mouse monoclonal antibodies specific for chicken interleukin-18 (IL-18). Y. H. Hong*[1], H. S. Lillehoj[2], S. H. Lee[2], M.-S. Park[2], J. LaBresh[3], D. Tompkins[4], and C. Baldwin[4], [1]*Department of Animal Science and Technology, Chung-Ang University*, *Anseong, Gyeonggi-do Republic of Korea*, [2]*Animal and Natural Resources Institute, Agricultural Research Service-USDA*, *Beltsville, MD*, [3]*Kingfisher Biotech, Inc.*, *St. Paul, MN*, [4]*Department of Veterinary and Animal Sciences, Paige Laboratory, University of Massachusetts*, *Amherst*.

Two mouse monoclonal antibodies (mAbs) which are specific for chicken interleukin-18 (chIL-18) were produced and characterized

by enzyme-linked immunosorbent assay (ELISA), Western blotting, quantitative real-time PCR and functional assays. The mAbs specific for chIL-18 identified a 23 kDa yeast-expressed chIL-18 and a 66 kDa *E. coli*- MBP fusion protein by Western blot analysis. Bioassays for chIL-18 were carried out to evaluate its ability to induce IFN-γ production in primary chicken spleen cells, and nitric oxide (NO) secretion in the HD11 macrophage cell line. Two mAbs showed neutralizing activity. Taken together, we have developed mouse monoclonal antibodies specific for chicken IL-18. These immune reagents will be useful tools to analyze IL-18 secretion during infections and to do basic and applied research for poultry.

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Key Words: chicken, IL-18, monoclonal antibody

T21 Influence of two different doses of infectious bovine rhinotracheitis virus (IBRV) on immune and physiological parameters in steers. S. M. Falkenberg*[1], T. B. Schmidt[1], T. Elsasser[4], J. L. Sartin[3], J. O. Buntyn[1], and J. A. Carroll[2], [1]*Mississippi State University*, *Mississippi State*, [2]*Livestock Issues Research Unit, USDA-ARS*, *Lubbock, TX*, [3]*Auburn University College of Veterinary Medicine*, *Auburn, AL*, [4]*Bovine Functional Genomics, USDA-ARS*, *Beltsville, MD*.

To evaluate the effects of IBRV on immunological and physiological parameters of cattle, 18 Holstein steers (450.11 ± 75.70 kg) were randomly assigned to either a Control group (Cg) or 1 of 2 IBRV challenged groups. Prior to the challenge, steers were fitted with indwelling rectal probes, BW recorded, and a blood sample obtained. On d 0, steers received either an intra-nasal dose of IBRV [3 mL/nostril (IBR1) or 4mL/nostril (IBR2); Cooper strain, 1 X 10^7 PFU/ml] or saline (3 mL/nostril; Cg). IBRV steers were placed in a paddock that was isolated from the Cg as well as all other cattle on the research farm. Blood samples were collected via jugular venipuncture every 24 h on d 1 and 2, and every 12 h on d 3, 4, 5, 6, and 7 post-challenge. All IBRV steers had elevated rectal temperatures ($P < 0.05$) as compared with Cg by d 2, returning to baseline on approximately d 5. Serum was analyzed for interleukin-6 (IL-6), interferon-γ (IFN-γ), tumor necrosis factor-α (TNF-α), growth hormone (GH) and insulin-like growth factor-1 (IGF-1). An increase in IFN-γ for the overall effect of IBRV as compared with the Cg ($P < 0.05$) was observed though no differences were found for IFN-γ in IBR1 vs. IBR2. Where a numerical increase in the mean concentrations of TNF-α and IL-6 were measured in IBRV vs Cg, the response was not different ($P > 0.05$). Furthermore, no differences ($P > 0.05$) in mean concentrations of GH and IGF-1 were found between Cg and IBRV. Results indicate that both doses of IBRV elicited immune responses; however there were no measured differences between the 2 dose concentrations. Collectively, the data suggest that measurable immune responses to IBRV at the doses chosen may be highly selective in regard to cytokine and metabolic parameters.

Key Words: cytokines, IBRV, dose response

T22 The effect of thymol on reactive oxygen species production by bovine neutrophils. L. M. Nemec*, C. Wu, S. Cordova, K. Davison, and T. F. Gressley, *University of Delaware*, *Newark*.

Neutrophils produce intracellular and extracellular reactive oxygen species (ROS) to destroy engulfed and extracellular bacteria, respectively. However, extracellular ROS production during mastitis can also damage healthy tissue and impede recovery. This study evaluated the effect of the antioxidant thymol on intracellular and extracellular ROS production by bovine neutrophils. Neutrophils were activated with phorbol myristate acetate (PMA) or zymosan in the presence of 0, 0.0001, 0.001, 0.01 or 0.1 g/L thymol. Neutrophil ROS production was assessed by measuring luminescence or fluorescence (arbitrary units) every 5 min for 75 to 120 min following addition of 1 of 4 reagents: luminol (LUM) for measurement of total ROS (intracellular+extracellular); isoluminol (ISO) for extracellular ROS; methyl cypridina luciferin analog (MCLA) for extracellular superoxide; 5-(6)-chloromethyl-2′, 7′-dichlorodihydrofluorescein diacetate, acetyl ester (CMH2) for intracellular ROS. All activator/thymol combinations were assessed using neutrophils isolated from 4 different cows. Area under the curve (auc) for each activator/thymol/cow combination was calculated and log-transformed before statistical analysis. The MIXED model of SAS included fixed effects of thymol concentration and activator and random effects of assay date and cow. Least squares means and *P*-values for overall thymol effect and linear and quadratic thymol contrasts are presented in the table. Overall, addition of thymol to activated neutrophils decreased extracellular ROS and increased intracellular ROS, which may reduce tissue damage during mastitis without negatively impacting neutrophil killing.

Table 1. Effect of Thymol on Neutrophil ROS Production

	LUM, log(auc)	ISO, log (auc)	MCLA, log (auc)	CMH2, log (auc)
Thymol, g/L				
0	5.61	4.82	4.05	5.35
0.0001	5.56	4.88	4.25	5.35
0.001	5.54	4.73	4.30	5.35
0.01	5.38	4.12	4.49	5.41
0.1	4.80	3.38	3.24	6.20
P-values				
Thymol	0.001	0.001	0.94	0.001
Linear	0.001	0.001	0.06	0.001
Quadratic	0.001	0.002	0.002	0.001

Key Words: neutrophil, thymol, reactive oxygen species

T23 Bovine hepatic and adipose retinol binding protein gene expression. P. Rezamand*, K. M. Hunt, R. D. Schramm, and M. A. McGuire, *University of Idaho*, *Moscow*.

Retinol is primarily transported in circulation to target organs by retinol-binding protein (RBP). The protein is relatively small (21 kDa), has one binding site for retinol in the all-trans form, is bound to transthyretin (TTR), and primarily synthesized in the liver. Circulating TTR and RBP may decrease in response to inflammation. Induction of transcription factor NF-IL6 by pro-inflammatory cytokine TNF-α results in down-regulation of the hepatic synthesis of proteins such as TTR. Our previous findings, however, indicated that circulating RBP concentration was greater in cows with a new intramammary infection (IMI) as compared with cows without a new IMI. Our objective was to determine whether there was a relation between hepatic and adipose mRNA expressions of RBP with that of TNF-α. Liver and intestinal adipose tissues were sampled from dairy cows (n = 28) at slaughter and frozen in liquid nitrogen. Total RNA was extracted from each tissue sample and cDNA was generated using the High Capacity Reverse Transcription Kit. Gene expressions of RBP, TNF-α, and β-actin, as a housekeeping gene, were measured in relative quantification using real time rt-PCR. Data were analyzed using original Ct values, adjusted to β-actin expression, in the MIXED and CORR procedures of SAS, and significance was determined at $P \leq 0.05$. Expression of RBP and TNF-α was detected in

all samples and for both genes, variations among cows were significant ($P < 0.001$). Relative to β-actin expression, RBP and TNF-α were more expressed in intestinal adipose than in liver ($P < 0.001$). Across tissues, RBP and TNF-α expressions were positively correlated (r = 0.66; $P < 0.001$). Within intestinal adipose, RBP and TNF-α expressions were weakly correlated (r = 0.38; $P < 0.001$). In the liver, however, mRNA expressions of RBP and TNF-α were strongly correlated (r = 0.64; $P < 0.001$). This implies that regulation of RBP at the transcription level may be independent from that of TTR, which is downregulated by pro-inflammatory stimuli via induction of transcription factor NF-IL6.

Key Words: bovine, retinol-binding protein, TNF-α

T24 Yeast supplementation alters the health status of receiving cattle. J. A. Carroll*[1], C. T. Collier[1], L. E. Hulbert1,3, J. R. Corley[2], A. G. Estefan[2], D. N. Finck[3], and B. J. Johnson[3], [1]*USDA-ARS, Livestock Issues Research Unit*, *Lubbock, TX,* [2]*Lesaffre Feed Additives*, *Milwaukee, WI,* [3]*Texas Tech University, Dept. of Animal and Food Sciences*, *Lubbock*.

Our objective was to determine if supplementation of yeast products during the receiving phase would improve the health status of beef calves before and following a low-dose lipopolysaccharide (LPS; 0.25 μg/kg BW) challenge. Twenty-four crossbred calves (203 ± 1.45 kg BW) were blocked by BW and assigned to 1 of 4 dietary treatments for 38 d before LPS exposure: 1) Control (Cont) calves fed an 83% concentrate diet; 2) Live Yeast (LY), calves fed the control diet with the addition of a LY; 3) Yeast Cell Wall (YCW), calves fed the control diet with the addition of a YCW product; and 4) LY plus YCW (LY/YCW). Calves on a common ration were group penned, and diets containing the yeast products were formulated to deliver 5 g•hd^{-1}•d^{-1} of either LY or YCW or 10 g•hd^{-1}•d^{-1} of the LY/YCW combination. On d 38, calves were fitted with jugular catheters and indwelling rectal probes, and moved to individual stanchions. On d 39, blood samples were collected at 30-min intervals from −2 to 8 h and then at 24 h relative to LPS challenge at 0 h. Rectal temperatures (RT) were collected at 1-min intervals from −24 to 24 h post-LPS. During the entire trial, basal RT before LPS tended ($P \leq 0.06$) to differ among groups with Cont calves having higher RT compared with LY/YCW ($P \leq 0.01$) and LY ($P \leq 0.04$) calves. After the LPS challenge, an interaction ($P \leq 0.05$) was observed such that RT remained higher in the Cont calves compared with all other groups. By 10 h post-LPS, RT were still greater ($P \leq 0.05$) in Cont calves compared with all other calves, and remained numerically higher throughout the study. Serum cortisol increased in all groups post-LPS with peak concentrations observed at 1 h. At 1 h post-LPS, serum cortisol concentrations were 26.5 ng/mL greater ($P \leq 0.04$) in Cont calves compared with LY/YCW calves. An interaction ($P \leq 0.01$) was observed for serum interferon-gamma (IFN) such that IFN concentrations tended ($P \leq 0.06$) to be greater in Cont calves compared with YCW calves before LPS exposure. These data indicate that supplementing the diet of receiving beef cattle with yeast products may improve their health during the early phase of the feedlot period, thus allowing for enhanced performance.

Key Words: cattle, immunity, yeast

T25 Impact of mature cow weights on farm profitability and economic weights of beef cattle traits. F. Szabó*[1], K. Keller[1], J. Wolf[2], and M. Wolfová[2], [1]*University of Pannonia Georgikon Faculty*, *Keszthely, Hungary*, [2]*Institute of Animal Science*, *Uhrinéves, Prague, Czech Republic*.

The impact of mature cow weight on the profitability of beef cattle farming and on the economic importance of 10 performance and functional traits was analyzed in Hungary. The examined traits were calving performance, stillbirth and calf losses till weaning, weight of calves at birth, at 120 and at 205 d of age, mature weight of cows, conception rates of heifers and cows and productive lifetime of cows. The cow weight was varied from 500 to 700 kg in 50 intervals. The economic efficiency of all farming systems was expressed as profit per cow and per year. The economic importance of a trait (marginal economic value) was defined as partial derivate of the profit function with respect to trait mean. The program package ECOWEIGHT was used for all calculations. The results showed that beef cattle farming with all cow weight classes could be profitable when including EU subsidies in the incomes of a FARM. Without subsidies, a positive profitable can be reached only when keeping small-framed cows (500 to 550 kg). In all modeled production systems, the most important trait was conception rate of cows followed by weaning weight of calves (at 205 d age) for light cows and productive life of cows in systems with heavy cows.

Key Words: beef cow, profitability, marginal and relative economic weight

T26 Carcass characteristics and chemical composition of *Longissimus* muscle of different genetic groups finished at tropical condition. R. H. de Tonissi Buschinelli de Goes*[1], D. M. Lambertucci[3], K. C. da Silva Brabes[1], A. B. Mancio[2], C. Mistura[4], and D. D. Alves[5], [1]*Universidade Federal da Grande Dourados*, *Dourados, MS, Brasil*, [2]*Universidade Federal de Viçosa*, *Viçosa, MG, Brasil*, [3]*Faculdade de Ciências Biomédicas de Cacoal*, *Cacoal, RO, Brasil*, [4]*Universidade do Estado da Bahia*, *Juazeiro, BA, Brasil*, [5]*Universidade Estadual de Montes Claros*, *Janaúba, MG, Brasil*.

The carcass characteristics and chemical composition of *Longissimus* muscle (LM) of steers at different genetic groups, grazing *Brachiaria brizantha* cv. Marandu, were evaluated. The animals were finished during the rainy season, receiving a protein/energetic supplement, of lower intake, contained corn and soybean meal, with 24% of CP; supplied at 1.1 kg/day. Eighteen beef steers (6 Nellore × Santa Gertrudis-SG, 6 Nellore × Simental-SI and 6 Nellore-NE) were slaughtered at 24 mo of age at 478 ± 6.2 kg. The experiment was analyzed as a complete randomized design and the averages compared by Tukey's test, at 5% of probability. There was no effect for genetic groups for slaughter weight, hot carcass weight (HCW), carcass yield, beef round weight, beef round yield, hind quarter with short ribs weight, spare rips, loin eye area (LEA), fat thickness (FT), yield grade estimated (YG = 72,92–0,489FT-0,02HCW+0,119 LEA), and Brazilian comercial cuts (BCC = 60,33–0,015HCW-0,462FT+0,11 LEA), with the averages of 478,8kg, 254.2kg, 53.05%, 118.6kg, 46.86%, 95.77kg, 13.41kg, 74.02cm^2, 4.09mm, 74.61% and 64.45%, respectively. It was observed difference ($P < 0.05$) for the percentages of moisture, ash, protein, total lipid and cholesterol between the genetic group, in LM. Fat for SG steers was of 3.24g/kg, while SI was of 2.58g/kg and NE of 2.29g/kg, however the fat thickness possesses lower value, what could be inferred that fat in the LM. Lipids could explain the low moisture presented by the crossbreeding animals (73.6%). The meat of the NE presented moisture of 74.1%, with ash of 1.10% and protein of 24.02%. The crossings of SG and SI of 0.98% and 1.02% for ash, 22.71% and 23.4% for protein, respectively. The SG presented a concentration of cholesterol of 48.29 mg/100g of total lipids; while the SI was 46.9 and the NE 46.44mg/100g. The difference in the cholesterol concentration in the muscle is probably associated with the structure of the cells that composes the muscle. The different genetic groups evaluated do not alter the carcass characteristics, but differ in chemical composition of *Longissimus* muscle

Key Words: yield grade, cholesterol, fat thickness

T27 Efficacy of day 23 GnRH for CIDR-Select estrus synchronization for beef heifers bred 12 hours after estrus or by fixed-time AI. J. L. Seabrook*, R. K. Peel, G. E. Seidel, and J. C. Whittier, *Colorado State University*, *Fort Collins*.

The objective of this study was to compare AI pregnancy rates resulting from administration of the CIDR Select synchronization protocol either with or without administration of d 23 GnRH. Angus and Hereford heifers at 4 locations were randomly assigned to treatments, blocking for body condition score and frame score. All heifers received 100 µg GnRH i.m. and a CIDR (1.38 g progesterone) d 0 – 14. Heifers assigned to the CIDR Select with GnRH received 100 µg GnRH i.m. on d 23; controls were processed through the facilities but did not receive GnRH. All heifers received 25 mg dinoprost tromethamine (PG) i.m. on d 30. The breeding protocol for Experiment 1, conducted at 3 locations (n = 270), was to breed heifers 12 ± 2 h after exhibition of estrus (n = 132); heifers that were not observed in estrus within 60 h from PG received 100 µg GnRH i.m. and were fixed-time AI (TAI) 60 ± 2 h after PG administration (n = 138). For Experiment 2, heifers at a fourth location (n = 326) were fitted with heat detection patches at the time of PG administration, which were scored when all were TAI 60 ± 2 h later. Treatment was not a source of variation in conception rates for heifers in Experiment 1: GnRH treated 56.4%, no GnRH 52.9% ($P = 0.58$). Heifers observed in estrus within 60 h after PG had a higher conception rate, averaged over the d 23 GnRH treatments, than heifers TAI (63.9%, 45.1% respectively; $P < 0.01$). Conception rates for heifers in Experiment 2 also were not affected by treatment: GnRH treated 57.1%, no GnRH 55.9% ($P = 0.83$). Patch score was correlated with a positive pregnancy diagnosis ($P < 0.01$); heifers with pristine patches had lower conception rates (34.8%) than those with fully worn patches (62.8%). Administering GnRH on d 23 of the CIDR-Select synchronization protocol was not associated with higher conception rates in these experiments.

Key Words: beef heifer, CIDR-Select, GnRH

T28 Fatty acid profile of feedlot Brangus bullocks fed with monensin or polyclonal antibodies. R. S. Barducci*[1,2], L. M. N. Sarti[1], M. D. B. Arrigoni[1], R. D. L. Pacheco[1], D. D. Millen[1], C. L. Martins[1], S. R. Baldin[1], F. S. Parra[1], J. R. Ronchesel[1], T. M. Mariani[1], J. P. S. T. Bastos[1], T. C. Putarov[1], D. Tomazella[1], and H. D. Rosa[1], [1]*FMVZ/UNESP*, *Botucatu, São Paulo, Brazil*, [2]*Apoio FAPESP*, *São Paulo, Brazil*.

This study was designed to test the effects of polyclonal antibody preparation (PAP) against lactate-producing rumen bacteria or monensin (MON) on fatty acid profile of feedlot Brangus (BR) bullocks. The experiment was designed as a 2 × 2 factorial arrangement, with 6 replications (3 bullocks/pen), which 72 9-mo-old bullocks (285.9 ± 38.7 kg) were distributed in 4 treatments and the animals were fed diets containing no additive (control), MON at 30 mg•kg^{-1} of DM, PAP at 450 mg•kg^{-1} of DM and PAP+MON (30 mg•kg^{-1} + 450 mg•kg^{-1}) for 112-d. Animals were adapted for 21-d before a high concentrate diet. The diet contained 47.5% high moisture corn, 20% citrus pulp, 12.8% soybean meal, 13.7% sugarcane bagasse, 4.6% Cynodon hay and 1.5% supplement. After slaughter, the carcass were chilled for 24-h and samples of back fat thickness of Longissimus dorsi muscle were collected from 48 animals (12 animals of each treatment) and stored for fatty acid profile analysis. No significant effects were observed among treatments ($P > 0.05$) for the variables of fatty acid profile. However, a significant ($P < 0.05$) PAP x MON interaction was observed for PUFA, which animals fed MON presented lower value ($P < 0.05$) than those fed PAP+MON (2.179 vs. 2.534 g/100g, respectively). Thus, the supplementation of PAP or MON separated was not a good alternative to improve fatty acid profile; however when both additives are fed together (PAP+MON) can be a useful tool to get better fatty acid profile, in this study there was a synergism between both additives.

Key Words: PAP, profile fatty acids, monensin

T29 Shelf-life characteristics of longissimus muscle of feedlot bullocks supplemented with vitamin D and E. S. R. Baldin*[1,2], F. S. Parra[1], J. R. Ronchesel[1], N. R. B. Consolo[3], M. D. B. Arrigoni[1], D. D. Millen[1], C. L. Martins[1], R. D. L. Pacheco[1], R. S. Barducci[1], L. M. N. Sarti[1], D. Tomazella[1], A. L. Campanini[1], J. M. P. Silva[1], A. S. C. Pereira[1], D. P. D. Lanna[4], [1]*FMVZ/UNESP*, *Botucatu, São Paulo, Brazil*, [2]*Apoio FAPESP*, *São Paulo, Brazil*, [3]*USP*, *Pirassununga, São Paulo, Brazil*, [4]*ESALQ*, *Piracicaba, Sã Paulo, Brazil*.

The objective of this study was to evaluate the effects of vitamins D and E supplementation on shelf-life characteristics: color, pH and fatty acid profile of longissimus muscle (LM) of feedlot bullocks. It was used 36 7-mo-old bullocks: 18 Nellore (NE) and 18 Canchim (CC; 5/8 Charolais, 3/8 Nellore), arranged in a 2 × 2 factorial design. During 47 d and 10 d before slaughter, 9 bullocks from each breed type were supplemented daily with vitamin E at 1300 IU and vitamin D at 7.5 × 10^6 IU, respectively. LM samples were harvested between 12th and 13th ribs and placed on polystyrene trays, covered with PVC plastic film and exposed to cooling, all of wich simulated retail display conditions. Temperature varied between 0°C and 4°C and light controlled (125 lx), during 7 d. Daily, samples were unpacked, exposed to the environment for 20 min and then, measurements of color and pH were taken. For the fatty acids profile analysis, it was collected subcutaneous fat subsamples at the day zero (PO) and at d 7 (P7). There was no effect ($P > 0.10$) of vitamin D and E supplementation for the variables in this study. There was an effect ($P < 0.05$) of period on color and pH, but on P3, samples of all treatments presented undesirable color for consumption. According to the fatty acids profile (g/100g), there was an effect of genetic group ($P < 0.05$) for: C14:0 (NE:23.75 vs. CC:25.83), C18:1 (NE:47.31 vs. CC:43.13), C18:2C9T11 (NE:0.79 vs. CC:0.67), SFA (NE:41.83 vs. CC:46.60), UFA (NE:56.59 vs. CC:51.77) and MUFA (NE:54.47 vs. CC: 49.59). Also, there was an effect of period ($P < 0.05$) on C18:1 (P0:44.78 vs. P7:45.76), C18:2C9T11 (P0:0.69 vs. P7:0.76) and C18:1T10T11T12 (P0:1.21 vs. P7:0.36). All in all, vitamin D and E supplementation did not improve shelf-life characteristics in this study.

Key Words: cooling, color, fatty acid profile

T30 Effect of Vitamin D and E supplementation on attributes of meat tenderness of feedlot bullocks. S. R. Baldin*[1,2], F. S. Parra[1], J. R. Ronchesel[1], N. R. B. Consolo[3], M. D. B. Arrigoni[1], D. D. Millen[1], C. L. Martins[1], R. D. L. Pacheco[1], R. S. Barducci1[1], L. M. N. Sarti[1], D. Tomazella[1], A. L. Campanini[1], F. A. S. Miquilin[1], A. S. C. Pereira[3], D. P. D. Lanna[4], [1]*FMVZ/UNESP*, *Botucatu, São Paulo, Brazil*, [2]*Apoio FAPESP*, *São Paulo, Brazil*, [3]*USP*, *Pirassununga, São Paulo, Brazil*, [4]*ESALQ*, *Piracicaba, Sã Paulo, Brazil*.

The study, conducted at São Paulo State University feedlot, Botucatu campus, was carried out to evaluate the effects of vitamins D and E supplementation on attributes of meat tenderness of 2 different genetic groups of feedlot bullocks. It was used 36 7-mo-old bullocks: 18 Nellore (NE) and 18 Canchim (CC; 5/8 Charolais, 3/8 Nellore), with average initial body weight of 234.53 ± 22.15 and 248.13 ± 34.67 kg, respectively, arranged in a 2x2 factorial design (supplementing vitamins x genetic group). Cattle were fed for 135 d, including 27 d of adaptation (AD). During 47 d before slaughter, 9 bullocks from each genetic group were daily supplemented with vitamin E at 1300 IU Also, the same bullocks 10 d before slaughter, were daily supplemented with vitamin D at 7.5 × 10^6 IU. On 10th d of vitamin D supplementation, blood samples were collected from jugular vein for plasmatic Ca evaluation. Rib eye samples were harvested between 12th and 13th ribs for analysis of Shear Force (SF), miofibrilar fragmentation index (MFI), total lipids (TL) and vitamin D and E meat concentrations. There was no effect ($P > 0.10$) of

vitamin D and E supplementation on SF, MFI, TL and vitamin D and E meat concentrations. Nevertheless, cattle fed with vitamin D and E had greater ($P < 0.05$) plasmatic Ca level in relation to control (189.7 vs. 152.40 mg/L). However, for genetic group, CC presented greater ($P < 0.05$) value of MFI than NE (69.07 vs. 62.61), and NE presented greater ($P < 0.05$) vitamin D and E meat concentrations (mg/kg) in relation to CC (0.19 vs. 0.03 and 2.88 vs. 1.29, respectively). The supplementation of vitamin D and E increased plasmatic Ca concentration, but it was not effective to enhance attributes of meat quality of 2 different genetic groups of feedlot bullocks.

Key Words: vitamin E, vitamin D, meat

T31 Influence of weaning strategy on growth and immunity in beef calves. L. B. Krebs*, A. Loyd, and E. G. Brown, *Stephen F. Austin State University*, *Nacogdoches, TX*.

The prevailing method of weaning calves involves abrupt separation from cows resulting in change in feed and living environment. These changes result in behavioral and physiological responses indicative of distress that are unfavorable to beef production and animal welfare. Twenty-six crossbred beef calves and their dams were used to evaluate stress and performance responses to 2 weaning strategies (2-stage and fenceline) independent of each other and in combination compared with traditional abrupt weaning. Cows and calves were assigned to treatments based on calf body weight and parity of the cow. Four days before weaning, one group of calves (n = 13) were fitted with an antisuckling device (2-stage) while remaining with the herd. At weaning, devices were removed and half of these calves were moved to a remote location (abrupt) and half placed in a pasture adjacent to their dam (fenceline). The calves not fitted with an antisuckling device before weaning (n = 13) were moved to a remote location or placed in a pasture adjacent to the dam in the same proportion as the previous group. Blood samples were collected on all cows and calves on d −4, 0, and 4 to measure white blood cell count, lymphocytes and neutrophils. Cows and calves were weighed on d −4, 0, and 28. Body condition scores were collected on cows on d −4, 14, and 28. No difference ($P = 0.38$) was observed for ADG in calves before weaning between treatments, but ADG was greater ($P < 0.001$) in fenceline weaned calves compared with abrupt separation. No differences ($P < 0.25$) were observed for white blood cell count, lymphocytes, neutrophils, or lymphocyte:neutrophil ratio in cows or calves. Average daily gain and body condition scores in the cows were not affected ($P < 0.20$) by weaning strategy. Results suggest that fenceline weaning may be an alternative to traditional weaning practices.

Key Words: weaning, fenceline weaning, immunity

T32 Effects of origin, breed, sex and season on productive performance of cattle arriving to feedlots located in northern Mexico (Mexicali, B.C.). L. C. Muñoz-Salas[1], C. F. Arechiga*[1], J. I. Aguilera-Soto[1], M. A. Lopez-Carlos[1], S. Mendez de Lara[1], F. Mendez-Llorente[1], M. Rincon[1], F. J. Gutierrez[1], C. A. Medina-Flores[1], L. Avendaño-Reyes[2], and A. Correa-Calderon[2], [1]*Universidad Autonoma de Zacatecas*, *Zacatecas, Mexico*, [2]*Universidad Autonoma de Baja California*, *Mexicali, BC, Mexico*.

Objective of present trial was to determine the effects of place of origin and nutritional source, breed, sex, season and initial weight on productive performance of cattle arriving to feedlots located in northern Mexico. Average daily gain (ADG), feedlot feeding period (FFP), and carcass quality (CQ; i.e, dressing percentage) was evaluated. Cattle (n = 12,437), were allotted into 236 feedlots. The study included mostly heifers (n = 8,342), but also yearling bulls, steers and cows. Data was analyzed by SAS proc GLM including origin, breed, sex, year and initial weight as main effects. Feedlot feeding period and average daily gain was 95.2 d and 1.55 kg for cattle consuming forage; 114 d and 1.42 kg for cattle already consuming a mixed ration in another feedlot; 124 d and 1.42 kg for cattle coming from irrigated prairies; 131 d and 1.42 kg for cattle coming from commercial reception pens; and 133 d and 1.46 kg for cattle coming directly from pasture. Carcass quality was 60.9, 64.7, 61.1, 61.6 and 61.9%, respectively. Breed affected ADG, FFP, CQ ($P < 0.05$) whereas sex did not ($P > 0.05$). Summer season compromised productivity compared with the other seasons ($P < 0.05$). Initial weight entering feedlot also affected FFP and ADG. Heavier animals had a shorter feeding period and a greater weight gain. Thus, we conclude that cattle origin, breed, season and initial weight entering feedlot surely affected feedlot feeding period, average daily gain and dressing percentage.

Key Words: beef cattle, feedlot, Mexico

T33 Number of days to accurately measure individual feed intake in lactating females. K. A. Gray*, B. L. Winslow, M. H. Poore, and J. P. Cassady, *North Carolina State University*, *Raleigh*.

The objective of this study was to evaluate relationships among feed intake over different periods of time within a 104 d period in Angus females. Data were collected at the Upper Piedmont Research Station in Reidsville, NC. In February lactating Angus females (n = 35) began the feeding period weighing 470 ± 7.8 kg at 3 years of age while calves ranged in age from 7 to 70 d of age. All cows in this study were previously trained and adapted to the Calan gates for a period of 98 d when they were growing heifers. Cows were assigned the same gate as they had when they were heifers. Cows were allowed a 2-wk period of readaptation to Calan gates and were fed a roughage-based ration targeted to maintain body weight. Following readaptation, cows began a 104 d test. Feed offered was recorded daily and body weights for both cow and calf were taken every 14 d. Linear regression of weight on time was used to estimate ADG for cow and calf. Cow ADG was slight at 0.25 ± 0.025 kg/d and calf ADG was 0.84 ± 0.033. Average daily dry matter intake (DMI) was estimated for different periods of time within the 104 d test. Every combination of 28, 35, 42, 49, 56, 63, 70, 77 and 84 d period within the 104 d test was used to estimate different DMI for each period consisting of a total of 146 different periods. Correlations were then calculated among all combinations of DMI periods to determine if a shorter test trial would be sufficient to estimate DMI and to determine if feed intake differed due to stage of lactation. It was found that the best estimate for the 104 d DMI were the 4 84 d periods specifically the middle 2 84 d periods ($r_p = 0.99$). As duration of DMI periods decreased correlation between the period and 104 d DMI slightly decreased, as expected. Among the 10 42 d periods it was found that the correlation between the 42 d period and the 104 d DMI had only decreased to 0.90 - 0.95. It was concluded that DMI measured over 104 d and 42 d had a high correlation making it possible to decrease the duration of the testing time while maintaining accurate estimates of DMI.

Key Words: Angus cows, lactating, dry matter intake

T34 Effect of cutting time and maceration on nitrogen utilization of trefoil-grass hay by growing steers. A. F. Brito*[1], C. Lafrenière[2], and R. Berthiaume[2], [1]*University of New Hampshire*, *Durham,* [2]*Agriculture and Agri-Food Canada*, *Sherbrooke, QC, Canada*.

Feeding forage cut at sundown (PM) has been shown to improve N utilization by cattle. However, nutritional value of PM forage may be

compromised due to rainfall, prolonged wilting time, leaching, and respiration. Maceration can enhance field drying and reduce wilting time. A birdsfoot trefoil-grass field was divided in 4. Half was cut at 1800 h (PM) with 50% of the PM herbage macerated after 12 h (PMM) and left to wilt. The other half was cut at 0600 h (AM) the next morning with 50% of the AM herbage macerated after 4 h (AMM) and left to wilt. The 4 hays were field dried, baled at the same time, and chopped before feeding. Four steers were used in a 4 × 4 Latin square with a 2 × 2 factorial arrangement of treatments to investigate the effects of forage cutting time (CT) and maceration (MAC) on N balance. Total collection of urine and feces were done for 6 consecutive days at the end of each 21-d period. Concentration (% DM) of CP averaged 11.6 (PM), 11.2 (AM), 10.2 (PMM), and 10.2 (AMM), while that of water soluble carbohydrates averaged 9.0 (PM), 7.0 (AM), 9.5 (PMM), and 8.1 (AMM). Intake of N was lowest in the macerated hays reflecting hay composition. Fecal N excretion (% of N intake) was greater (P = 0.04) in macerated vs. non macerated hays. Steers fed PM-cut hays had reduced (% of N intake) excretions of urinary N (P = 0.08) and manure N (P = 0.03), and enhanced retained N (P = 0.03). Significant CT x MAC interactions were observed for manure N and retained N as % of N intake, showing that non macerated PM-cut hay had the lowest excretion of manure N and the greatest N retention. Maceration had no effect on N retention by cattle fed trefoil-grass hay.

Table 1. Effect of cutting time and maceration on N intake (g/d) and N balance (% of N intake)

	Treatments					P		
Item	PM	AM	PMM	AMM	SED	CT	MAC	CT x MAC
N intake	129	112	106	108	4.93	0.08	<0.01	0.04
Fecal N excretion	40	43	46	44	1.77	0.63	0.04	0.08
Urinary N excretion	32	37	33	35	2.66	0.08	0.70	0.47
Manure N excretion	72	81	78	79	2.32	0.03	0.24	0.05
Retained N	28	19	22	21	2.32	0.03	0.24	0.05

Key Words: maceration, cutting time, steers

T35 Temperature during summer transport of Canadian feeder cattle at high and low loading densities. C. Goldhawk*[1,2], E. Janzen[1], L. González[4], T. Crowe[3], J. Kastelic[2], E. Pajor[1], and K. Schwartzkopf-Genswein[2], [1]*University of Calgary*, *Calgary, Alberta, Canada*, [2]*Agriculture and AgriFood Canada*, *Lethbridge, Alberta, Canada*, [3]*University of Saskatchewan*, *Saskatoon, Saskatchewan, Canada*, [4]*University of Manitoba*, *Winnipeg, Manitoba, Canada*.

A recent survey of cattle transport in Canada found that despite traveling similar distances, feeder cattle have greater shrink and spend more time on truck than fat cattle. These results create concern about the conditions during transport for feeder cattle. Preliminary temperature results are available from a larger study evaluating the effects of loading density during feeder cattle transport (700–900 kg BW). The temperature in the belly (B) and top deck (TD) of 7 commercial loads were monitored over an 11 h journey. Loading density (H = 0.767 m^2/animal; L = 0.876 m^2/animal) was alternated between compartments within loads, yielding 3 replicates of HB, 4 LB, 4 HTD and 3 LTD. Twelve temperature loggers were placed throughout each compartment, 1 on each side mirror of the truck and 1 on the ear tags of 4 focal animals in each compartment. Ambient temperature ranged from 10 to 34°C in the am and 24–34°C in the pm. The average temperature at the ceiling of a compartment was 2.3°C higher than the ambient temperature. On average, temperatures at the animal level were 0.78°C higher than at the ceiling of the compartments during stationary periods and 1.07°C higher than the ceiling temperature during transit. During transit, temperatures at animal level ranged from 13.7 to 29.6°C in the HB treatment and from 8.3 to 29.5°C in the HTD treatment. Similarly, during transit, temperatures at animal level ranged from 10.5 to 29.8°C in LB and from 12.5 to 31.3°C in LTD. The highest temperatures at animal level were recorded during prolonged stationary periods of 1.5–3.5 h (border crossing). During the first 10 min of the stationary period, before unloading the cattle for inspection, compartment temperatures at animal level rose by 0.9°C in the B and 2.4°C in the TD. Upon reloading, compartment temperature at animal level peaked after 20 min at 26–32°C and stayed within this range for the remainder of the stationary time at the border. Given the concurrent stressors experienced by cattle during transportation, the range of temperatures recorded during these loads warrant further investigation to determine the relationship between trailer microclimate and cattle well-being.

Key Words: cattle, transportation

T36 Comparative genomics: The Guinea Fowl satiety center. N. Bonner*, J. Tyus, and S. Nahashon, *Tennessee State University*, *Nashville*.

Genetic influence of the mechanisms driving feeding behavior and energy homeostasis in avians has not been fully elucidated; hence there is a paucity of such information in the Guinea Fowl (GF). Recent advances in genomics, proteomics and bioinformatics have made these mechanisms less difficult to evaluate, but assays aimed at developing GF genetic improvement programs continue to lag. The GF has tremendous potential as a viable poultry meat species in the US and globally. Generating genetic information for the GF is essential for its improvement and in comparative mapping of avian species of economic importance. The primary aim of this study was to compile a comprehensive database of genes expressed in GF center of satiety. Messenger RNA was isolated from ventromedial hypothalamus and pituitary of adult GF. Following reverse transcription, cDNAs were cloned into the pBluescript plasmid vector using the Stratagene cDNA Library Construction Kit. Approximately 1000 clones were selectively screened via blue-white selection, restriction digestion and PCR. Positive clones were cycle-sequenced by PCR and analyzed with the ABI PRISM 3100-Avant Genetic Analyzer. A second objective was to comparatively analyze GF gene fragments against homologs from other poultry species. Guinea fowl nucleotide sequences were subjected to sequence homology searches using the megablast option of NCBI's Basic Local Alignment Search Tool. Nucleotide sequence similarity between GF and other avian species averaged 76.5%. Nucleotide sequences exhibiting high homology (~80%) with other avian species averaged 685.6 bases in length and ranged from 293 to 1,025 bases. Nearly 12% of the nucleotide sequences analyzed showed no significant similarity to any available sequence data. Gene fragments generated from this work are currently being used to develop oligonucleotide primers for quantitative PCR and expressed sequence tags for selective breeding.

Key Words: Guinea Fowl genomics, satiety, hypothalamus

T37 Divergent selection for 4-week body weight in Japanese quail: Relationship between blood parameters and carcass characteristics. H. Beiki*, A. Pakdel, and M. Moradi Shahre Babak, *University of Tehran*, *Iran*.

The current study has been carried out to investigate the relationship between blood parameters and carcass characteristics in Japanese quail. Quail lines utilized were 2 lines divergently selected for high (HW) and low (LW) 4-wk body weight following 7 generations and also a control line (C). To investigate quail blood parameters, 15 quail from each line were selected randomly at 42-d of age. Blood samples were taken from the jugular vein just before slaughter and carcasses were measured individually. The plasma cholesterol content of HW line quail were significantly higher than for quail from the LW and C lines. There was a significant correlation (0.99) between serum hematocrit level and breast depth in the HW, LW and control (0.99) lines ($P < 0.01$). There was also a significant correlation between ovary weight and serum triglyceride level (TG) in the HW (0.82) and LW (0.87) lines ($P < 0.01$). Liver weight in the LW line was significantly correlated with TG level (0.82) ($P < 0.01$), and the correlation between testis weight and TG in the LW line (−0.96) was also significant ($P < 0.01$). The results of current study indicated that carcass characteristics and blood parameters of Japanese quail were greatly affected by short-term divergent selection. Thus, to prevent undesirable side effects of selection in this species, like those that have occurred in broilers, we must refine the breeding goal into a broader perspective and consider changes in physiological traits in the breeding goal.

Key Words: quail, divergent selection, blood parameters

T38 Genetic variation in physiological responses following heat stress in laying hens. J. N. Felver-Gant*[1], L. A. Mack[1], R. L. Dennis[2], and H. W. Cheng[2], [1]*Purdue University*, *West Lafayette, IN,* [2]*Livestock Behavior Research Unit, USA-ARS*, *West Lafayette, IN*.

Heat stress (HS), also known as hyperthermia, is a major problem experienced by poultry during high-temperature conditions. The ability to manage the detrimental effects of HS can be attributed to many factors, including genetics. The objective of the present study was to determine the variation of effects that HS poses on the well-being of laying hens. Ninety 28-wk-old White Leghorns of 2 strains were used; a line of individually selected hens for high productivity and survivability, DeKalb XL (DXL), and a line of group-selected hens, kind gentle bird (KGB). Hens were randomly paired, housed by strain and assigned to hot (H) or control (C) treatments for 14 d (mean: C = 24.3°C, H = 32.6°C). Physiological measures were collected at d 8 and 14. Behavior data was collected at d 1, 2, 6, 9, and 13. Compared with controls, H-hens core temperature (CT) was significantly higher at d 8 and 14 ($P < 0.05$). Heterophil:lymphocyte ratios were significantly higher in H-hens at d 14 ($P < 0.05$). H-hens had significantly reduced liver wt (LW) and spleen wt (SW) at d 8 and 14 ($P < 0.05$) and body wt (BW) at d 14 ($P < 0.05$). H-hens tended to have reduced BW at d 8 ($P < 0.10$) and heart wt (HW) at d 14 ($P < 0.10$). H-DXL had significantly reduced LW than H-KGB at wk 1 ($P < 0.05$). Behaviorally, H-hens opened their wings significantly more than C-hens ($P < 0.05$). C-hens did not initiate thermal panting. H-KGB hens exhibited panting behavior significantly more than H-DXL ($P < 0.05$). The data suggest that HS has detrimental effects on the physiology of laying hens. However, differences can be observed in the results of this study due to the genetic basis for variations in heat stress response.

Key Words: heat stress, genetics, laying hen

T39 Genome-wide copy number variation and temporal gene expression analysis in Marek's disease-resistant and -susceptible inbred chickens. Y. Yu[1], A. Mitra[1], H. Zhang[2], F. Tian[1], G. Liu*[3], and J. Song[1], [1]*University of Maryland*, *College Park,* [2]*USDA-ARS-ADOL*, *East Lansing, MI,* [3]*USDA-ARS*, *Beltsville, MD*.

Viruses that cause cancers are a great threat to human and animal health. Marek's disease (MD) in chickens is a lymphoproliferative disease caused by Marek's disease virus (MDV). The overexpression of Hodgkin's disease antigen in MD makes it an ideal model to study the progression mechanism of Hodgkin's disease in vivo. Three inbred chicken lines (L63, L72 and LM) with different reactions to MDV were used to perform array-based comparative genomic hybridization (CGH) and gene expression microarray experiments at different time points (5dpi, 10dpi and 21dpi) of virus infection, with the objective of comparing copy number variation (CNV) with MDV indicator traits. A total of 43 CNV were found in the 3 chicken lines with the total size ranging from 1.4 Mb in L72 to 1.6 Mb in LM. While only 22% of the sequence found within CNV regions in L63 (MD-resistant) and LM (intermediate in MD-resistance) is unique, about 62% is unique in L72 (MD-susceptible) chickens. Several anti-viral pathways, and particularly the NF-κB pathway, were found activated in the early cytolytic stage (5dpi) in L63 chickens. The array-CGH and gene expression microarray

results revealed a CNV loss located on chromosome 4 present in both L63 and LM chickens but absent in L72 chickens that is associated with the expression of a CD8α homolog before and after MDV infection. To our knowledge, this is the first time a CNV loss has been found that might be related to MD-resistance in chickens.

Key Words: copy number variation, microarray, genetics

T40 Broiler breeders with an efficient innate immune response are more resistant to coccidial infections. C. L. Swaggerty*[1], K. J. Genovese[1], H. He[1], J. R. Nerren[1], I. Y. Pevzner[2], and M. H. Kogut[1], [1]*United States Department of Agriculture*, *College Station, TX,* [2]*Cobb-Vantress, Inc.*, *Siloam Springs, AR*.

Coccidial infections cost the poultry industry an estimated $600 million in low carcass weights and prophylactic drugs per year. For the past several years we have characterized the innate immune response of 2 broiler breeder lines (A and B) and their F1 reciprocal crosses (C [B sire x A dam] and D [A sire x B dam]) and compared their resistance against Salmonella, Enterococcus, and Campylobacter challenges. In all cases, line A and cross D are more responsive and more resistant than line B and cross C. Now, we want to determine if the trend is also observed following separate challenges with the protozoan parasites, *Eimeria tenella* (ET), *E. maxima* (EM), or *E. acervulina* (EA). Fourteen-day-old chickens from lines A and B and cross C and D were challenged orally with 15–50 × 10^3 ET, 10–40 × 10^3 EM or 25–50 × 10^3 EA oocysts. Birds were sacrificed 6 d post-challenge and the appropriate region of the gut was removed and scored for lesions (ET in the ceca; EM in the mid-gut; EA in the duodenum) and final body weight (BW) compared with non-infected controls. Regardless of the challenge species or dose administered, line A and cross D birds were more resistant to intestinal pathology as demonstrated by lower lesion scores compared with B and C, respectively. As might be expected, the lower lesion scores in line A and cross D chickens were accompanied by higher final BW compared with line B and cross C chickens, thus reducing potential revenue loss associated with low carcass weights in coccidia-infected birds. The results from this study showed that in addition to improved resistance against bacterial infections line A and cross D chickens are also more resistant to coccidial infections compared with line B and cross C birds. Taken together with all of our earlier studies utilizing these lines, an efficient innate immune response protects against a broad range of food-borne and poultry pathogens including costly coccidial infections.

Key Words: genetics, coccidia, innate immunity

T41 Expression of the peptide transporter, PepT1, in chickens from high and low weight-selected lines and their F1 and F2 crosses. B. Zwarycz*, E. A. Wong, P. B. Seigel, and C. R. Mott, *Virginia Polytechnic Institute and State University*, *Blacksburg*.

PepT1, a peptide transporter located in the brush border membrane of the small intestine of chickens, is important in the uptake of amino acids in the form of di- and tri-peptides. Thus, PepT1 plays an important role in growth and feed efficiency. The objective of this study was to determine PepT1 expression and inheritance in the duodenum, jejunum, and ileum of chickens selected for high or low body weight and their F1 and F2 progeny. Parental line chickens selected for 51 generations for high (H) or low (L) 8-week body weight were mated to produce 4 types of progeny. These were parental lines (LxL and HxH) and reciprocal F1 crosses (HxL and LxH). Only males were used in the analysis. On d7 posthatch, LxL chicks had the lowest body weights and the highest levels of PepT1 mRNA in the small intestine, whereas the HxH chicks had the heaviest body weights and lowest levels of PepT1 mRNA. The reciprocal F1 chicks were intermediate in body weight and PepT1 levels. An F2 generation, produced by random matings of LxH and HxL parents, had a greater range in body weights and PepT1 expression levels than the F1 crosses. This 3 generation mating study suggests polygenic inheritance for PepT1 in chickens

Key Words: chicken, PepT1, transporter

T42 Genetic properties of feed utilization efficiency parameters. S. E. Aggrey*[1], A. B. Karnuah[1], and N. B. Anthony[2], [1]*University of Georgia*, *Athens,* [2]*University of Arkansas*, *Fayetteville*.

Feed costs constitute about 70% of the total production costs; however, the efficiency of feed utilization has not kept up with the growth potential of today's broilers. Improvement in the efficiency of feed utilization will reduce the amount of feed required for growth, which will directly reduce production cost, increase profitability, and subsequently reduce the amount of manure produced. We estimated genetic parameters of feed conversion ratio (FCR) and residual feed consumption (RFC) in a random mating broiler control population using DFREML and determine nutrient factors that affect both traits. The heritability of FCR and RFC were 0.22 and 0.11, respectively with genetic correlation of 0.72. However, when maternal effects were included in the model, the genetic correlation increased to 0.98, probably suggesting that maternal components influence feed utilization efficiency and as a result both nuclear and mitochondrial genomes are important in deciphering the genetic factors affecting feed utilization efficiency. Among the nutrient factors, it was determined that protein energy and calcium retentions greatly affected feed efficiency.

Key Words: feed efficiency, genetic parameters, chicken

T43 Analysis of ascites susceptibility using genetic markers in commercial broilers. S. Krishnamoorthy*, N. Anthony, D. Rhoads, R. Wideman, and G. Erf, *University of Arkansas*, *Fayetteville*.

Although the ascites syndrome in chickens has been investigated for years, it continues to inflict financial losses within the global poultry industry. It is estimated that annually 5% of the 40 billion world broiler population succumbs to ascites, thus leading to yearly losses of millions of dollars. Efforts to curb the incidence of ascites are typically designed to slow early growth. This limits the bird's ability to show its true genetic potential and impacts later yields. In 1994, lines divergent for susceptibility to ascites were established from a commercial sire line through sibling selection of birds reared at local altitude, after testing sibs reared under simulated high altitude conditions. We used a whole genome SNP array to identify 7 potential regions associated with susceptibility. After 16 generations of selection, the selected lines changed in allele frequency for 2 regions on chromosome 9, as compared with each other and with the line of origin. Changes were consistent with patterns of susceptibility and resistance to ascites. In addition to the research populations, we determined that 2 ascites susceptible commercial lines are also segregating for resistance related alleles in these regions. The data support the predictive nature of these loci, in that the presence of a specific genotype is associated with resistance to ascites, which suggests that one or more genes within these regions might play an important role in ascites development. Future research will include reducing the incidence of ascites in susceptible commercial lines through marker-assisted selection.

This work has been supported by NIH/NHLBI Grant 1R15HL092517 01 and The Arkansas Biosciences Institute.

Key Words: ascites, genetic markers

T44 Using quantitative PCR to investigate three candidate genes related to pulmonary hypertension in the chicken. A. A. Al-Rubaye*, N. B. Anthony, G. F. Erf, R. F. Wideman, and D. D. Rhoads, *University of Arkansas*, *Fayetteville*.

Idiopathic pulmonary arterial hypertension syndrome (IPAH) is a disease of humans and chickens that results from chronic high pulmonary arterial pressure. IPAH in broiler chickens results in right-sided congestive heart failure leading to ascites that, if not aggressively treated, will result in death. We have been mapping chicken genes affecting resistance or susceptibility to IPAH. Previously, we identified 2 regions on Gga9 and one on Gga27 that show significant linkage disequilibrium to IPAH in our lines. Within these regions we identified 3 candidate genes that are known to be related to susceptibility to pulmonary hypertension in humans. Those genes are ACE, HTR2B, and AGTR1. We are examining the expression of these 3 genes in chicken IPAH using reverse transcriptase quantitative PCR. Initial analyses have detected significant differences in the expression levels for 2 of the candidate genes in whole blood RNAs. We are expanding the analyses to include increased numbers of samples and a wider range of tissues.

This work was supported by grants from the Arkansas Biosciences Institute and NIH/NHLBI Grant 1R15HL092517 01.

Key Words: QPCR, pulmonary hypertension syndrome, chicken IPAH

T45 Selection of the best model for estimation of genetic parameters for growth traits in Iranian Moghani sheep. N. Ghavi Hossein-Zadeh*[1] and M. Ardalan[2], [1]*Department of Animal Science, Faculty of Agriculture, University of Guilan*, *Rasht, Iran*, [2]*Department of Animal Science, University College of Agriculture and Natural Resources, University of Tehran*, *Karaj, Iran*.

The objective of this study was to estimate the genetic parameters for birth weight (BW), 3 mo weight (3MW), 6 mo weight (6MW), 9 mo weight (9MW), and yearling weight (YW) of Iranian Moghani sheep using restricted maximum likelihood via the MTDFREML program. The data and pedigree information used in this research were collected at Breeding Station of Moghani sheep (Ardebil province, Iran) during 1987–2005. Six different animal models were fitted, differentiated by including or excluding maternal effects, and including or excluding a covariance between maternal and direct genetic effects. The estimates for direct heritability ranged from 0.31 to 0.54, 0.21 to 0.34, 0.13 to 0.25, 0.11 to 0.22 and 0.10 to 0.17 for BW, 3MW, 6MW, 9MW and YW, respectively. These estimates were substantially higher when maternal effects, either genetic or environmental, were ignored in the model. The results of this study show the importance of including maternal genetic and environmental effects when estimating genetic parameters for body weight traits in Moghani sheep.

Key Words: growth traits, genetic parameters, Moghani sheep

T46 Estimates of genetic trends for body weight traits of Moghani sheep obtained by a multivariate animal model analysis. N. Ghavi Hossein-Zadeh*, *Department of Animal Science, Faculty of Agriculture, University of Guilan*, *Guilan, Rasht, Iran*.

The objective of the present study was to estimate genetic changes for body weights at different ages in Moghani sheep. Traits included were birth weight (BW, n = 4208), 3 mo weight (3MW, n = 4175), 6 mo weight (6MW, n = 3138), 9 mo weight (9MW, n = 2244), and yearling weight (YW, n = 1342). The data and pedigree information used in the current research were collected at the Breeding Station of Moghani sheep (Ardebil province, Iran) during 1989–2005. Variance components were estimated from a 5-trait analysis, based on the best model of analysis for each trait, using the MTDFREML program. Level of significance for the inclusion of effects into the model of analysis was declared at $P < 0.05$. The final model included the fixed class effects of year-season (68 levels), sex of lamb and parity of dam, birth type (single, twin, triplet), the linear covariate effect of age of dam (from 2 through 7 years old) and random direct and maternal genetic effects. The most suitable model was determined based on likelihood ratio tests for each trait. Breeding values of individual animals were predicted with Best Linear Unbiased Prediction (BLUP) methodology and obtained from a multivariate animal model analysis and genetic trends were obtained by regressing the means of predicted breeding values on year of birth for each trait. Estimates of direct heritabilities for BW, 3MW, 6MW, 9MW, and YW were 0.29, 0.13, 0.14, 0.10, and 0.31, respectively. Estimates of maternal heritabilities were 0.29 for BW, 0.08 for 3MW, 0.11 for 6MW, 0.06 for 9MW, and 0.10 for YW. Direct genetic trends were positive and significant ($P < 0.05$) for BW, 3MW, 6MW, 9MW and YW and were 1.63, 69.20, 79.38, 66.83 and 110.22 g/year, respectively. Also, maternal genetic trend for BW, 3MW, 6MW, 9MW and YW were positive and significant ($P < 0.05$) and were 2.36, 49.18, 37.33, 17.73 and 9.67 g/year, respectively. The results showed that improvement of body weights of Moghani sheep seems feasible in selection programs.

Key Words: Moghani sheep, growth traits, genetic trend

T47 Association of polymorphisms in the FecB gene with litter size in Wadi sheep. Y. Ren*[1,2], Z. Shen[1,2], M. Li[3], N. Xiao[3], W. Dong[3], and S. Fu[1], [1]*Binzhou Animal Science & Veterinary Medicine Institute*, *Binzhou Shandong, China*, [2]*Research and Development Center of Wadi Sheep Breeding Technology*, *Binzhou Shandong, China*, [3]*Shandong Lvdu Biotechnology Co., Ltd.*, *Binzhou Shandong, China*.

Wadi sheep in the Shandong proving of China are known for fecundity and antireversion. About 20–30% Wadi sheep have 4 nipples, which leads to a tendency for fecundity and high galactosis. The FecB gene, a major gene for fecundity in the Booroola Merino breed, is caused by a 1-base mutation of BMPR-IB and increases litter size by increasing ovulation rate. Polymorphisms within the FecB gene of Wadi sheep and associations with litter size were analyzed by PCR-RFLP to study the fecundity of Wadi sheep on molecular level. This results showed that there was FecB mutation in Wadi sheep that was the same as in Booroola, and the frequencies of 3 genotypes (B/B, B/+, +/+) were 0.29, 0.56 and 0.15, respectively. An association between genotype frequencies and number of nipples was observed. Average litter sizes for the 3 genotypes were 2.81 ± 0.42, 2.49 ± 0.53 and 1.96 ± 0.28, respectively. Statistical analysis showed that litter size of Wadi sheep with B/B and B/+ genotype was significantly greater than that of sheep with the +/+ genotype ($P < 0.01$), but differences between the B/B and B/+ genotype were not significant. In conclusion, the FecB gene could of great interest in the Wadi sheep breed due to its association with fecundity.

Key Words: Wadi sheep, FecB gene, litter size

T48 Inbreeding effects on different weights and population structure of Santa Inês sheep. M. L. Santana Júnior*, V. B. Pedrosa, P. S. Oliveira, J. P. Eler, and J. B. S. Ferraz, *Animal Breeding and Biotechnology Group, Department of Basic Sciences, College of Animal Science and Food Engineering, University of São Paulo, C. Postal 23, 13635-970, Pirassununga, SP, Brazil*.

The aim of this study was to describe the population structure and inbreeding and to quantify its effect for different weights of Santa Inês sheep in Brazil. By this reason, 6,161 production data and 17,097 animals in the pedigree data, of 6 previous generations were utilized to evaluate birth weight (BW), weight at 60 d (W60) and weight at 180 d (W180). The genetic structure analysis of population was realized by the software ENDOG (v.4.6.), resulting in some level of inbreeding for 21.72% of the animals in the pedigree data, with a maximum value of 41.02%, and average of 10.74% for the inbreed individuals. The population average inbreeding was 2.33%, and the average kinship was 0.73%. The ancestral effective number was 156 animals, and the number of population founders was 211 individuals. Parameters related to genetic variability in this population must be monitored to prevent a decrease in genetic progress. The utilization of a program for directed mating, as is presently the case in this flock, is an appropriate alternative to keep the level of inbreeding under control.

Key Words: effective population size, inbreeding, generation interval

T49 Estimates of variances due to direct and maternal effects on birth weight in Moghani sheep. M. Bayeri Yar*[1], S. Alijani[1], T. Farahvash[2], and A. Rafat[1], [1]*University of Tabriz*, *Tabriz, East Azerbijan, Iran*, [2]*Islamik Azad University,Shabestar Branch*, *Tabriz, East Azerbijan, Iran*.

Data from a total of 6,758 Moghani lambs were collected from 1995 to 2006 at the Jafar Abad sheep breeding station in the Ardebil province of Iran. Data were analyzed by DFREML using an animal model. The full general model used was as follows: $Y = Xb + Z_a a + Z_m m + Z_p pe + e$. In particular, use of model 1 resulted in high estimates of additive genetic and direct heritability (0.33). Inclusion of maternal effects (models 2, 4 and 5) resulted in much smaller estimates of h^2. Comparing models with likelihood ratio tests showed that model 5 performed significantly better than other models. Based on use of the most appropriate model for birth weight (BW), the estimated ratios of variance components (±SE) were: h^2= 0.26 (± 0.01), m^2 = 0.09 (± 0.009), pe^2 = 0.06(±0.01). Maternal effects therefore included heritable components of phenotypic variance that will respond to selection. Although estimates of h^2 also varied between the models with different maternal effect structures, these differences were minor in comparison. It has been suggested that this antagonism will limit the potential for genetic improvement of commercial flocks through artificial selection. The idea that an evolutionary response to selection on birth weight could be similarly constrained through this mechanism is supported by the negative values estimated for rams. In conclusion, there were important maternal genetic effects influencing birth weight in this population.

Table 1. Estimates of (co)variance components, genetic and phenotypic parameters of BW from a univariate analysis

Models	h^2 (±SE)	m^2 (±SE)	pe^2 (±SE)	ram	logL
1	0.33(±0.01)	—	—	—	−796.45
2	0.31(±0.01)	0.22(±0.01)	—	—	−794.68
3	0.31(±0.01)	—	0.29(±0.01)	—	−793.78
4	0.28(±0.01)	0.19(±0.009)	0.02(±0.01)	—	−793.7
5	0.26(±0.01)	0.18(±0.01)	0.12(±0.01)	−0.97	−783.85

h^2: direct heritability; m^2: maternal heritability; pe^2: maternal permanent environmental variance; ram: direct-maternal genetic correlation.

Key Words: Moghani sheep, maternal effects, birth weight

T50 Estimation of additive and non-additive genetic parameters for growth traits of Moghani sheep. M. Bayeri Yar*[1], s. Alijani[1], and T. Farahvash[2], [1]*Univeraity of Tabriz*, *Tabriz, East Azerbijan, Iran*, [2]*Islamic Azade University, Shabestar Branch*, *Tabriz, East Azerbijan, Iran*.

A total 6,758 records from Moghani lambs were collected from 1995 to 2006 at the Jafar Abad sheep breeding station in the Ardebil province of Iran. Five traits were considered; birth weight (BW),weaning weight (WW), 6-mo weight (6W), 9-mo weight (9W), and yearling weight (YW). Data were analyzed using a single-trait animal model via the DFREML software. The model was: $Y = Xb + Z_a a + Z_m m + Z_p p + e$, where Y is a vector of observations; b is a vector of fixed effects; a is a vector of direct animal genetic effects; m is a vector of maternal genetic effects; p is a vector of maternal permanent environmental effects; e is a vector of residuals, and X, Z_a, Z_m and Z_p are incidence matrices relating records for trait to fixed, direct genetic, maternal genetic, and permanent environmental effects, respectively. Results of the univariate analyses are shown in Table1. Direct heritability for body weight increased after weaning. This study showed important effects of maternal effects on growth traits, which should be considered in genetic evaluations. Direct and maternal heritability estimates obtained in this study indicated that it would be possible to improve growth traits through genetic selection at all ages.

Table 1. Estimates of (co)variance components, genetic and phenotypic parameters of growth traits from a univariate analysis

Trait	h^2 (±SE)	m^2 (±SE)	p^2 (±SE)	$r_{a,m}$
BW	0.26(±0.01)	0.18(±0.02)	0.12(±0.01)	−0.97
WW	0.23(±0.02)	0.16(±0.01)	0.07(±0.03)	−0.95
W6	0.28(±0.07)	0.12(±0.01)	0.06(±0.02)	−0.89
W9	0.33(±0.07)	0.06(±0.02)	0.024(±0.01)	−0.869
YW	0.3(±0.1)	0.02(±0.005)	0.015(±0.008)	−0.79

h2: direct heritability; m2: maternal heritability; p2: maternal permanent environmental variance; ra,m: direct-maternal genetic correlation.

Key Words: Moghani sheep, genetic parameters, growth

T51 Estimation of variance components for reproductive traits of Moghani sheep. M. Bayeri Yar*[1], s. Alijani[1], and T. Farahvash[2], [1]*Univeraity of Tabriz*, *Tabriz, East Azerbijan, Iran*, [2]*Islamic Azade University, Shabestar Branch*, *Tabriz, East Azerbijan, Iran*.

A total of 3652 records were collected from 1995 to 2006 at the Jafar Abad sheep breeding station in the Ardebil province of Iran. Four traits were measured, including conception rate (CR), litter size (LS), mean litter weight per lamb born and mean litter weight of lambs at weaning. Mixed model methodology was used to analyze all traits using a multiple-trait animal model with repeated records. Covariance components and genetic parameters were estimated using the restricted maximum likelihood method based on a derivative-free algorithm (DFREML). Estimates of direct and maternal heritability, direct-maternal genetic correlation and fraction of variance due to permanent environmental effect of the ewe and ewe-mate, as well as phenotypic variances for each trait are shown in Table1. The low estimates of heritability for LS and CR may be due to the importance of random environmental effects on variability of the observations and due to the categorical expression of the trait. Because the heritability estimate was quite low, improvement of CR by selection would be difficult even though CR has great economic importance. Results showed that all traits were influenced by genetic effects and permanent environmental effects, and to improve these traits one should improve environmental effects in first step. Estimates of genetic variances and heritability are necessary for genetic

evaluation of sheep and also for choosing the best selection scheme. Economic weights of traits can be determined to build an advantageous overall selection index.

Table 1. Estimates of (co)variance components, genetic and phenotypic parameters of reproductive traits from a univariate analysis

Traits	Mean ± SD	h^2 (± SE)	m^2 (± SE)	Pe^2 (± SE)	ram
LS	1.4 (± 0.51)	0.08(± 0.01)	0.038(± 0.01)	0.25(± 0.05)	0.33
CR	0.7(± 0.25)	0.03(± 0.01)	—	—	—
LMWLB	4.85(± 0.78)	0.1(± 0.02)	0.03(± 0.02)	0.03(± 0.01)	0.31
LMWLW	22.86(± 5.14)	0.09(± 0.01)	0.05(± 0.01)	—	0.1

Direct (h2) and maternal heritability, direct-maternal genetic correlation (ram), fraction of variance due to permanent environmental (pe2).

Key Words: Moghani sheep, reproduction

T52 Determination of intrinsic tolerance for high dietary nitrate in ewes using hepatic gene expression. R. R. Cockrum*, K. J. Austin, and K. M. Cammack, *University of Wyoming*, *Laramie*.

Ruminants differ in their ability to efficiently reduce nitrate (NO_3^-) to nitrite (NO_2^-). It was hypothesized that these differences may be due to intrinsic differences in ability to metabolize NO_3^-. In a previous study, differentially expressed ($P < 0.05$) hepatic genes (n = 13) were identified in ewes determined as highly tolerant (n = 6) and lowly tolerant (n = 6) to 300 mg of NO_3^-/kg BW administered for an 8-d period. The objective of this study was to determine if those genes were also differentially expressed between highly tolerant and lowly tolerant ewes a priori to NO_3^- treatment, indicating a potential for marker–assisted selection. Thirteen genes involved in metabolism and stress response were identified as differentially expressed ($P < 0.05$) in liver samples from highly tolerant and lowly tolerant ewes after NO_3^- treatment using both 24k bovine oligonucleotide microarray and real–time RT–PCR techniques. Of those genes, 4 were up–regulated ($P \leq 0.05$; *HOPX*, *GPX3*, *ITIH4*, and *HP*), 8 were down-regulated ($P \leq 0.03$; *CYP25A1*, *PFKFB1*, *AOX1*, *ASL*, *SCP2*, *KIK-1*, *FADS2*, and *THRSP*), and *CSAD* tended ($P = 0.07$) to be down–regulated in lowly tolerant ewes compared with highly tolerant ewes. Relative expression of those genes was determined in liver samples collected from the same highly tolerant and lowly tolerant ewes before NO_3^- treatment. Relative expression levels were tested for treatment differences using the GLM procedure in SAS. No differences ($P > 0.05$) in expression before NO_3^- administration were detected, confirming that the changes in expression observed post–treatment were due to the NO_3^- administration. These results also indicated that selection for tolerance to high dietary NO_3^- cannot be made before exposure based on differences in expression of genes involved in metabolism or stress. Instead, differences in microbial populations in the rumen may be key to disparities observed in response to high dietary NO_3^-.

Key Words: nitrate toxicity, gene expression, tolerance

T53 Genetic parameters for growth traits in the progeny of Nubian, French Alpine Saanen, Toggenburgh, and Spanish goats mated naturally to Boer sires. A. Pérez*, J. S. Saucedo, L. Avendaño, J. F. Ponce, and M. F. Montaño, *Universidad Autónoma de Baja California, México, Instituto de Ciencias Agrícolas*, *Mexicali, Baja California, México*.

Data came from a commercial goat farm at Imperial Valley California. The objectives were to compare the performance of the progeny of goats involving inheritance of Nubian(N), French Alpine (A), Saanen (S) Toggenburgh (T), and Spanish (SP), (n = 160), and to estimate genetic parameters for growth traits. Traits analyzed were weight at birth BWT and weaning WWT, and average daily gain (ADG) from birth to weaning. Separate analysis for each trait used least squares mixed model SAS (1999). The analytical model included: breed of dam, age of dam, sex of the kid, season of parturition as fixed effects; sire × breed of dam interaction and the residual as random. The overall mean values for weight at birth and weaning were: 1.99 and 12.89 kg, respectively. The average values for weight at birth were (2.12 ± 0.66, 2.11 ± 0.56, 2.04 ± 0.55, 1.95 ± 0.63, 2.10 ± 0.55 and 1.98 ± 0.67, 1.97 ± 0.68, 1.93 ± 0.58, 1.83 ± 0.63, 1.96 ± 0.66) for males and females kids, respectively. The average values for weaning weight were (13.99 ± 0.59, 13.29 ± 0.53, 13.25 ± 0.54, 12.67 ± 0.51 and 13.51 ± 0.43, and 12.50 ± 0.59, 12.48 ± 0.50, 11.98 ± 0.58, 12.68 ± 0.56 and 12.60 ± 0.57 kg) for male and female kids, respectively. The estimated ADG from birth to weaning was 181 ± 0.32 g. The average values for daily gain were: 187 ± 0.46 and 175 ± 0.49 g for male and female kids, respectively. Estimates of heritability direct values were ($h^2 = 0.20 \pm 0.67$, $h^2 = 0.15 \pm 0.68$, and $h^2 = 0.25 \pm 0.64$) to BWT, WWT, and ADG, respectively.

Key Words: genetic parameters, growth traits, boer goat

T54 Student organization sponsored dog training classes provide experiential learning opportunity for students and community participants. L. K. Karr-Lilienthal*[1] and J. S. Morstad[3,2], [1]*University of Nebraska-Lincoln*, *Lincoln,* [2]*Union College*, *Lincoln, NE,* [3]*Prairie Skies Inc.*, *Lincoln, NE*.

The goal of this project was to determine the effectiveness of dog training classes organized by a student organization offered to members of the community at large. Students contracted a local professional dog trainer to provide training services. Two different class types were offered: an 8-week Canine Good Citizen (CGC) class for dogs taking a CGC test upon completion of the class and a 4-week basic obedience course. Using exit surveys, community participants and student organization members ranked a series of items on a 1 (strongly disagree) to 5 (strongly agree) scale. Students (n = 9) indicated completion of the course provided a better understanding of dog training (mean = 4.67), could see the importance of dog training in their future career (mean = 4.44, SD = 0.73), and would be interested in applying similar concepts in the training of their own dog (mean = 4.89, SD = 0.33). Students also indicated an understanding of the need for organizational (mean = 4.33, SD = 0.71) and communication skills (mean = 4.56, SD = 0.73) when working with the public. Students indicated assisting with the course allowed them to apply class content (mean = 4, SD = 0.87) and a desire for more hands on opportunities (mean = 4.56, SD = 0.73). The community dog handlers (n = 12) indicated they felt the class improved their dog′s behavior (mean = 4.7, SD = 0.6), the bond between them and their dog (mean = 4.7), and they would recommend it to others (mean = 4.8). They indicated that they felt the university was providing a valuable service by offering the class (mean = 4.75) and that they enjoyed interacting with the students (mean = 4.1). Participants in the 8-week course rated their interactions with the students higher than those in the 4-week course possibly due to both more students attending the 8-week course sessions and more time for interaction. Overall, providing community dog training classes improved student learning and improved community awareness and support of the companion animal programs offered at the University of Nebraska–Lincoln.

Key Words: dog, experiential learning, undergraduate

T55 Tail deflection as a measure of emotional state in canines. C. L. Terrill*, T. H. Friend, and J. E. Sawyer, *Texas A&M University*, *College Station*.

Previous research indicates that negative emotions may be processed in the right hemisphere of the brain and positive emotions in the left; which may be evident in lateral movement of the tail. Dogs and other species could use asymmetry of behavioral displays as a sign of dominance or aggression that is not normally noticed by people. If emotionally linked asymmetry of tail movement occurs, it may aid in reducing the nearly 4.7 million dog bites in the United States each year. The objective of this study was to determine if lateral tail movement in dogs varies with emotional state. Fourteen dogs (7 female, 7 male), ages 2 to 12 years old were selected for the study. Dogs were held in a wooden test box (1.83 × 0.91 × 1.22 m) with a 20 cm × 20 cm viewing slot in one end to reduce distractions until a test stimulus was presented. The dogs were individually exposed to 2 negative stimuli (unknown person, α dog) and 1 positive stimulus (owner) for 0.5 min per stimulus, with a 2 min break between each stimulus to mitigate any potential overlap of emotional response. Still photos of the first 2 full responses of each dog's tail were captured from video, and the maximum angle during each response was averaged to determine left and right deflection. Six of the 14 unknown person tests elicited barking and growling behaviors, indicating that tests were efficacious. Data were analyzed as a mixed model with stimulus as a fixed effect and subject as a random block. Orthogonal contrasts were used to compare positive with negative stimuli, and to compare the types of negative stimuli. Dogs' maximum tail deflections were markedly different among positive and negative stimuli ($P < 0.01$; 36.1° right, 36.0° left, and 34.6° ± 2.5° left for owner, unknown person, and α dog, respectively). Responses to negative stimuli were similar (α dog with unknown person; $P < 0.69$). These results suggest that right and left-brain asymmetry is measurable by quantifying maximum tail deflection in canines, and this methodology may be useful in behavioral studies to estimate positive and negative emotions.

Key Words: emotional state, tail wagging, canine

T56 Galactoglucomannan oligosaccharide (GGMO) supplementation affects nutrient digestibility, fermentation end-product production, and large bowel microbiota of the dog. T. A. Faber*[1], A. C. Hopkins[2], I. S. Middelbos[1], N. P. Price[3], and G. C. Fahey, Jr.[1], [1]*University of Illinois*, *Urbana,* [2]*Temple-Inland*, *Diboll, TX,* [3]*National Center for Agricultural Utilization Research, USDA*, *Peoria, IL*.

A galactoglucomannan oligosaccharide (GGMO) obtained from fiberboard production was evaluated as a dietary supplement for dogs. The GGMO substrate contained high concentrations of oligosaccharides containing mannose, xylose, and glucose, with the mannose component typically 46%. Adult dogs assigned to a 6x6 Latin square design were fed 6 diets, each containing a different concentration of supplemental GGMO (0, 0.5, 1, 2, 4, and 8%) that replaced dietary cellulose. Total tract dry matter (DM) and organic matter (OM) apparent digestibilities increased ($P < 0.0001$) linearly, while total tract crude protein (CP) apparent digestibility decreased ($P < 0.0001$) linearly as the dietary GGMO substrate concentration increased. Fecal concentrations of acetate, propionate, and total SCFA increased ($P \leq 0.0001$) linearly whereas butyrate concentration decreased ($P < 0.0009$) linearly with increasing dietary concentrations of GGMO. Fecal pH decreased ($P \leq 0.0003$) linearly as dietary GGMO substrate concentration increased whereas fecal score increased quadratically ($P \leq 0.0001$). Fecal phenol ($P \leq 0.05$) and indole ($P \leq 0.01$) concentrations decreased linearly with GGMO supplementation. Fecal biogenic amine concentrations were not different among treatments except for phenylethylamine, which decreased ($P < 0.0001$) linearly as dietary GGMO substrate concentration increased. Fecal microbial concentrations of *E. coli*, *Lactobacillus* spp., and *Clostridium perfringens* were not different among treatments. A quadratic increase ($P \leq 0.01$) was noted for *Bifidobacterium* spp. as dietary GGMO substrate concentration increased. Data suggest positive nutritional properties of supplemental GGMO when incorporated in a high quality dog food.

Key Words: dog, galactoglucomannan oligosaccharide, fermentation end-products

T57 Evaluation of cellulose and beet pulp as dietary fibers for use in raw meat-based diets fed to captive exotic felids. K. R. Kerr*[1], C. Morris[2], S. Burke[2], and K. S. Swanson[1,3], [1]*Division of Nutritional Sciences, University of Illinois*, *Urbana,* [2]*Henry Doorly Zoo*, *Omaha, NE*, [3]*Department of Animal Sciences, University of Illinois*, *Urbana.*

The optimal fiber type and level of inclusion in raw meat-based diets for captive exotic felids has not been determined. The effects of fiber type and level on total tract digestibility, fecal characteristics, and fecal fermentative end products were evaluated using jaguars (n = 4), cheetahs (n = 4), Malayan tigers (n = 4), and Siberian tigers (n = 4) using a factorial design. Dietary fibers [cellulose (C); beet pulp (BP)] were added to diets at 2% or 4% (as-is). Statistical analyses were conducted using Mixed Models procedure of SAS. Dry matter (DM) and organic matter (OM) digestibilities were lower ($P < 0.05$) in cats fed 4C (76.7%; 80.6%) compared with those fed 2C (81.9%; 86.3%), 2BP (80.39%; 85.2%), and 4BP (82.3%; 87.9%). Fecal DM percentage was higher ($P < 0.05$) and fecal scores were lower ($P < 0.05$; i.e., stools were drier) in cats fed C compared with cats fed BP, and in cats fed 2BP compared with cats fed 4BP. The ratio of fecal DM output to DM intake (g DM feces/g DM intake) was higher($P < 0.05$) in cats fed 4C compared with those fed 2C, 2BP, and 4BP. The ratio of fecal output as-is to DM intake (g feces as-is/g DM intake) was higher($P < 0.05$) in cats fed C compared with those BP. Fecal acetate, propionate, butyrate, total short chain fatty acid, and ammonia concentrations were lower ($P < 0.05$) in cats fed C compared with cats fed BP. The proportion of acetate was greater ($P < 0.05$) and the proportion of butyrate was lower ($P < 0.05$) in cats fed BP compared with cats fed C. Total fecal branched-chain fatty acid concentrations were higher ($P < 0.05$) in cats fed 2BP than cats fed 4BP and 2C, and higher ($P < 0.05$) in cats fed 4C compared with cats fed 4BP. To conclude, cellulose at the 4% level decreased diet digestibility and increased fecal DM output, thus beet pulp (2% and 4%) or cellulose (2%) may be preferred dietary fiber options for raw meat-based diets for captive exotic felids. However, cats fed beet pulp had wetter/looser stools, increased fecal as-is output, and higher concentrations of fecal fermentative end products, which may have implications for animal management and gut health.

Key Words: exotic felids, digestibility, fiber

T58 The influence of fish versus mammalian and avian protein sources on satiety hormone response in dogs. B. M. Vester Boler*[1], T. A. Faber[1], L. L. Bauer[1], K. S. Swanson[1], S. Smiley[2], P. J. Bechtel[2,3], and G. C. Fahey Jr.[1], [1]*University of Illinois*, *Urbana,* [2]*University of Alaska*, *Fairbanks,* [3]*USDA/ARS*, *Fairbanks, AK*.

Satiety is affected by macronutrient composition of the diet. Proteins, specifically, are the most satiating, and fish proteins have been reported to be more satiating than meat proteins. The objective of this study was to determine the effect of beef, chicken, pork, or fish protein pre-meals on postprandial satiety hormone and 24 h food intake responses. Ten purpose-bred, intact female hounds were used. Pork loin, beef loin, chicken breast, salmon fillet, and pollock fillet were tested. During phase I, dogs were fed 100 g of protein from each substrate mixed with 200 mL of water. Blood was collected before feeding the substrate (0 min), and at 5, 15, 30, 60, 90, and 120 min postprandial, and analyzed for glucose, insulin, total ghrelin, and glucagon-like peptide-1 (GLP1). Dogs were fed 2-times their metabolizable energy (ME) requirement of food 3 h following the feeding of the protein substrate, and orts were weighed at 30, 60, and 180 min, and 24 h, after food presentation to determine intake. During phase II, dogs were fed 100 g of substrate mixed with 200 mL of water. Two-times the ME requirement of food then was offered 3 h following the protein meal and orts were weighed at 30, 60, and 180 min, and 24 h, after food presentation. In phase I, glucose decreased over time ($P < 0.001$), but was lowest ($P = 0.01$) when dogs were fed pollock or chicken substrates. Insulin increased ($P < 0.0001$) over time, and tended to be greater ($P = 0.09$) when dogs consumed the salmon treatment. Food intake and GLP1 increased ($P < 0.001$) over time, but did not differ due to treatment ($P = 0.60$ and $P = 0.33$, respectively). Total ghrelin decreased ($P < 0.01$) over time, but did not differ ($P = 0.86$) due to diet. In phase II, food intake tended to be greater ($P = 0.06$) when dogs consumed the beef pre-meal compared with when dogs consumed the pork or pollock pre-meals. Protein source appears to influence blood markers of satiety in dogs, but has little effect on decreasing food intake.

Key Words: satiety, dog, protein source

T59 Dietary magnesium alters urinary histamine excretion in domestic felines. S. K. Martin*[1], C. E. Conway[1], M. R. C. de Godoy[1], D. L. Harmon[1], E. S. Vanzant[1], S. Zicker[2], R. M. Yamka[2], and K. R. McLeod[1], [1]*University of Kentucky*, *Lexington,* [2]*Hill's Pet Nutrition, Inc.*, *Topeka, KS*.

Magnesium (Mg) deficiency has been associated with increased histamine production in rats. Limitation of Mg with acidifying foods is common practice for management of urinary tract health in domestic cats. Nine healthy adult female shorthair cats were used in a 3 period random crossover experiment with fixed treatment sequences to test the effects of dietary Mg (0.06, 0.12, and 0.18% DM) on histamine in blood and urine. The dry-extruded test foods were fed in sufficient amounts to maintain ideal body weight and obtain a target urine pH of 6.3. Each experimental period was preceded by a 7d wash out period, in which the 0.06% Mg was fed, followed by a 14d feeding period of the appropriate food. Two 24h total urine collections were performed (d13: acidified, d14: unacidified; immediately iced) and blood was collected on d14. Dry matter intake ($P = 0.70$) and BW ($P = 0.30$) were not affected by treatment. Plasma Mg increased linearly with increasing dietary Mg (0.54, 0.56, 0.58 m*M*; $P = 0.001$). Urinary histamine excretion responded quadratically ($P = 0.02$) to treatment (3483, 3369, 3986 ng/d), whereas plasma histamine concentration ($P = 0.8$) was unaffected. Differences were not detected among treatments in total histamine, cellular + noncellular histamine, ($P = 0.70$) or antigen-induced ($P = 0.21$) histamine release in whole blood. Urine output ($P = 0.48$), pH ($P = 0.95$), NH3 ($P = 0.21$), and titratable acidity of urine ($P = 0.78$) were similar across treatments. These data suggest that dietary Mg concentration at 0.06- 0.12% has little effect on histamine in blood or urine, however, supplying Mg at 0.18% increased urinary histamine.

Key Words: cat, magnesium, histamine

T60 Dietary effects of dietary cation anion balance on histamine metabolism and urine acidity in domestic felines. S. K. Martin*[1], C. E. Conway[1], M. R. C. de Godoy[1], D. L. Harmon[1], E. S. Vanzant[1], S. Zicker[2], R. M. Yamka[2], and K. R. McLeod[1], [1]*University of Kentucky*, *Lexington,* [2]*Hill's Pet Nutrition, Inc.*, *Topeka, KS*.

Dietary cation anion balance (DCAB) has been extensively studied in relation to urinary pH and stone formation. However, there is a paucity of data concerning the relationship between DCAB and histamine; the latter has been suggested as a mediator of inflammation in human interstitial cystitis which displays similarities with feline idiopathic cystitis. Eight healthy adult female shorthair cats were used in a 3 period random crossover with fixed treatment sequences to test the effects of DCAB (6.3, 6.6, and 6.9 target urine pH) on histamine kinetics and urine acidity. Dry-extruded test foods were fed to maintain ideal body weight. Each experimental period (14d) was preceded by 7d wash out period in which the low DCAB diet was fed. Two 24hr total urine collections were performed (d13: acidified, d14: unacidified; immediately iced) and blood was collected on d14. Dry matter intake ($P = 0.73$), BW ($P = 0.62$), and urine output ($P = 0.50$) were similar across treat-

ment. Urinary pH (6.11, 6.37. 6.69) increased linearly ($P = 0.004$), while titratable acidity of urine (0.14, 0.13, 0.10 mL 0.1 *M* NaOH to achieve 7.4 pH) tended to decrease linearly ($P = 0.09$) with increasing DCAB. Urine NH_3 decreased linearly ($P = 0.03$) with increasing DCAB (445.7, 418.6, 324.5 mmol/L). Urinary histamine excretion ($P = 0.03$) and concentration ($P = 0.02$) increased linearly with increasing DCAB (6164, 8513, 8356 ng/d; 113.8, 129.9, 135.2 ng/mL); where as plasma histamine concentration ($P = 0.42$) was unaffected. Differences were not detected among treatments in antigen-induced ($P = 0.21$) histamine release in whole blood, however total, cellular + noncellular histamine release ($P = 0.07$) demonstrated a quadratic trend with treatment (12.7, 6.9, 11.2 ng/mL). These data indicate that DCAB alters urinary acidity and histamine excretion, but does not affect circulating plasma concentrations or antigen-induced release of histamine.

Key Words: cat, dietary cation anion balance, histamine

T61 The effects of graded arginine levels on nitrogen metabolism in the lean adult dog. C. E. Conway*[1], M. R. C. de Godoy[1], S. K. Martin[1], K. R. McLeod[1], N. Z. Frantz[2], R. M. Yamka[2], and D. L. Harmon[1], [1]*University of Kentucky*, *Lexington*, [2]*Hill's Pet Nutrition, Inc.*, *Topeka, KS*.

Arginine (ARG) is considered to be conditionally essential in the diet of adult omnivores, indicating that addition of supplemental ARG may be beneficial. These potential benefits include enhanced hepatic urea synthesis aiding ammonia clearance and increased glomerular flow rates via the vasodilatory effects of nitric oxide. The objectives of this study were to determine if feeding increased supplemental ARG affects indices of renal function, inflammation, and whole body nitrogen metabolism in the adult dog. Three isocaloric foods were used in this study: a control (0.99% total ARG on a DMB), control plus 0.5% supplemental ARG (1.42% total ARG on a DMB), and control plus 1.0% supplemental ARG (1.85% total ARG on a DMB). The foods were fed to maintain ideal body condition of 9 adult (ages 2–3 years) spayed Beagles (7.62 ± 0.67 kg) in a replicated 3x3 Latin Square design. Experimental periods were 28 d in length with blood collection on d 14 and 28, and total urine and fecal collections for the final 6 d of each period. Nitrogen intake was increased ($P < 0.0001$) by increasing supplemental ARG. Dry matter digestibility was 1.7% lower ($P = 0.0025$) for the 1.0% ARG food. Nitrogen digestibility was greatest ($P = 0.0013$) for the 0.5% ARG food. Nitrogen absorbed was greater ($P < 0.0001$) for both the 0.5% and 1.0% ARG foods than control, yet nitrogen retained ($P = 0.3188$) and urea excretion ($P = 0.3153$) did not differ between treatments. Inflammatory biomarkers, PGE2 and HMGB1, hormone IGF1, and kidney markers, ADMA, albumin, and MCP1, were evaluated in urine or serum samples. No differences were detected in any of these biomarkers indicating that increased supplemental ARG did not have an anti-inflammatory effect or improve markers of kidney function at the levels tested. Despite some subtle changes in N metabolism, it does not appear, based on the variables measured, that addition of dietary arginine to the adult dog at maintenance is beneficial.

Key Words: arginine, dog, nitrogen metabolism

T62 The effects of carob (*Ceratonia siluqua*) on some reproductive parameters of male New Zealand White rabbits. A. Ata, M. S. Gulay*, O. Yildiz-Gulay, and S. Gungor, *Mehmet Akif Ersoy University, Faculty of Veterinary Medicine*, *Burdur, Turkey*.

Carob is used locally in many Mediterranean countries for its aphrodisiac properties. Thus, the aim of this study was to determine the effect of carob on reproductive parameters of male New Zealand White rabbits. The experiment consisted of 2 stages. The first stage was the adaptation period which 6–8 mo old rabbits were trained for the semen collection for 15 d. At the end of the first stage rabbits were divided into 2 groups of 8; a control and treatment groups administered daily with 10cc tap water and carob extract by oral gavages, respectively. Second stage of the experiment was 49 d (1 spermatogenesis duration). During second stage semen samples were collected weekly from all rabbits and samples taken at wk 1 and wk 7 were analyzed separately. There were no differences in control and treatment groups for ejaculate volume (0.71 ± 0.06 vs. 0.64 ± 0.03mL), ejaculate pH (7.01 ± 0.02 vs. 7.00 ± 0.01), sperm concentration (347.5 ± 45.1 vs. 380.9 ± 29.4 × 10^6 mL), percent progressive motility (78.9 ± 1.44 vs. 79.1 ± 0.91%), percent live spermatozoa by eosin-nigrosine staining mixture (EET; 82.5 ± 1.25 vs. 78.3 ± 3.06%), percent sperm membrane response by hypo-osmotic swelling test (HOS; 79.0 ± 1.21 vs. 74.9 ± 2.54%) and seminal plasma protein levels (2.6 ± 0.3 vs. 2.9 ± 0.3gr/dL) at the beginning of stage 2 ($P > 0.1$). Similarly, there were no differences in control and treatment groups for ejaculate volume (0.68 ± 0.06 vs. 0.63 ± 0.03 mL), ejaculate pH (7.06 ± 0.03 vs. 7.02 ± 0.02), percent progressive motility (78.0 ± 2.9 vs. 84.0 ± 2.12%), EET (80.1 ± 3.51 vs. 80.4 ± 2.41%), HOS (77.5 ± 2.37 vs. 80.9 ± 2.54%) and seminal plasma protein levels (2.6 ± 0.19 vs. 2.4 ± 0.25 g/dL) at the end of stage 2 ($P > 0.1$). However, sperm concentration (337.6 ± 43.4 vs. 460.7 ± 44.1 × 10^6 mL, $P < 0.05$) and percent changes on spermatozoa concentrations between groups (percentage of spermatozoa at the end of stage 2 ÷ percentage of spermatozoa at the beginning of stage 2; 98.9 ± 6.38 vs. 122.9 ± 6.56%, $P < 0.02$) were affected by the treatment at the end of stage 2. Data suggested that use of carob cures by boiling the fruit of carob has beneficial influences on sperm concentration in rabbits.

Key Words: carob, rabbit, spermatological parameters

T63 The effects of carob (*Ceratonia siluqua*) on some hematological parameters and organs of male New Zealand White rabbits. M. S. Gulay*[1], O. Yildiz-Gulay[1], A. Ata[1], A. Balic[2], and A. Demirtas[1], [1]*Mehmet Akif Ersoy University, Faculty of Veterinary Medicine*, *Burdur, Turkey*, [2]*Sakarya Toyota Hospital*, *Sakarya, Turkey*.

Carob, also known as St. John's Bread, is used locally in many Mediterranean countries for its curative properties. However, the long-term use of carob may also have toxic effects. Thus, the present study was conducted to determine the effects of dietary carob on some hematological parameters and organs of male New Zealand White rabbits. Rabbits (6 to 8 mo old) were divided into 2 groups of 8 rabbits. Rabbits in the control group received 10cc tap water for 49 d. Rabbits in the treatment group received the same amount of carob cures by boiling the fruit of carob for 49 d. All treatments were given by oral gavage. At the end of the experiment, 10 mL of blood was withdrawn from the ear arteries of each rabbit and sacrificed. Total erythrocyte, leukocyte, plasma protein, percent hemoglobin, hematocrit, mean corpuscular volume, mean corpuscular hemoglobin, mean corpuscular hemoglobin concentration, percent neutrophil, eosinophil, basophil lymphocyte and monocyte for rabbits in control and treatment groups did not differ and were 5.77 ± 0.22 and 6.37 ± 0.31 × 10^6/μL, 6.7 ± 0.99 and 7.34 ± 0.34 × 10^3/μL, 6.51 ± 0.20 and 6.48 ± 0.30 g/dL, 13.8 ± 0.32 and 13.7 ± 0.24 g%, 41.0 ± 1.59 and 40.8 ± 0.96%, 71.4 ± 2.8 and 64.6 ± 3.3 μm^3, 24.0 ± 0.7 and 21.8 ± 1.3 μg, 33.8 ± 1.18 and 33.7 ± 0.96%; 33.6 ± 4.54 and 38.4 ± 1.20%, 3 ± 0.89 and 2.8 ± 0.20%, 58.7 ± 4.73 and 53.8 ± 5.14%, and 4.7 ± 1.05 and 5 ± 1.04%, respectively. Liver, kidney, lung, heart and body weights between control and treatment groups were not significant ($P < 0.1$). Moreover, no apparent changes in liver, kidney, liver, heart, testis and brain were detected by gross post mortem and histopathologi-

cal examination to suggest toxic effect of oral use of carob extract for 49 d. Thus, the results suggested no toxic effect subacute use of carob extract in male New Zealand White rabbits.

Key Words: carob, rabbit, hematological parameters

T64 The effects of feeding *Pinus pinea* seeds on some blood values in male New Zealand White rabbits. O. Yildiz-Gulay*[1], M. S. Gulay[1], A. Ata[1], A. Balic[2], and A. Demirtas[1], [1]*Mehmet Akif Ersoy University, Faculty of Veterinary Medicine*, *Burdur, Turkey*, [2]*Sakarya Toyota Hospital*, *Sakarya, Turkey*.

A trial involving 16 male New Zealand White rabbits was conducted to determine whether there is any effect of *Pinus pinea* seed supplementation on hematological parameters and organs. Rabbits (6 to 8 mo old) were divided into 2 groups of 8 rabbits. Rabbits in the control group received 10cc tap water for 49 d. Rabbits in the treatment group received 1 g/kg of *Pinus pinea* seeds in 10 mL of tap water for 49 d. All treatments were given by oral gavage. At the end of the experiment, 10 mL of blood was withdrawn from the ear arteries of each rabbits and sacrificed. No significant differences were detected in mean hemoglobin (13.8 ± 0.31 vs. 13.5 ± 0.25 g%), hematocrit (41.0 ± 1.59 vs 40.4 ± 0.87%), red blood cell count (5.8 ± 2.24 vs. 5.7 ± 2.51 × 10^6/μL), white blood cell count (6.70 ± 9.94 vs. 6.54 ± 3.54 × 10^3/μL), plasma protein (6.5 ± 0.20 vs. 6.3 ± 0.12 g/dL), mean corpuscular hemoglobin concentration (33.8 ± 1.18 vs. 33.5 ± 1.20 g/dL) percent neutrophil (34.5 ± 4.01 vs. 38.5 ± 3.66%), eosinophil (3.0 ± 0.89 vs. 2.0 ± 0.40%), basophil (0.60 ± 0.33 vs. 0.50 ± 0.29%), lymphocyte (57.2 ± 4.17 vs. 53.2 ± 2.92%) and monocyte (4.7 ± 1.05 vs. 5.8 ± 0.85%) of rabbits in control and treatment groups, respectively. Overall blood parameters remained within the physiological range in both groups. Liver, kidney, lung, heart and body weights between control and treatment groups did not differ. Moreover, no apparent changes in liver, kidney, liver, testis and brain were detected by gross post mortem and histopathological examination to suggest toxic effect of oral use of *Pinus pinea* seeds for 49 d. In conclusion, 49 d of *Pinus pinea* seed supplementation did not cause any negative effects on the parameters tested in this study.

Key Words: *Pinus pinea* seeds, hematological parameters, histopathology

T65 Spermatological parameters of male New Zealand White rabbits supplemented with *Pinus pinea* seeds. A. Ata, M. S. Gulay*, O. Yildiz-Gulay, S. Avki, and S. Gungor, *Mehmet Akif Ersoy University, Faculty of Veterinary Medicine*, *Burdur, Turkey*.

The experiment was designed to evaluate whether supplementing male New Zealand White rabbits with *Pinus pinea* seeds affected spermatological parameters. Six to 8 mo old male rabbits (n = 16) were trained for semen collection for 15 d. Rabbits were assigned randomly to control and treatment groups (8 per group). Control and treatment groups were administered daily with 10cc tap water and 1 g/kg of *Pinus pinea* seeds in 10 mL tap water by oral gavage, respectively for 1 spermatogenesis duration (49 d). During the entire experimental period semen samples were collected weekly from all rabbits. During the experiment, 2 semen samples taken at wk 1 and wk 7 were combined and analyzed separately. There were no differences in control and treatment groups for initial values for ejaculate volume, ejaculate pH, progressive motility, head defect, tail defect, sperm concentration, percent live spermatozoa by eosin-nigrosine staining mixture (EET), percent sperm membrane response by hypo-osmotic swelling test (HOS) or seminal plasma protein levels ($P > 0.1$). Similarly, there were no differences in control and treatment groups for ejaculate volume (1.02 ± 0.13 vs. 0.90 ± 0.18 mL), ejaculate pH (7.02 ± 0.04 vs. 7.00 ± 0.02), progressive motility (75.7 ± 2.63 vs. 79.8 ± 1.94%), head defect (2.02 ± 0.09 vs 2.12 ± 0.09%), tail defect (13.0 ± 0.99 vs. 10.9 ± 1.22%), EET (73.3 ± 2.26 vs. 81.6 ± 4.98%), HOS (73.1 ± 2.28 vs. 77.1 ± 3.15%) and seminal plasma protein levels (2.3 ± 0.23 vs. 2.8 ± 0.34 g/dL) at the end of experiment ($P > 0.1$). However, sperm concentration (327.6 ± 44.3 vs. 464.7 ± 45.8 × 10^6 mL, $P < 0.05$) and percent changes on spermatozoa concentrations between treatment groups (percentage of spermatozoa at the end of experiment ÷ percentage of spermatozoa at the beginning of experiment; 97.2 ± 8.05 vs. 124.9 ± 5.74%, $P < 0.02$) were affected by the treatment at the end of experiment. Data suggest the daily dietary supplementation of *Pinus pinea* seeds to rabbits may improve sperm concentration in rabbits.

Key Words: *Pinus pinea* seeds, rabbit, spermatological parameters

T66 An x-ray system to assess Ragusano PDO quality. G. Impoco[1], C. Pasta[1], G. Portelli[1], G. Marino[1], M. Caccamo*[1], S. Carpino[1], and G. Licitra1,2, [1]*CoRFiLaC, Regione Siciliana*, *Ragusa, Italy*, [2]*D.A.C.P.A., University of Catania*, *Catania, Italy*.

Accept/reject judgments in Ragusano Protected Designation of Origin (PDO) quality assessment are highly subjective due to the lack of standard evaluation protocols. Moreover, assessment takes place on aging centers. X-ray scanning is a mature technology used in the industrial chain to inspect the inner structure of food. The use of x-ray images of cheese blocks was investigated to judge cheese quality, the main reason being that this technique is non-destructive. Moreover, evaluating quality on a common ground would open the possibility of devising quantitative image analysis tools, inspired by objective evaluation protocols. An evaluation scale was created to objectively score cheese blocks by visual inspection of x-ray images. According to inspectors' suggestions, 7 relevant criteria were chosen. Six inspectors assessed these parameters on a few test images of Ragusano PDO and assigned a weight to each of them. Then, a 7-item on a 9-point semantic differential scale was created. A data set of 223 images manually evaluated cheese blocks was collected. From this data set, 64 images were randomly extracted. Images were evaluated using the scale Furthermore, inspectors also assessed cheese acceptability only based on images by using a yes/no criterion. Two weeks later, inspectors observed the same 64 images only to evaluate cheese block acceptability, with no scale use. Results of both experiments were compared with the on-field evaluation to determine whether the scale was useful for quality assessment. The scale presented a final reliability with both Cronbach's α test and standardized Cronbach's α of about 0.81. Construct validity assessed on all 7 items resulted in a 2-factor solution that explained 79.5% of the scale variance. By using the scale, cheese acceptability evaluated by images was consistent with on-field evaluation for 62% of cheese blocks, whereas without the scale consistency dropped down to 37%.

Key Words: quality evaluation, cheese, x-ray imaging

T67 Effects of rapid visco analyzer on the functional properties of imitation mozzarella cheese. S. He[1,2], X. Li*[1,2], Y. Ma[3], C. Yao[2], and B.Wu[1,2], [1]*Key Laboratory of Dairy Science, Northeast Agricultural University, Ministry of Education*, *Harbin, Heilongjiang, China*, [2]*College of Food Science, Northeast Agricultural University*, *Harbin, Heilongjiang, China*, [3]*School of Food Science and Engineering, Harbin Institute of Technology*, *Harbin, Heilongjiang, China*.

A small-scale manufacturing method of imitation cheese was developed by a rapid visco analyzer (RVA). In this work, imitation mozzarella cheeses with similar chemical compositions, made by RVA at a stirring speed of 200, 300 or 450 rpm and by the Stephan cooker at 1,500 rpm, were investigated through functional properties, microstructure and sensory evaluation. A color measurement instrument (model ZE-6000, Nippon Denshoku Industries CO., Ltd., Japan) revealed that the increase of stirring speed in RVA method made the color more white. Within the range of speeds in the present study, the relationship between the minimum apparent viscosity (y, cP) and speeds (x, rpm) was best described by a linear model y = 0.9x + 685.3 (r2 = 0.968). Through free-oil release analysis, the fat leakage of imitation cheese at 450 rpm was significantly higher than the others. On the Texture profile analysis (TPA), the hardness of imitation cheese significantly increased, and the adhesiveness sharply decreased while the springiness and cohesiveness values remained unchanged. However, there was not a significant effect on functional properties of imitation cheeses between RVA at 450 rpm and Stephan cooker at 1,500 rpm. The microstructure of imitation cheeses observed by scanning electron microscopy, showed that increasing stirring speed seemed to reduce the fat globules size and form a uniform protein matrix. In the sensory evaluation, the imitation cheese manufactured by RVA at 450 rpm was not a significant difference with the control made by the Stephan cooker. The RVA can be used as a small-scale manufacturing tool for making the imitation cheeses with similar functional properties.

Key Words: imitation mozzarella cheeses, rapid visco analyzer (RVA), functional properties

T68 A sensor technology for monitoring and controlling syneresis in the cheese vat. T. G. Ferreira*[1], M. Castillo`, F. A. Payne[1], C. O'Donnell[3], and D. O'Callaghan[4], [1]*University of Kentucky*, *Lexington*, [2]*Universitat Autònoma de Barcelona*, *Spain*, [3]*University College Dublin*, *Ireland*, [4]*Moorepark Food Research Center, Teagasc, Fermoy, Co. Cork, Ireland*.

Cheese quality is affected by curd moisture content which is determined during the whey syneresis step. The syneresis step in cheese processing is currently controlled empirically by the processor as there are no on-line sensor technologies available for monitoring curd syneresis. A novel non-destructive optical sensor technology that is able to monitor both milk coagulation and curd syneresis in a stirred cheese vat has been developed. The objective of this study was to evaluate the performance of the sensor technology over a wide range of coagulation and syneresis rates. A 5-factor, fully randomized, fractional, factorial central composite design (CCD) was employed. The 5 experimental factors selected were milk coagulation temperature, milk pH, fat to protein ratio, calcium chloride addition level, and gel cutting time. The CCD consisted of a 2k-1 factorial (k = 5) with 2k axial points and 7 center points (33 runs). A homogeneous sample of curd and whey was removed from the cheese vat from 5 until 85 min after cutting on 10 min intervals. Fat, protein and total solids content of whey, curd, and milk were determined. Also, the weight of curd and whey produced was expressed as a percentage of the initial weight of milk to provide the actual curd and whey yield. A curd aliquot was pressed for determination of pressed cheese moisture content. Results confirmed previously observations for both curd moisture content and light backscatter ratio changes during curd syneresis. The largest change in curd moisture content was observed during the first 15–30 min of syneresis. However, significant moisture content changes were observed in pressed cheese samples at all different post-cutting times. These results clearly suggest an important role of syneresis end point selection on moisture content consistency of fresh, pressed cheeses. Successful validation and of the syneresis sensor technology scale up and subsequent transference to the industry will have a large impact on cheese production efficiency and cheese yield. Not only will the sensor have industrial applications, it could also serve as a powerful tool for research.

Key Words: on line sensor, syneresis, moisture content control

T69 Method to quantify retention of lipid soluble substances in a cheese curd model system. M. Tippetts* and S. Martini, *Utah State University*, *Logan*.

The purpose of this study was to find a way to quantify how much of an emulsion′s lipid soluble substances are retained in a cheese curd model

system by image analysis rather than alternate methods such as HPLC. Soybean oil (SBO) was the oil phase and it was saturated with Nile red, which is an indicator for liposoluble substances. The oil-in-water emulsion was made using a 1 wt % protein non-fat dairy powder aqueous solution, and a 5 wt% oil phase. The saturated Nile red SBO was added to the system as 0, 20, 40, 60, 80, and 100% of the total SBO. Each emulsion was homogenized using a microfluidizer. After emulsion formation 5 mL of the emulsion were pipetted into pre-heated 3.36 wt% protein milk protein concentrate solution. The ratio of emulsion to milk solution was 1:40. Curd was made and then samples were taken of each sample, placed in a mold and under UV light images were taken using an ethium bromide filter, which excited the Nile Red in the curd. The images were then analyzed using ImageJ software′s macro for RGB histogram. The intensities of red (histogram) for the mean and mode were plotted with respect to the concentration of Nile red. Data was fitted using linear regression with R2 values of 0.994 (mean) and 0.996 (mode). The correlation found for each measurement is: $y = 0.379x + 7.361$ and $y = 0.392x + 5.385$ for the mean and mode, respectively. These results show that a good linear correlation exists between the amount of Nile red added to the emulsion and the final red intensity found in the curd. Correlations found with the mode measurements seem to be more sensitive to changes in Nile red concentration due to the slightly steeper slope obtained in the linear correlation. Since Nile red is a lipid-soluble compound, this technique can be used to quantify the amount of lipid soluble substances retained in a model system for cheese curd.

Key Words: lipids, emulsion, cheese

T70 Effect of storage at ambient temperature on calcium lactate crystallization in Cheddar cheese. F. Su, P. Rajbhandari, and P. Kindstedt*, *University of Vermont*, *Burlington*.

Supermarkets sometimes hold cheese at ambient temperature in unrefrigerated aisle displays to enhance sales. Storage temperature is an important risk factor in calcium lactate crystal formation, but the effect of ambient storage followed by refrigerated storage has not been reported. In this study, Cheddar cheese was made at the University pilot plant and aged for 3 mo at 5°C. The cheese block (9 kg) was then sectioned into retail-sized (ca. 14.5 × 4.5 × 4.5 cm; 350 g) chunks and 9 chunks were randomly chosen for study. For each of the 9 samples, one of the large (ca 14.4 × 4.5 cm) surfaces was from the exterior of the 9 kg block and thus relatively rough due to curd granule junctions and press cloth indentations; the opposite surface was cut smooth with a wire cutting device. The samples were vacuum packed at 50 mbar and randomly assigned to 3 temperature treatments. Two sets of 3 samples were held at 20°C for either 24 or 48 h, respectively, before being stored at 1°C. A third set was immediately stored at 1°C, which served as the control. Digital photos of rough and smooth surfaces were taken triweekly for 28 wk and the number and area of crystal regions were determined by image analysis. Data were analyzed by repeated measures ANOVA. The number and area of crystal regions were significantly affected by surface roughness, storage temperature and storage time. Rough surfaces crystallized more profusely than smooth surfaces, and ambient storage for 24 or 48 h caused substantial reductions in crystal formation rates relative to control cheeses. The results indicate that short-term ambient storage rendered cheese surfaces less susceptible to crystallization, especially the rough surfaces that were heavily predisposed to crystallization. The mechanism for this effect is unclear but may involve temperature-induced alteration of the cheese surface and potential nucleation sites.

Key Words: Cheddar cheese, calcium lactate, storage temperature

T71 Effect of addition of calcium chloride and sodium chloride on aflatoxin M1 content during Egyptian Domiatti cheese processing. M. M. Motawee*[1], K. Genedy[1], and T. A. Nassib[2], [1]*National Organization for Drug Control and Research*, *Giza, Cairo, Egypt*, [2]*Faculty of Agriculture, Mansoura University, Mansoura, Egypt*.

Aflatoxins are highly toxic, mutagenic and carcinogenic compounds producing by some common molds as *Aspergillus flavus* and *Aspergillus parasiticus* during their growth on feedstuffs. Domiatti cheese is the most popular soft white pickled cheese in Egypt and makes up about of the 75% of the cheese produced and consumed in our country. The proportion of salt (5 to 14%) depends on the season of manufacture and on the temperature of cheese ripening. The present study was aimed to analyze the level of aflatoxin M1 (AFM1) by thin layer chromatography method in pasteurized milk, curd and whey after spiked milk with (AFM1) during Domiatti cheese processing. The results indicated that, the addition of $CaCl_2$ at the different concentration (0.01, 0.02, 0.03, 0.04 and 0.05%) had slight significant effect of AFM1 content in pasteurized milk. AFM1 content decreased from 1.4 ppb to 1.26 ppb with the addition of 0.01 and 0.05% of $CaCl_2$, respectively. While AFM1 content in curd was significantly ($P < 0.5$) increased from 6.7 to 7.5 ppb with the addition of 0.01 and 0.05 of $CaCl_2$ respectively. The increase of $CaCl_2$ concentration was accompanied with decrease of AFM1 content in whey of cheese. On the other hands, the addition of different concentration of NaCl (6, 8, 10 and 12% caused slight decreased of AFM1 in pasteurized milk from 1.38 ppb at 6% of NaCl to 1.26 ppb at 12% NaCl. Opposed results was showed in the curd, where AFM1 decreased from 6.7 ppb at 6% NaCl to 6.1 ppb at 12% NaCl. The same trend was observed in whey.

Key Words: aflatoxin M1, NaCl, $CaCl_2$, Domiatti cheese

T72 Effect of milk fat content on goat cheese proteolysis elaborated with the traditional method. D. Sánchez-Macías*, I. Moreno-Indias, L. E. Hernández-Castellano, A. Morales-delaNuez, A. Torres, M. D. Ruiz-Díaz, A. Argüello, and N. Castro, *Department of Animal Science, Las Palmas de Gran Canaria University*, *Arucas, Las Palmas, España*.

Three different milk fat contents (5%, 1.5% and 0.4%) were used to manufacture full-fat cheese (FFC), reduced-fat cheese (RFC) and low-fat cheese (LFC) goat raw milk cheese according to traditional hand-made cheese practices in Canary Islands (Spain). Cheeses were ripened for 1, 7, 14 and 28 d. Water-soluble proteins were extracted at 1, 7, 14 and 28 d of ripening and they were separated on SDS-PAGE gel. The SAS PROC MIXED procedure for repeated measurements was used to evaluate the effect of differing fat content and ripening time on the proteolysis. Tukey's test was used to evaluate the differences between groups. β-casein was the greatest proportion in all type of cheese and at all ripening time. α_{s2}-casein and α_{s1}-casein were the most abundant after β-casein. Quantitative analysis showed a general reduction in each casein as ripening progressed. In the 3 types of cheese, the degradative rates of intact caseins was higher throughout the period of ripening in the α_{s1}-casein (60–70%), followed by β-casein (38–45%) and then by α_{s2}-casein (25–40%) than d 1 of ripening. Furthermore, the rate of degradation during the experimental time was lower as the fat content decreased. At d 28, the percentage of total principal caseins remaining was 62, 66.5 and 70% in FFC, RFC and LFC, respectively. The remaining α_{s2}-casein and α_{s1}-casein in FFC and RFC were lower than in LFC. In contrast, β-casein also showed degradation along the ripening, differences in degradation between the 3 types of cheese were not significant at 28 d. α_{s1}-casein was degraded faster and cheese contained 28–40% at 28 d of ripening. α_{s2}-casein was degraded slower in LFC

than in FFC and RFC. The electrophoretic bands of degradation products increased with the ripening time in all cheeses. The appearance of these fragments was higher in FFC than RFC and LFC. This statement is correlated to previous information, that the degradation rate of caseins was increased as cheese was fatter resulting in a greater appearance of degradation bands in FFC.

Key Words: cheese, low-fat, proteolysis

T73 Impact of salt substitutes on the sensory characteristics of reduced sodium process cheese. A. Kommineni*, J. Amamcharla, and L. E. Metzger, *Midwest Dairy Foods Research Center, South Dakota State University*.

Process cheese (PC) is an integral part of the American diet. However, consumption of PC is limited by its high sodium content (typically 1265 to 1596 mg/100g). A high dietary intake of sodium has been associated with hypertension. The major ingredient sources of sodium in PC are sodium based emulsifying salts, sodium chloride (NaCl) and natural cheese, contributing 38%, 39%, and 20% of the total sodium, respectively. As per the Code of Federal Regulations (CFR) the sodium content should be less than 950 to 1100mg/100g to be labeled as "reduced sodium" PC. One of the challenges in formulating an acceptable sensory quality reduced sodium PC is the elimination of bitter-metallic flavor that is typically associated with the potassium based salt substitutes. The objective of this study was to determine if new commercially available salt substitutes improve the flavor and acceptability of reduced sodium PC. Newly available salt substitutes (SOLO, NeutralFres, Modified potassium chloride (Nu-Tek: 14500 and Nu-Tek: 14510), potassium chloride) were utilized in the formulations. Metallic blockers and salt flavor enhancers were also incorporated in the formulation either in combination or alone along with salt substitutes to evaluate their ability to mask off-flavors. Potassium citrate was used as emulsifying salt in all the formulations. A triangle test was used to determine if there was any detectable difference in any sensory characteristic between control PC (1540 mg Na/100g) and reduced sodium PC. The reduced fat reduced sodium (RFRS) formulation containing NuTek-14510 and sodium gluconate was not significantly ($P < 0.05$) different from control PC. Similarly, low-fat- reduced-sodium (LFRS) formulation containing NuTek-14510, xylitol, and sodium gluconate was not significantly ($P < 0.05$) different from the control PC. The sodium content of the acceptable RFRS and LFRS were 700 and 710 mg/100g. In conclusion, Nu-Tek:14510 and sodium gluconate can be used to improve the flavor of reduced sodium PC.

Key Words: process cheese, sodium, salt substitutes

T74 Comparison of identified flavor compounds, texture and sensory properties in regular cream cheese and cream cheese made from whole milk powder. S. S. Jeon*, C. H. Chung, and H. S. Kwak, *Sejong University*, *Seoul, South Korea*.

This study was carried out to compare identified flavor compounds, texture and sensory analysis in regular cream cheese and cream cheese made from whole milk powder which were stored at 7°C for 4 weeks. To identify the flavor compounds, the cheeses were extracted and analyzed by solid phase microextraction (SPME) and gas chromatography-mass spectrometry (GC-MS), respectively. Tentatively identified flavor compounds were mainly 13 from acids, however, octadec-9-enoic acid and Z-11-tetradecenoic acid was not present. Z-7-tetradecenoic acid was produced only from the cheese made with whole milk powder. Two ketones, 1 amine, 1 alcohol and 2 alkene were produced from both cheeses, but 6-heptyltetrahydro-2H-pyran-2-one as lactone and 2,6,10,15,19,23-hexamethyl-,(all-E)-2,6,10,14,18,22-tetracosahexaene as alkene were produced only from cream cheese made from whole milk powder. Also 1 imide and 1 alkane were showed only from the sample cheese. The identified flavor components from the whole milk powder-made cheese were different from regular cream cheese due to heat treatment. However, in rheological properties, hardness, adhesiveness, cohesiveness, springiness and gumminess were not significantly ($P < 0.05$) different between control and sample. In sensory analysis, appearance, flavor, taste and texture properties were not significantly ($P < 0.05$) different between control and sample cheese. In addition overall acceptability in the cream cheese made from whole milk powder was similar to that in control. On the basis of our results, we conclude that the cream cheese made from whole milk powder showed almost no adverse changes in texture and sensory characteristics except few identified flavor components.

Key Words: cream cheese, whole milk powder, flavor, texture, sensory evaluation

T75 Identification of neutral volatile compounds, texture and sensory properties in cholesterol-removed cream cheese. S. S. Jeon*, S. J. Lee, and H. S. Kwak, *Sejong University*, *Seoul, South Korea*.

This study was carried out to identify neutral volatile compounds, and examine texture and sensory evaluation in cholesterol-removed cream cheese which was treated by closslinked β-cyclodextrin and stored at 7°C for 4 weeks. To identify the volatile compounds, the 4 week-stored cream cheeses were extracted and analyzed by solid-phase microextraction (SPME) and gas chromatography-mass spectrometry (GC-MS), respectively. Tentatively identified neutral volatile compounds were detected 12 acids, 2 ketones, 1 amine, 1 alcohol, 1 lactone and 1 alkene. The main components were acids, such as hexanoic acid, n-hexadecanoic acid, tridecanoic acid, octanoic acid, octadec-9-enoic acid, 9,12-octadecadienoic acid, n-decanoic acid, benzoic acid, dodecanoic acid, tetradecanoic acid, z-11-tetradecenoic acid and oleic acid. Other components were 2-tridecanone and 2-pentadecanone as ketones, 5-(p-aminophenyl)-4-(o-tolyl)-2-thiazolamine as amine, 4,6-di(1,1-dimethylethyl)-2-methyl phenol as alcohol, tetrahydro-6-pentyl-2H-pyran-2-one as lactone and 3,7,11,15-tetramethyl 2-hexadecene as alkene. The identified components from cholesterol-removed cream cheese were same as those from regular cream cheese. In rheological properties, hardness, adhesiveness, cohesiveness, springiness, gumminess and chewiness were not significantly ($P < 0.05$) different between control and cholesterol-removed cheese during storage at 7°C for 4weeks. In sensory analysis, appearance, flavor, taste and texture properties were also not significantly ($P < 0.05$) different between control and 4week storage periods. In addition, overall acceptability in the cholesterol-removed cheese was closely similar to that in control. On the basis of our results, we conclude that the cholesterol-removed cream cheese showed no adverse changes in flavor, texture and sensory characteristics.

Key Words: cream cheese, cholesterol removal, identification of flavor, sensory analysis

T76 Changes of Ragusano cheese aroma due to different levels of pasture intake. S. Carpino*[1], T. Rapisarda[1], I. Schadt[1], C. Pasta[1], G. Belvedere[1], and G. Licitra[1,2], [1]*CoRFiLaC, Regione Siciliana*, *Ragusa, Italy*, [2]*D.A.C.P.A. Catania University*, *Catania, Italy*.

In the Hyblean region of Sicily, 3 groups of 15 Holstein cows have been selected in one dairy farm, during the pasture season. At the beginning of the experiment, milk production and fat content were not different between groups, averaging 26.1 ± 8.1 (kg/cow/day) and 4.0

± 0.6 (%), respectively. The control group (CNT) was exclusively fed a total mixed ration. The remaining groups had additionally pasture access, either for 6 h (LP) or for 16 h (HP). After a 2 weeks adaption period, milk of each group was collected separately, 4 times with a 15 d interval, and 2 Ragusano cheeses were produced. In total, 24 forms were made: 12 aged at 4 (4M) and 12 at 7 (7M) months. The aim of the study was to evaluate the effect of different levels of pasture intake on Ragusano cheeses aroma. Differences in volatile compounds were detected and analyzed by Smart Nose system (LDZ, Switzerland) with principal component analysis (PCA). Odor active compounds were also analyzed by gas chromatography–olfactometry extracted by both, steam distillation and headspace solid-phase microextraction. Odor active compounds were classified into "good" (G): flower, fresh, fruit, green, honey, nut, milk, butter, sweet, vanilla; "bad" (B): animal, broth, burnt, plastic, fried, potato, garlic, onion, rancid, and "not good, not bad" (N): hay, soil, mushroom, pungent, spicy. Differences between compound frequencies were evaluated using the Tukey's HSD test. Mean pasture intakes and standard deviation, relative to total dry matter intake, were 30.6 ± 6.9% in the LP group, and 68.1 ± 2.7% in the HP group. In both, 4M and 7M cheeses, CNT, LP and HP samples were clearly separated by PCA analysis, indicating differences in volatile composition. Feeding differences had no effect on the numbers of N or B odour active compounds, neither in the 4M nor the 7M cheeses. In the 4M cheeses, but not in the 7M cheeses, "good" compounds were more frequent when milk derived from the LP or HP compared with CNT ($\alpha = 0.05$; Q = 3.72). Pasture nutrition of cows might have less importance for aroma quality of 7M compared with 4M aged cheeses.

Key Words: Ragusano cheese, pasture, aroma compounds

T77 Enzyme accelerated ripening of Turkish Mihalic hard cheese: proteolysis and lipolysis. T. Ozcan* and E. Kurdal, *Uludag University, Department of Food Engineering*, *Bursa, Turkey*.

Mihalic cheese, a traditional Turkish hard cheese variety, is mostly produced around Bursa and Balikesir, and also known as Maglic, Mahlic or Kelle cheese. It is white with roundish holes, hard and crusty and made from high-fat sheep or cow milk. Ripening of hard cheese varieties is a slow and consequently an expensive process. During manufacturing and ripening proteolysis, glycolysis and lipolysis reactions, mainly driven by accelerating agents such as starter culture or enzymes, determine the sensory, chemical and textural properties of the cheese. The objective of the present work was to observe the effect of fungal lipase (Piccantase A from *Mucor miehei*), and a bacterial neutral protease from *Bacillus subtilis* (Fermizyme B500) alone or combined with a starter culture on the acceleration of the ripening process of Mihalic cheese made from cow's milk. Cheeses were analyzed at 2, 15, 30, 60 and 90 days of ripening. Casein fractions of Mihalic cheese samples were analyzed by urea polyacrylamide gel electrophoresis (PAGE) and lipolysis rates were measured as acid degree value (ADV). The proteolysis and lipolysis rate of Mihalic cheese samples displayed significant differences due to treatment and ripening period ($P < 0.01$). The highest lipolysis rate was noted monitored in lipase added cheese (as 5.56 ADV) with highest γ-casein ratio and β-casein degradation. Breakdown of casein was higher in starter + protease + lipase added cheese. At the end of ripening period, it was observed that α_s-casein ratios decreased in starter added, starter + protease added and protease added cheeses. Breakdown of β-casein continued throughout ripening, and there was an increase at the end of ripening regarding the ratios of other fractions. In view of sensorial acceptance, protease added cheeses having bitterness and crumbly textural properties due to intense breakdown of β-casein scored lower than lipase added samples.

Key Words: Mihalic cheese, proteolysis, lipolysis

T78 Seasonal variation in milk composition affects textural properties of low-moisture part-skim Mozzarella cheese. V. Jai*, U. Lund, and N. Farkye, *California Polytechnic State University*, *San Luis Obispo*.

The chemical composition of milk (specifically casein, fat and calcium contents) affects quality and functional properties of Mozzarella cheese. The objective of this study was to determine the effects of seasonal variation of milk components on texture properties of low-moisture part-skim (LMPS) Mozzarella in California. Concentrations of protein fractions (i.e., total protein (TP), true protein (TrP) and casein), fat, Ca, total solids (TS) and pH were measured in silo milk samples collected weekly over 15 mo from a dairy plant. LMPS mozzarella from the same plant was also collected biweekly during the same period. Seven days post manufacture the cheeses were analyzed for TP, fat, TS, total Ca, Ca in cheese filtrate, pH and texture properties e.g., hardness (g), cohesiveness, springiness, aggregation index (AGI) and % loss during shredding. Significant seasonal variation of casein, TP, Ca in milk were explained using a linear regression model equivalent to a basic single cosinor model with sine and cosine of week (converted into radians) as predictors ($y = \beta o + \beta 1 \cos(\text{time}) + \beta 2 \sin(\text{time}) + \varepsilon$) with *P*-values <0.05 and R-sq values >0.6. TP in cheese correlated positively with TP, TrP and casein in milk (Pearson correlation coefficient $r > 0.6$; $P < 0.001$). Ca in milk correlated positively with total Ca in cheese and cheese filtrate ($r > 0.4$; $P < 0.05$). Positive linear correlation between hardness, springiness and TP, casein in milk and cheese ($r > 0.3$; $P < 0.05$) were significant. Protein fractions and Ca in milk; TP and total Ca in cheese correlated negatively with the loss in shredding ($r < -0.5$; $P < 0.05$). The protein fractions in milk and cheese negatively correlated with AGI in cheese ($r < -0.45$; $P < 0.05$). Total Ca in cheese and milk correlated positively with springiness of cheese ($r > 0.4$; $P < 0.05$). Results show that concentrations of Ca and protein fractions in cheese milk significantly effect the texture and composition of LMPS mozzarella.

Key Words: low-moisture part-skim Mozzarella, seasonal variation of milk, textural properties

T79 A study of bioactive peptides in US Cheddar cheeses of different ages. Y. Lu*, S. Govindasamy-Lucey, and J. A. Lucey, *University of Wisconsin-Madison*, *Madison*.

Bioactive peptides (BP) have been found in fermented dairy products with various bioactive properties, such as, antihypertensive, angiotensin-I-converting-enzyme (ACE)-inhibitory, immunomodulatory, antimicrobial, mineral transport and opioid activities. The objective of this study was to determine the types and levels of BP produced during ripening of Cheddar cheese. Water-soluble extracts were prepared from Cheddar cheeses. Centrifugation and ultra-filtration were used to remove fat and to fractionate water-soluble extract into 2 fractions with molecular weight (MW) between 1000 to 3000 Da and MW ≤1000 Da, respectively. The fractions were subjected to HPLC -tandem mass spectrometry to identify peptides. HPLC - electrospray ionization (ESI) - time-of-flight (TOF) mass spectrometry was also used to identify peptides present in the fraction of MW ≤1000 Da. BP were identified by comparison with already published milk protein derived BP. A range of Cheddar cheeses of various ages was studied to identify the specific types and determine the levels of BP produced during ripening. In young (~6 d old) and mature (2 years old) Cheddar cheese, 8 and 34 ACE-inhibitory peptides, and 77 and 157 casein phosphopeptides, respectively, were found. With age more potent forms of ACE-inhibitory peptides were found. For some of the ACE-inhibitory peptides (including dipeptides, tripeptides, tetrapeptides and pentapeptides that had high ACE-inhibitory activity or low

IC_{50} values), the content appeared to increase with age as indicated by HPLC-ESI-TOF. Confirmation of the type and quantification of levels of BP in a range of different aged commercial Cheddar cheese is ongoing. Aged Cheddar cheese could be a good source of BP.

Key Words: bioactive peptide, angiotensin-I-converting-enzyme, mass spectrometry

T80 Effect of curd milling on the characteristics of Queso Fresco during storage. D. L. Van Hekken*[1], M. H. Tunick[1], N. Y. Farkye[2], J. B. Luchanski[1], S. Mukhopadhyay[1], and P. M. Tomasula[1], [1]*USDA, Agricultural Research Service*, *Wyndmoor, PA,* [2]*California Polytechnic State University*, *San Luis Obispo*.

Queso Fresco (QF) is one of the most popular fresh Hispanic-style cheeses in the US Manufacture of QF varies from country to country with many practicing fine milling of the curd before forming the cheese block. This study was undertaken to determine the effect of milling of the curd with different sized blades on the chemical, functional, and rheological properties of QF. QF was prepared from pasteurized, homogenized milk containing 0.1% of added $CaCl_2$. It was coagulated with chymosin and the curd was cooked at 39°C for 30 min and wet salted at 12.5% salt (wt salt/wt cheesemilk). Portions of the curds were then finely milled using different-sized meat grinder blades and hand-packed into molds for storage overnight at 4°C. Cheeses were removed from the molds the next day, sliced into smaller blocks, vacuum packaged, and stored at 4°C for up to 8 wks. Fresh QF contained 56.5 to 58.0% moisture, 22.2% fat, 15.7 to 17.6% protein, 2.5% lactose, and 2.4% salt. Moisture content decreased with aging ($P \leq 0.05$) because of wheying off; control QF (not milled or passed through grinder without blade) had the highest amount of wheying off (3%), while the finest milled QF had the lowest amount of wheying off (0.5%). All other properties were not affected significantly ($P \geq 0.05$) by the milling treatment or by storage for up to 8 weeks at 4°C. In QF, the homogenization step, know to alter milk protein-protein interactions, was sufficient to disrupt the cheese matrix and resulted in a crumbly cheese. The fine milling step did reduce the amount of whey lost from the cheese during storage but did not affect other functional or rheological properties of the QF.

Key Words: Queso Fresco, milling, wheying-off

T81 Pigments from nonthermal browning formed in Gouda and Parmesan cheeses. A. Lopez-Hernandez*[1], L. E. Rodriguez-Saona[2], M. M. Giusti[2], M. E. Johnson[3], D. A. Sommer[3], and S. A. Rankin[1], [1]*University of Wisconsin-Madison*, *Madison,* [2]*The Ohio State University*, *Columbus,* [3]*Wisconsin Center for Dairy Research*, *Madison*.

Under certain conditions, some cheeses develop a brown discoloration during the course of aging thus yielding changes in flavor and color. Parmesan and Gouda cheeses are some typical examples of the products where excessive browning and the concomitant caramel-like flavor have been noted. To date, very little definitive science exists to describe, define or control the reaction chemistry of non-thermal browning (NTB) in cheese from either the flavor or pigmentation perspective. Factors such as redox potential, available oxygen, the type and concentration of α-dicarbonyls, amino acid type and concentration, the presence of Mn^{2+} ions, and microbial tyrosinase activity are some of the suggested pathways proposed to explain the development of NTB. In the present work, the brown pigments from several Parmesan and Gouda cheese samples exhibiting various degrees of discoloration were extracted using methyl tert-butyl ether (MTBE) and further separated from the fat fraction by TLC. The L*, a* and b* values for the different samples were measured and ranged from 89.5 to 91.07, −0.923 to −2.14, and 1.14 to 3.99, respectively. The UV-Visible spectra of the colored compounds in the isolated fractions were characterized by the presence of unique absorption bands at 425, 451 and 472 nm. Attenuated total reflectance Infrared analyses (ATR-FT-IR) of the brown pigments revealed the presence of characteristic bands at 1103 and 1037 cm-1. These results suggest that the pigments may be comprised of lipid-containing moieties since those bands are very characteristic of in-plane C−H bending vibrations.

Key Words: browning, FT-IR, cheese pigments

T82 Whey ricotta: A scientific reevaluation. J. W.-M. Heick*, R. Jimenez-Flores, and H. Khalil, *California Polytechnic University*, *San Luis Obispo*.

Ricotta cheese is one of the first attempts in the dairy industry to utilize the whey left over during the manufacturing of chesses. Currently, ricotta is exclusively made from whole or skim milk and has a low commercial value. However, whey ricotta as made following the classic style (as described by Kosikowski) has great modern potential because it utilizes the by-product of cheese manufacturing (sweet or acid whey) and has an excellent nutritional profile and organoleptic properties. Our research focused on manufacturing high protein ricotta from whey while retaining the desired sensory and nutritional profile. An Italian style low acid cheese was manufactured at the Cal Poly Creamery, and the whey was collected after cutting at a pH of 6.60. The whey was then skimmed and/or ultrafiltrated before it was added to the steam kettle for processing. Three treatments were applied to the whey: fat skimming, ultra filtration and acidification, and the final ricotta was either pressed or left to drain naturally. Whey and ricotta samples were analyzed qualitatively and quantitatively for total protein before and after protein precipitation. Total protein was measured using the MilkoScan FT2 from FOSS, and the protein profiles were determined using sodium dodecyl sulfate PAGE (SDS- PAGE). Compositional analysis of the finished ricotta was conducted using the Babcock method for percent fat, Elementar rapid-n cube for protein, and CEM LabWave 9000 for moisture. The ricotta curd was analyzed along with the pre/post whey: skimming the whey resulted in a 80% drop in final fat content while ultrafiltration resulted in a increase in the effectiveness of protein removal from the post whey. Moisture levels were dependent on the whey treatments: 70–80% in non-pressed ricotta and 65–78% in pressed ricotta, protein content also varied with a range of 9–14%. Acidification occurred at 2 levels, high pH target of 5.5 resulted in the most neutral flavor while low pH 4.5 had more complete protein precipitation. The results highlight a practical methodology to manufacture a high quality whey cheese from by-product using equipment that is readily available to small cheese makers.

Key Words: whey, ultrafiltration, ricotta

T83 Evaluation of the addition of urea to refrigerated raw milk on the crude protein, milk fat, lactose, and total solids contents determined by mid-infrared spectrometry. E. G. Esteves[1], M. M. O. P. Cerqueira*[2], L. M. Fonseca[2], M. O. Leite[2], M. R. Souza[2], C. F. A. M. Penna[2], R. Rodrigues[2], and L. R. Abreu[3], [1]*Ministry of Agriculture*, *Brasília, Distrito Federal, Brasil*, [2]*Federal University of Minas Gerais*, *Belo Horizonte, Minas Gerais, Brasil*, [3]*Federal University of Lavras*, *Lavras, Minas Gerais, Brasil*.

To detect the effect of fraudulent addition of urea to refrigerated raw milk, 32 samples of milk from 32 samples of milk from bulk tanks were collected at different dairy farms. A control sample and 3 test samples added with different levels of urea (0.0723, 0.1445 and 0.2891 wt%) were made. Both, the bulk tank and the test samples were analyzed to determine the crude protein, lactose, milk fat, and total solids contents by mid-infrared spectrometry. The crude protein, lactose, and total solids contents increased in 0.110, 0.17, and 0.140 wt%, respectively, on a 0.2891 wt% of urea added to milk. On the same conditions, the milk fat content decreased in 0.032 wt%. The equations of linear regression among the urea levels added (in wt%) and the crude protein and the total solids contents (both in wt%) were established. The changes on refrigerated raw milk composition submitted to the addition of urea detected by mid-infrared spectrometry analysis show that this fraudulent addition can increase the profits of the dairy farmer when milk payment is applied by the dairy industry.

Key Words: urea, milk composition, mid-infrared spectrometry

T84 Cheese whey compositional analysis using infrared spectroscopy. F. A. Pinto[1], L. A. Clementino[1], D. L. S. Oliveira[1], L. R. Abreu[2], L. M. Fonseca*[1,3], R. Rodrigues[1,3], M. O. Leite[1,3], and M. M. O. P. Cerqueira[1,3], [1]*Federal University of Minas Gerais/Escola de Veterinária/DTIPOA*, *Belo Horizonte, MG, Brazil*, [2]*Universidade Federal de Lavras/DCA*, *Lavras, MG, Brazil*, [3]*Laboratory for Milk Quality Analysis*, *Belo Horizonte, MG, Brazil*.

Compositional analysis of whey is necessary for its best utilization. To perform physicochemical analysis, infrared spectroscopy techniques are useful, as they are fast and precise. The objective of this research was to evaluate infrared spectroscopy for measurement of cheese whey composition from typical Brazilian cheeses. Twenty-one samples of whey from Minas padrao cheese and 22 samples of whey from Prato cheese were analyzed, using standard methods and a filter infrared equipment (Combisystem 2300, Bentley). The results for fat, protein and total solids using infrared instrument based on filters and standard methods were compared by Friedman test for related samples. The mean values are presented in Table 1.

The differences between results from both methods were significant. The pasteurization process can affect the results, as compounds formed during heating may interfere with infrared spectrum readings, and the whey samples used for equipment calibration were made from raw milk. After a linear transformation of the results with curve approximation, measurement of whey composition from Minas padrao cheese by infrared and standard methods were statistically equivalent. Therefore, results show that it is necessary to perform an equipment calibration for cheese whey analysis using infrared equipment based on filter. However, for whey from Prato cheese, even after transformation, the difference was significant. This whey has a water excess, as showed by the high freezing point. Moreover, it has a dye that is added for typical orange color during Prato cheese production. Water and pigment may affect the absorption of infrared radiation by the whey constituents. Therefore, infrared spectroscopy based on filters can be used for component analysis of whey from Minas padrao cheese, as long as a calibration adjustment is used. For Prato cheese whey, the infrared method based on filters did not provide accurate results.

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Table 1. Compositional analysis of cheese whey using standard methods and infrared spectroscopy

	Minas Cheese Whey		Prato cheese whey	
Component	Standard Methods	IR Spectroscopy	Standard Methods	IR Spectroscopy
Fat (g/100g±SD)	0.38±0.12	0.33±0.12	0.40±0.08	0.26±0.15
Protein (g/100g±SD)	0.78±0.08	0.67±0.11)	0.78±0.08	0.73±0.07
Total solids (g/100g±SD)	6.42±0.21	6.79±0.20	6.19±0.75	6.85±0.54
Ashes (g/100g±SD)	0.49±0.03	–	0.48±0.05	–
Chloride (g/100g±SD)	0.20±0.01	–	0.19±0.02	–
Freezing point (°C)	–0.507	–	–0.492	–

SD-standard deviation.

Key Words: cheese whey composition, infrared spectroscopy, infrared milk analyzer

T85 Comparison of Mojonnier and Gerber methods for analyzing the fat content of fermented milk beverages. E. H. P. Andrade, M. O. Leite, C. F. A. M. Penna, M. R. Souza, L. M. Fonseca*, and M. M. O. P. Cerqueira, *Federal University of Minas Gerais*, *Belo Horizonte, Brasil*.

The objective of this study was to compare 2 methods to estimate fat content in fermented milk beverages. The samples of fermented milk beverages were collected in large supermarket chains from Belo Horizonte, Minas Gerais, Brazil. Both methods are described in Brazilian legislation, but Mojonnier is the official method to analyze fat content in milk beverages and Gerber is the official method to analyze fat content in fluid milk. Gerber is a simpler and easier method to perform than Mojonnier method. Thirty samples of fermented milk beverages were analyzed using the 2 methods. There was no difference ($P > 0.05$) between Mojonnier and Gerber methods for fat content measurement in these samples. So, both of them could be used to measure the fat content in fermented milk beverages.

Key Words: fermented milk beverages, Mojonnier method, Gerber method

T86 Quantitative analysis of the distribution of fat globules in milk. G. Impoco[1], N. Fucà[2], and G. Licitra*[1,2], [1]*CoRFiLaC, Regione Siciliana*, *Ragusa, Italy*, [2]*DACPA, University of Catania*, *Catania, Italy*.

This study aims at devising image analysis methods to quantify the distribution of fat globules in confocal laser scanning microscope

(CLSM) images. Milk was collected from a local farm and subject to eight different treatments. Ten images were recorded for each milk specimen using CLSM at 40X and classified according to five parameters (small globules count, large globules count, globule density, presence of clusters, and distribution homogeneity). Each image was classified through visual inspection by assigning a numeric score to each parameter. Visual evaluation provided qualitative, subjective information. Automatic quantitative analysis was performed onto the same images to obtain objective, repeatable estimates. Each image was partitioned into cells. For each cell, nine numerical descriptors were computed (e.g., number of globules in a cell, area covered by globules). For each descriptor, a measurement was obtained at each cell. The variances of such measurements over all cells were recorded. Nine descriptors were thus obtained for each image. Factor analysis on manual evaluation data revealed that count of small and large globules were strongly inversely correlated (−0.85), as well as density and homogeneity to the presence of clusters (−0.40 and −0.61, respectively). Density and homogeneity had a moderate correlation factor (0.66). Principal component analysis showed that the first three components accounted for 80% of the total variance in scores. Factor analysis was also performed on software measurements. As expected, several descriptors were highly correlated since they capture similar aspects of the images. After grouping correlated factors, numerical description was consistent with qualitative parameters. Automatic classifications turned out to be a good interpretation of manual annotations. This suggests that quantitative characterization of dispersed phases of fluids in CLSM micrographs is promising.

Key Words: image analysis, milk treatments, milk microstructure

T87 Evaluation of Sprint rapid protein analyzer for total protein analysis of Cheddar cheese. H. M. Zhang*, P. Salunke, J. K. Amamcharla, and L. M. Metzger, *Midwest Dairy Foods Research Center, South Dakota State University*, *Brookings*.

The Kjeldahl method is widely used as a reference method for protein measurement of numerous dairy products including cheese. However, it is labor intensive, time consuming, and utilizes hazardous chemicals. A new protein analysis instrument called the Sprint rapid protein analyzer (CEM Corporation) was recently developed. This instrument utilizes an automated protein-tagging technology and is rapid, easy to operate, and does not utilize hazardous chemicals. In previous research we have demonstrated that the Sprint method is applicable for analysis of milk and cream samples. The objective of this study was to evaluate the applicability of the Sprint method for the analysis of Cheddar cheese. In this study 6 Cheddar cheese samples were analyzed for protein in duplicate using the Sprint method and the Kjeldahl method at 1 week, 3, 6, 9, and 12 mo on ripening. The protein content of each sample measured by Kjeldahl analysis remained relatively constant throughout ripening (mean difference between 1 week and 12 months was - 0.23%), whereas the protein content of each samples measured by the Sprint method decreased during ripening (mean difference between 1 week and 12 months was 2.68%). The average protein differences between the methods (Sprint – Kjeldahl) at 1 week, 3, 6, 9, and 12 month samples was 2.04, 1.34, 0.90, 0.11, and -0.79%. These results indicate that the Sprint method over estimated the protein content during early ripening and underestimates the protein content after extended ripening. As Cheddar cheese ages the level of intact protein decreases and the level of hydrolyzed protein increases. Since the protein-tagging technology utilized in the Sprint method is influenced by protein hydrolysis it is not surprising that the results of this method are influenced by the age of the cheese. In order to utilize the Sprint method for protein analysis of Cheddar cheese the level of protein hydrolysis in the cheese needs to be controlled.

Key Words: Sprint rapid protein analyzer, Cheddar cheese, total protein

T88 Determination of true proteins in dairy products: A comparative study between Kjeldahl and Sprint protein analyzer. D. Zhao*, V. Jai, and N. Y. Farkye, *California Polytechnic State University*, *San Luis Obispo*.

True proteins (TP) in milk play a major role in yield, functionality and nutritional value of dairy products and products containing dairy components. It is standard practice in milk procurement for milk processing plants to pay premium for protein content of milk. However, in the dairy industry, TP is of greater economic value than total protein content hence the need for rapid determination of TP is of significant interest. In this study, the Sprint Rapid Protein analyzer, SPR (CEM Corporation, Matthews, NC) was compared with the standard Kjeldahl method to measure the TP in selected dairy products. The SPR is based on the Orange G dye binding method that measures the TP directly unlike Kjeldahl in which TP is calculated as the difference between total nitrogen and non-protein nitrogen multiplied by 6.38. Cheddar and mozzarella cheeses, and milk protein powders such as whey protein concentrate 80, milk protein concentrate, milk protein isolate, whole milk powder, and non fat dry milk were analyzed for true proteins by both the methods and the results were compared. The results were not statistically different for Cheddar cheese ($P > 0.05$), Mozzarella cheese ($P > 0.05$) and the milk protein powders ($P > 0.05$). The repeatability within the samples for Cheddar cheese, Mozzarella cheese and milk powders were similar in both methods (standard deviation 0.02–0.42 from Kjeldahl; and 0.04–0.49 for SPR). The relative standard deviation for all the products measured in both the methods was always less than 2%. Therefore, the precision and accuracy in measuring true protein by SPR in dairy products is comparable to Kjeldahl. The SPR offers rapid (less than 5 min), easy determination of true proteins in dairy products. It can be a good alternative to Kjeldahl in a dairy processing plant where faster results are needed

Key Words: true proteins, Kjeldahl, Sprint rapid protein analyzer

T89 Application of FTIR spectra for early detection of spore contamination in fluid milk. J. C. Huber-Rockow* and R. Jimènez-Flores, *California Polytechnic State University*, *San Luis Obispo*.

FTIR is shown to be a useful tool for the analysis of spores in several food products and processes. This research aims to improve milk safety and processing practices through the development of a fast and reliable FTIR method to document and quantify the metabolic changes in spores in raw milk and milk after a germination-induction heat treatment. In this study, basic FTIR-ATR spectral analysis and principal component analysis properly differentiates 11 reference strains of *Bacillus* in their 1200–900 cm^{-1} fingerprint regions (*B. megaterium*, *B. subtilis* (2), *B. pumilus*, *B. licheniformis* (2), *B. coagulans*, *B. circulans*, *B. amyloliquefaciens*). Subsequently, using the whole spectra generated by the FOSS MilkoScan FT2, we successfully identified individual strains at different stages of heat-induced germination in a milk system, however no significant difference between strains was identified. Further analysis will improve differentiation between strain variability and natural variability of milk. Completion of this work will continue to highlight the utility of FTIR as a tool for safety and quality screening in the dairy industry.

Key Words: FTIR, spores, milk quality

T90 Oxidation stability of milk rich in α-linolenic acid produced through duodenum infusion of high-linolenic perilla fatty acid into dairy cows. Q. S. Liu, J. Q. Wang*, D. P. Bu, E. Khas, G. Yang, L. Y. Zhou, P. Sun, and K. L. Liu, *State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences*, *Beijing, China*.

Our objective was to determine the effect of storage condition on oxidation stability of milk samples which were stored in dark under different storage conditions. The milk samples came from 4 primiparity Chinese Holstein cows infused with increasing amounts of high-linolenic perilla fatty acid into the duodenum (0, 100, 200, 300, 400 g/d), then stored in dark at either 4°C or 20°C for period of 0, 72, and 120 h. Data were analyzed statistically by using PROC MIXED of SAS. It was observed that at 0 h, the activity of total superoxide dismutase (T-SOD), total antioxidant capacity (T-AOC) in milk samples were tended to decrease linearly ($P = 0.21$, $P = 0.14$), but the content of thiobarbituric acid reactive substances (TBARS) was tended to increase linearly ($P = 0.18$) with the infusion increased, the oxidation stability of milk samples showed the tendency of decreasing at 0 h. Furthermore, the activity of T-SOD was not changed, the T-AOC decreased sharply $P = 0.0086$, the content of TBARS increased significantly ($P = 0.029$) with the infusion increased, the oxidation stability of milk decreased significantly when them stored at 4°C for 72 h, however, when stored for 120 h, the activity of T-SOD, T-AOC and the content of TBARS were not changed, which showed the oxidation stability of milk tended to remain stable at 4°C for 120 h. Milk samples stored at 20°C for 72 h, the activity of T-SOD, T-AOC tended to decrease ($P = 0.055$, $P = 0.07$). Content of TBARS tended to increase linearly ($P = 0.082$), which indicated that the oxidation stability of milk have the tendency of decreasing with the increasing amounts of α-linolenic acid, but for 120 h, the activity of T-SOD did not change significantly, the T-AOC tended to decrease quadratically ($P = 0.052$), the content of TBARS increased sharply ($P = 0.023$), therefore, the oxidation stability of the milk was decreased. Our results suggested that the oxidation stability of milk rich in α-linolenic acid produced through duodenum infusion perilla oil is decreased at the different storage conditions.

Key Words: milk samples, storage condition, oxidation stability

T91 Activity and viability of lactic acid bacteria in yogurts fortified with predigested non-germinated or germinated whole soy powder. U. Nsofor*[1,2] and Z. Ustunol[1], [1]*Michigan State University*, *E. Lansing,* [2]*Food and Drug Administration*, *College Park, MD.*

We have previously shown that pre-digestion and germination of soybeans hydrolyzes the non-bioavailable compounds into bioactive compounds and fermentation during yogurt manufacturing further increases their yield. The overall goal of this research was to determine the activity and viability of lactic acid bacteria in yogurt that has been fortified with predigested and non-germinated, or germinated soy powder, over the 6 week refregerated storage of the product. Swiss style reduced-fat strawberry flavored cow's milk yogurts fortified with germinated (GSP) or non-germinated (NGSP) spray dried whole soy powders (50:50 blend) and cultured with *Streptococcus salivarius* ssp. *thermophilus*, *Lactobacillus delbrueckii* ssp. *bulgaricus* and a probiotic *Lactobacillus acidophilus* NCFM were manufactured using standard yogurt manufacturing procedures. The soybean varieties utilized for yogurt making were Vinton 81 and DF 222. Treatments investigated were 50:50 blends of, GSP Vinton 81 + cow's milk, NGSP Vinton 81 + cow's milk, GSP DF 222 + cow's milk, NGSP DF 222 + cow's milk. All soy and all dairy yogurt controls were also included. Proximate analysis of all yogurt samples was conducted according to AOAC procedures. Activity and viability of the lactic acid bacteria was monitored at 7 d intervals over 6 weeks of refrigerated storage at 4°C. MRS, MRS-sorbitol and M17 agar were utilized to enumerate *Lactobacillus delbrueckii* ssp. *bulgaricus*, *Lactobacillus acidophilus* NCFM and *Streptococcus salivarius* ssp. *thermophilus*, respectively. The pH of each yogurt was determined at time of manufacture and also monitored at 7 d intervals for 6 weeks. The pH of the yogurts remained constant for up to 5 weeks of refrigerated storage. Cow's milk yogurt fortified with GSP DF 222 maintained highest ($P < 0.001$) activity and viability of lactic acid bacteria during the 6 weeks of the study, $>4 \times 10^7$ CFU/g. Activity and viability of the lactic acid bacteria was lowest in all soy yogurts during the same time frame, $<2.0 \times 10^6$CFU/g.

Key Words: yogurt, soy, lactic acid bacteria

T92 Sensory attributes of yogurt fortified with predigested, non-germinated or germinated whole soy powder. U. Nsofor*[1,2] and Z. Ustunol[1], [1]*Michigan State University*, *E. Lansing,* [2]*Food and Drug Administration*, *College Park, MD.*

Fortification of yogurt with soy and soy ingredients has been of interest to combine health benefits of soy with dairy ingredients. We have previously shown that pre-digestion and germination of soybeans hydrolyzes the non-bioavailable compounds into bioactive compounds and fermentation during yogurt manufacturing further increases their yield. The overall aim of this research was to determine the sensory attributes of cow's milk yogurt fortified with predigested and non-germinated, or germinated soy powder and compare these yogurts to their all soy and all dairy counterparts. Swiss style reduced-fat strawberry flavored cow's milk yogurts fortified with germinated (GSP) or non-germinated (NGSP) spray dried whole soy powders (50:50 blend) and cultured with *Streptococcus salivarius* ssp. *thermophilus*, *Lactobacillus delbrueckii* ssp. *bulgaricus* and a probiotic *Lactobacillus acidophilus* NCFM were manufactured using standard yogurt manufacturing procedures. The soybean varieties utilized for yogurt making were Vinton 81 and DF 222. Treatments investigated were 50:50 blends of, GSP Vinton 81 + cow's milk, NGSP Vinton 81 + cow's milk, GSP DF 222 + cow's milk, NGSP DF 222 + cow's milk. All soy and all dairy yogurt controls were also included. Proximate analysis of all yogurt samples was conducted according to AOAC procedures. A total of 112 untrained sensory panelists evaluated all 6 yogurt samples for appearance, body texture, flavor and overall acceptance on a 9-point hedonic scale. All yogurts had similar pH of 4.55 at the end of manufacturing. There were no significant differences in their compositional analysis. Sensory results showed there were no significant differences in appearance, body texture, flavor and overall acceptance between the cow's milk yogurt and the 50:50 blends containing germinated or non-germinated soy powder. There were also no noted differences in sensory attributes investigated between the 2 bean varieties (Vinton 81 and DF 222) studied. However, all soy yogurts were scored significantly lower ($P < 0.001$) than all other yogurts.

Key Words: yogurt, soy, sensory

T93 Effect of lactose content on the post-acidification of yogurt. V. Sikand*, P. S. Tong, and S. Roy, *California Polytechnic State University*, *San Luis Obispo*.

The manufacturing of yogurt involves fermentation of milk by *Lactobacillus delbrueckii* ssp. *bulgaricus* and *Streptococcus thermophilus*. Two important properties of yogurt are that it contains live cultures and lactic acid. Because of the high residual lactose content in yogurt, lactic acid can continue to be produced during its refrigerated storage by *Lactobacillus bulgaricus*. This phenomenon is called "post-acidification." Yogurt can become too acidic (sour) because of its continued acidification and negatively affect the properties of the yogurt. The objective of this research was to control post acidification by reducing the amount of lactose in milk used for preparing yogurt. Two non-fat yogurt mixes were formulated to contain 5% protein and varying degrees of lactose as follows: Control yogurt mix containing 7% lactose made by adding 5.66% w/w nonfat dry milk powder to fluid skim milk and experimental yogurt standardized to 2% lactose by adding milk protein isolate (MPI) containing 87% protein to UF permeate obtained from skim milk. The UF permeate was used because of its similar mineral composition to milk. These mixes were stirred for 5 h and kept overnight in a refrigerator for complete hydration. On the next day, these yogurt mixes were heated at 85°C for 30 min, cooled to 42°C, mixed with commercial frozen yogurt culture (DVS YC-X11), and incubated until it reached pH 4.6. Basic composition analyses of these yogurt mixes showed similar mean protein values. The control yogurt mix had 0.18% fat content, 7% lactose, and about 13% total solids, while the experimental yogurt mix had 0.31% fat, 1.9% lactose, and 7.9% total solids. Relative to the experimental yogurt mixes, the control yogurt mixes showed a significant decrease in pH level from 4.53 to 4.24 ($P < 0.001$) and an increase in the titratable acidity (TA) from 0.98 to 1.21 ($P < 0.001$) over a 21-d refrigerated storage. However, for the experimental yogurt mixes, the decrease in pH and increase in TA was not significant ($P > 0.001$). Our results showed that limiting lactose content in the UF permeate used for yogurt mix help in controlling post-acidification of lactic acid development.

Key Words: yogurt, post-acidification, lactose

T94 Effect of a satiety ingredient on the properties of resulting yogurts during storage. D. Olson*[1], K. Aryana[1,2], D. Alexander[3], and T. Emmick[3], [1]*Louisiana State University Agricultural Center*, *Baton Rouge,* [2]*Louisiana State University*, *Baton Rouge,* [3]*Kemin Health*, *Des Moines, IA*.

Slendesta is an ingredient used for weight management by inducing satiety. The effect of the Slendesta level (0 (control), 150, and 300 mg/227 g yogurt) on the characteristics of the resulting vanilla yogurts during 0, 1, 3, 5, and 7 wk of 4°C storage was investigated. The resulting vanilla yogurts were analyzed for color (L*, a*, and b* values), pH, extent of syneresis, viscosity, log *Lactobacillus bulgaricus* and *Streptococcus thermophilus* counts, and sensory properties (flavor, body/texture, and appearance/color scores). The Slendesta level was significant for L* value, pH, extent of syneresis, viscosity, log *Lactobacillus bulgaricus* count, and appearance/color score. Increasing Slendesta level decreased L* value, pH, and extent of syneresis but tended to increase viscosity and log *Lactobacillus bulgaricus* count. The 150 mg Slendesta level yogurt had significantly higher appearance/color scores than the control. Age had a highly significant effect on L* value, a* value, pH, extent of syneresis, viscosity, log *Streptococcus thermophilus* count, and log *Lactobacillus bulgaricus* count and a significant effect on both the body/texture score and the appearance/color score. The highest L* value and a* value occurred at wk 0 and 1, and the pH decreased after wk 0. Both the extent of syneresis and the viscosity had a general tendency to increase with storage time. Although both log *Streptococcus thermophilus* counts and log *Lactobacillus bulgaricus* counts decreased with storage, the relative decrease in counts was more rapid for the log *Lactobacillus bulgaricus* counts. Body/texture scores were significantly higher at 3 wk than at 0 wk, while appearance/color scores were significantly higher at 0 wk than at 3 wk. Slendesta positively influenced some characteristics of yogurt.

Key Words: satiety, weight management, yogurt

T95 Chemical and sensory characteristics of set-type yogurts made from sheep, goat, and their mixed milks during refrigerated storage. A. C. Gürsoy-Balci[1], Z. Güler[1], and Y. W. Park*[2], [1]*Mustafa Kemal University*, *Antakya, Hatay, Turkey*, [2]*Fort Valley State University*, *Fort Valley, GA*.

In the countries of the Mediterranean basin, sheep and goat milk and their products have formed a vital part of its economy and cultural heritage. Sheep and goat milk products can provide a profitable alternative to cow milk products owing to their specific taste, texture, typicality and healthy image. Six types of yogurts were manufactured from pure goat milk of Damascus breed, pure sheep milk of Awassi breed, and mixed milk (50% each) of the 2 species using CH-1 and YF-3331 yogurt starter cultures to study chemical composition and sensory properties of the products in relation to free fatty acids (FFA) and volatile compounds (VC) profiles. Upon manufacture, the yogurts were stored at 4oC for 1, 7, 14 and 21 d before conducting chemical and sensory analyses. FFA and VC were determined on a capillary gas chromatography using aluminum adsorption and static headspace techniques. Results showed that cultures significantly affected acetaldehyde ($P < 0.05$), acetone ($P < 0.05$) and diacetyl ($P < 0.01$) contents, responsible for characteristic yogurt flavor, whereas type of milk had no effects. Type of milk influenced ethanol level, which was highest in goat yogurt. Significant variations occurred in acetaldehyde and diacetyl contents during the storage. FFA of hexadecanoic, octadecanoic and decanoic acids were significantly ($P < 0.05$) affected by type of milk. Type of culture influenced ($P < 0.05$) levels of C2 to C15 FFA, while type of milk affected C2 to C14 FFA contents. The mixed milk yogurt contained mean concentrations of 3.96 µg/g diacetyl, 6.69 µg/g acetoin, 41.43 µg/g acetaldehyde, 2.83 µg/g ethanol, 1.77 µg/g ethanoic acid, 1.33 µg/g hexanoic acid, 2.51µg/g decanoic acid, and 1.08 µg/g octanoic acid, respectively. It was concluded that yogurts made from the mixed milk had the highest sensory scores in taste and smell traits.

Key Words: sheep and goat milk, yogurts, chemical characteristics

T96 Oxidative stability of yogurt from bovine and caprine milks enriched with different levels of n-3 fatty acids. D. Dlders*, A. Mora-Gutierrez, R. Attaie, and G. L. Goodie, *Prairie View A&M University, Prairie View, TX.*

Incorporation of n-3 fatty acids into daily diet results in beneficial effects on vision, neural development, and lowers incidents of diseases such as coronary heart disease. The intake of n-3 fatty acids is generally low in the typical Western diet. Dietary intake of yogurt supplemented with physiologically significant amounts of n-3 fatty acid would contribute to a healthy life. However, the incorporation of n-3 fatty acids in foods would have to be limited due to their oxidative instability. The objective of this study was to evaluate the oxidative stability of yogurt from bovine and caprine milks enriched with different level of Menhaden oil containing 38% n-3 fatty acids. Non-fat yogurt from bovine and caprine milks were supplemented with 0.1, 0.2, and 0.4% Menhaden oil followed by homogenization. Yogurt samples were stored in the dark for 30 d at 4°C, and oxidative deterioration of samples were assessed at different intervals using thiobarbituric acid (TBA) test. As the level

of n-3 fatty acids increased in samples the TBA value also increased, regardless of storage time. Significant chelating activity ($P < 0.05$) was detected in yogurt samples containing iron as a chelating agent at 100 ppm. Furthermore, the yogurt made from caprine milk exhibited stronger chelating activity than the yogurt from bovine milk ($P < 0.05$). The high content of β-casein in yogurt from caprine milk is suggested to be involved in protection of n-3 fatty acids against lipid oxidation induced by iron. Yogurt in general seems to be a suitable vehicle for n-3 fatty acid fortification, particularly yogurt made from caprine milk.

Key Words: yogurt, oxidative stability, omega fatty acids

T97 Evaluation of non-essential and heavy minerals in three species milks, Torba yogurts, and whey. H. Sanal[1], Z. Guler[1], and Y. W. Park*[2], [1]*Mustafa Kemal University*, *Antakya, Hatay, Turkey*, [2]*Fort Valley State University*, *Fort Valley, Georgia, USA*.

Among concentrated yogurts, Torba yogurt is made by straining in a special cloth bag, which is the most commonly consumed in Turkey. Mineral contents of milk and dairy products are influenced by many factors such as animal species, feeds, environment, milking and manufacturing processes. This study was to determine non-essential and heavy metal concentrations in cow (Holstein), ewe (Awassi) and goat (Damascus) milks and their regular yogurts, Torba yogurt and whey. A Varian Vista-MPX simultaneous inductively coupled plasma optical emission spectrometer (ICP-OES) was used to quantify silver, aluminum, arsenic, boron, beryllium, cadmium, nickel, lead, antimony, titanium, thallium and vanadium in ashed milks and their respective products. Barium was not detected in goat and cow milk and their products. Among all elements, boron was most abundant, and highest in the cow milk. Species differences were observed between levels of certain health-related elements such as As, B, Ba, Cd, Ni, Sb and Ti in milk and their products. Mean lead contents of all 3 species milks were 3.0 ppm. Average contents (ppm) of Ag, Al, As, B, Ba, Be, Cd, Ni, Pb, Sb, Ti, Tl and V in cow milk and its Torba yogurt were: 0.27, 0.32; 5.31, 6.73; 1.91, 3.29; 24.0, 23.3; 0.0, 0.0; 0.04, 0.06; 0.21, 0.18; 2.47, 2.72; 3.05, 3.22; 1.27, 2.32; 0.31, 0.47; 7.01, 7.18; 0.72, 1.30, respectively. Milk, regular yogurt and Torba yogurt revealed good sources of non-essential elements, especially boron, lead, thallium and vanadium. The daily intake of these elements from these milks and yogurts appeared to exceed the provisional tolerable daily intake. Daily intake of toxic elements from milks and yogurts ranged between 2.16% (Be) and 116% (Pb). A long-term exposure of these elements from foods and environment has to be continuously monitored to maintain at their minimum levels for food safety.

Key Words: cow-sheep-goat milk, Torba yogurt, non-essential elements

T98 Impact of acidulant addition on yogurt fermentation times and physiochemical properties. T. A. Boomgaarden* and K. A. Schmidt, *Kansas State University*, *Manhattan*.

Consumers desire products that minimize their environmental impact; therefore, in recent years, a greater emphasis has been made for sustainable production of agricultural products. This research aimed at developing a yogurt process with reduced fermentation time, thus reducing energy needs and creating a more sustainable manufacturing process. Yogurt was manufactured by pre-acidifying nonfat yogurt mix (13.5% solids) with citric acid, lactic acid or concentrated lemon juice (CA, LA, LJ) at 200 ppm before or after heat treatment to pH 6.2, followed by fermentation at 42°C in a BioFlo 3000 (New Brunswick Scientific Co., Inc.) to a target pH of 4.6. Yogurts were analyzed for *L. bulgaricus* and *S. thermophilus* counts at the beginning and end of fermentation. Three randomized replications were completed and all tests were done in duplicate and averages were reported. Results showed that CA or LJ added after heat treatment reduced fermentation time by 13% compared with the control; whereas, CA and LJ added before heat treatment had no effect. LA added before or after heat treatment increased fermentation time by 16%. Counts of *L. bulgaricus* and *S. thermophilus* were similar, with initial counts of 6.9 and 7.7 log CFU/mL respectively, and end counts of 7.1 and 7.7 log CFU/mL respectively. In addition, control yogurt and yogurts with CA and LJ added after heat treatment were manufactured and fermented in 90 mL sterile cups and assessed for pH, texture and rheological (G', G") characteristics at d 1. Statistically, the CA and LJ yogurts had less firmness (202 g and 212 g) and greater pH (4.58 and 4.57) compared with the control yogurt (231 g and 4.53). Control yogurt had greater G' and G" values at a frequency of 1 Hz than CA and LJ yogurts. These results show that partial acidification of the yogurt mix with CA or LJ after heat treatment reduced fermentation time but some physiochemical parameters, particularly texture, were affected. This new yogurt has potential for success in the marketplace because it appeals to consumers seeking sustainable products and could be easily implemented by manufacturers.

Key Words: yogurt, fermentation time, sustainable manufacturing

T99 Antioxidative peptides isolated from fermented whey proteins by lactobacilli and their effects on aged mice. Y. Bao*[1], X. Liang[1], L. Qin[1], R. Li[1], and M. Guo[2], [1]*Northeast Forestry University*, *Harbin, China*, [2]*University of Vermont*, *Burlington*.

Natural proteins can be partially hydrolyzed to produce peptides that may have biological functions. The objectives of the study were to prepare functional peptides from fermented whey protein concentrate (WPC) by *Lactobacillus plantarum A9* and *Streptococcus thermophilus* S33, and to characterize their antioxidative properties. The optimum conditions for producing antioxidative peptides were: inoculate rate 5%, culture ratio 1:1, fermentation temperature at 37°C and pH at 6.4, and fermentation time for 16 h. Two fractions were obtained using ultrafiltration and their relative molecular weights were 328 and 2,031, respectively. The induced model aged mice were treated by neck back subcutaneous injection of D-galactose every day for 45 d. The mice were given 3 different doses of whey protein peptides (WPP) at 100, 200 and 400 mg/kg body weight per day, respectively. The effects of WPP on the levels of catalase (CAT), malondialdehyde (MDA), superoxide dismutase (SOD), glutathione peroxidase (GSH-PX) in serum, liver and brain were evaluated after 45 d. The CAT, SOD and GSH-PX activities in the induced aged group decreased while MDA increased compared with control mice. However, the activities of CAT, SOD, and GSH-PX in the organs of induced aged mice fed with the WPP were significantly increased especially for the higher dose group ($P < 0.05$). The results showed that antioxidative peptides could be prepared from fermented WPC using *Lactobacillus plantarum A9* and *Streptococcus thermophilus S33* for functional foods applications.

Key Words: peptides, whey protein, fermentation

T100 Zinc-binding activity of yak casein hydrolysate and the structural characteristics of hydrolysate-Zn complex. X. Y. Mao*[1], X. Wang[1], J. Zhou[1], and P. S. Tong[2], [1]*College of Food Science & Nutritional Engineering, Key Laboratory of Functional Dairy of Chinese Ministry of Education, China Agricultural University*, *Beijing, China*, [2]*California Polytechnic State University*, *San Luis Obispo*.

The bioavailability of zinc is very important for its absorption. Many factors can affect the bioavailability of dietary zinc in dairy food systems. Some proteins or peptides can form complex with zinc, which makes zinc soluble and increases its absorption and bioavailability in intestinal basic conditions. The aim of this work was to: 1) determine the Zn-binding activity of yak casein hydrolysate and 2) verify that casein hydrolysate can really form complex which is soluble in a simulated intestinal environment. The capacity of yak casein hydrolysate to form complexes with zinc was quantified. Zinc chelation by casein hydrolysate was described by means of UV-visible spectrophotometry (UV-vis) and Fourier transform infrared spectroscopy (FTIR). Results showed that casein hydrolysate prepared with Alcalase and trypsin possessed the highest Zn-binding activity compared with casein hydrolysates prepared with pepsin, Flavozyme or papain ($P < 0.05$). The 6h-hydrolysate obtained with Alcalase, which is an endopeptidase from *Bacillus licheniformis*, showed the highest Zn-binding activity and significantly higher than that of the native proteins. The UV-vis absorption spectra showed that absorbance spectra changed between yak casein hydrolysate and its zinc complex in the area of 230–300 nm. The absorbance of casein hydrolysate-Zn complex at 270–300 nm was significantly lower than that of casein hydrolysate itself at the same wavelength. The oxygen atom of the carbonyl group in peptides could chelate with Zn^{2+} and lead to the hypochromic shift of its typical bands. Furthermore, FTIR spectra showed that the absorption at wave numbers between 1 450 cm^{-1} and 1 000 cm^{-1} increased when yak casein hydrolysate and Zn^{2+} formed complexes. Casein hydrolysate-Zn complex exhibited strong bands at the wave numbers of 1449 cm^{-1} and 1406 cm^{-1} that are the characteristic stretching mode of C = N. The FTIR spectra verify that some sites of yak casein hydrolysate can bind with zinc, and the formed substance is a Zn-binding complex which may be useful and practical in the prevention and treatment of Zn deficiency.

Key Words: yak casein hydrolysate, Zn-binding capacity, characterization

T101 Functional and volatile properties of milk serum protein concentrates. L. E. Coppola*[1], S. A. Rankin[1], M. S. Molitor[2], and J. A. Lucey[1], [1]*University of Wisconsin-Madison*, [2]*Wisconsin Center for Dairy Research*, *Madison*.

Microfiltration, commonly used in the dairy industry for removal of fat and bacteria from milk, can also be an effective tool to isolate milk serum proteins for the production of milk serum protein concentrate (MSPC). MSPC has less fat, undergoes fewer heat treatments, and is free of rennet and other by-products of the cheese-making process, likely causing it to have improved functionality over traditional cheese whey protein concentrate (WPC). Because solubility, turbidity, foaming, and volatile composition are vital characteristics for many food applications, this study compared these features of MSPC and WPC. Milk permeate was produced from pasteurized, unhomogenized skim milk at temperatures of ~5°C and ~23°C using polymeric, cross-flow microfiltration. Permeates were concentrated by ultrafiltration and spray dried to obtain MSPC powders of ~80% protein. The MSPC powders were compared with a traditional WPC80 from Swiss cheese whey made at Babcock Dairy Plant and 3 commercial WPC. SDS-PAGE results showed that protein composition was significantly different with the MSPC made at 5°C containing more β-casein than the other MSPC or WPC samples (~15% vs. <5%). Both MSPC were significantly ($\alpha = 0.05$) different in standard foaming, turbidity, and solubility tests than WPC samples. MSPC generated larger foam overruns (>2000% vs. <800%) and more stable foams (>14 min vs. <5 min), solutions were less turbid (>90% vs. <25% transmission), and powder had higher solubility compared with WPC samples (over pH range 3–7). Furthermore, MSPC made at 5°C had significantly larger foam overrun (>30000%) and greater foam stability (>2 h) than MSPC made at 23°C (<1200% overrun, stability <15 min). Analysis of volatile content of the powders by SPME-GC/MS showed that the number of different types of volatile compounds present in both MSPC was significantly lower than the number present in WPC samples. In addition, accelerated storage of MSPC at 50°C for 28 d resulted in fewer types of volatiles increasing in intensity during storage compared with WPC samples where many volatiles increased in intensity during storage. MSPC has distinctive flavor and performance attributes that may result in enhanced functionality in specific types of food applications.

Key Words: milk serum protein, protein concentrate, whey

T102 Volatile profiles of commercial starter distillates and diacetyl levels in selected dairy food. M. I. Rincon*, A. Lopez-Hernandez, M. S. Surianto, A. R. Rankin, and S. A. Rankin, *University of Wisconsin-Madison*, *Madison*.

Starter distillates are used as ingredients in the formulation of many dairy products such as cottage cheese, margarine, spreads, processed cheese, and sour cream to increase the levels of naturally occurring aroma compounds associated with lactic acid bacteria (LAB) fermentation. Diacetyl is a highly volatile product of the citrate metabolism of certain LAB including *Lactococcus lactis* ssp. *diacetylactis* and *Leuconostoc citrovorum* that imparts a high level of "buttery" flavor notes. In the US, starter distillates are regarded as generally recognized as safe and usage in food products is only limited by good manufacturing practices. Little is known but the volatile composition of starter distillates and the level of diacetyl in finished products. The objective of this work was to characterize the volatile constituents of 11 commercial starter distillates and to quantitate the levels of diacetyl in several commercial dairy products where starter distillates are used as flavorants. The headspace volatiles were assessed using a solid phase microextraction fiber and analyzed by GC-MS. The identity of the aroma compounds present in the samples was confirmed by matching the corresponding mass spectra with those in a NIST database and by comparing the retention times to those of authentic standards. The levels of diacetyl in the 11 commercial starter distillates ranged from 5,000 to 30,000 ppm. In addition to diacetyl, significant levels of acetoin, acetic acid, acetaldehyde, furfural, benzaldehyde, fatty acids, ethyl acetate were found. A total of 10 samples of cottage cheeses, margarines, spreads, and butter sprays were found to contain diacetyl in the range of 10 to 100 ppm. The results obtained in this work summarize the volatile composition of commercial starter distillates and the approximate levels of diacetyl in selected foods.

Key Words: diacetyl, starter distillates, volatiles in dairy products

T103 Sensory properties of chocolate flavored, protein fortified, fluid milk based recovery beverages produced using indirect and direct thermal processing. A. Lammert*[1], A. Olabi[2], K. Brooks[1], S. Vink[1], and P. Tong[1], [1]*California Polytechnic State University*, *San Luis Obispo,* [2]*American University of Beirut*, *Beirut, Lebanon*.

Protein′s role in post exercise muscle recovery is well documented and numerous beverages are commercially available. However, fluid milk is typically not the first ingredient. The objective was to determine differences between sensory properties of a chocolate flavored, protein fortified fluid milk based recovery beverage that contained 25 g of protein per 12 ounce serving using indirect and direct thermal processing methods. Beverages were formulated using milk, whey protein concentrate (WPC), fructose, sucrose, carrageenan, salts, flavors and

cocoa. WPC was mixed and hydrated for 30 minutes in the milk. The remaining dry ingredients were blended and added to the hydrated WPC/milk mixture and mixed for an additional 5 minutes. The mixture was UHT processed at 285°F for 3 seconds using indirect or direct heat and bottled in a clean fill hood. Descriptive sensory analysis using a trained panel was completed on two week old beverages and the characteristics evaluated were appearance, odor, flavor, texture, and aftertaste. Results were analyzed using repeated measures ANOVA. WPC brand had a significant effect ($P < 0.05$) on mostly the appearance attributes in addition to sweet odor, chalkiness, viscosity and astringent and chalky aftertastes. There was no effect ($P > 0.05$) on most odor and flavor attributes. Processing method had a significant effect on two appearance attributes and burnt odor, cooked flavor, chalky texture, and aftertaste. There was a significant WPC brand and processing method interaction ($P < 0.05$) for most appearance, texture and aftertaste attributes. Given the lack of major effects on odor and flavor attributes, our work indicated that chocolate protein fortified fluid milk based recovery beverages can be developed using different WPCs with minimal impact on sensory properties.

Key Words: fluid milk, descriptive analysis, whey

T104 Physicochemical properties of pomegranate flavored carbonated symbiotic beverage. H. Walsh*, J. Cheng, and M. Guo, *University of Vermont*, *Burlington*.

Drinkable yogurt is becoming popular in the US and other countries and is considered a functional food. Carbonation of drinkable yogurt may create a niche in the functional foods market. The objectives of this study were to develop a manufacturing technology for drinkable carbonated symbiotic yogurts, and to evaluate their physicochemical properties. Two flavors of yogurt drink: pomegranate (P) and vanilla (V) were formulated, each containing inulin as prebiotic and probiotic bacteria to produce symbiotic dairy beverages. The products were successfully stabilized with high methoxyl pectin and whey protein concentrate. The carbonation process was achieved using a pressurized carbonator for these yogurt drinks with approximately 3 volumes of food-grade carbon dioxide. The samples were sealed in glass containers to maintain carbonation levels. Three trials of each product were carried out and 3 replicates from each trial were taken for analysis. Protein fat, total solids and ash were determined using standard dairy analysis methods. Carbohydrate was determined by difference. Viscosity and pH were also analyzed using standard methods. Bottled samples were held at refrigerated temperatures (4°C) for 8 weeks to evaluate the stability of the product over time. Chemical composition of the carbonated beverages were as follows: Protein: 1.58 ± 0.05% (P), 1.59 ± 0.06% (V), Fat: 1.24 ± 0.2% (P), 1.18 ± 0.11% (V), Total Solids: 14.78 ± 0.11% (P), 14.93 ± 0.05% (V), Ash: 0.49 ± 0.02% (P), 0.46 ± 0.03% (V), Carbohydrate: 11.47 ± 0.12% (P), 11.69 ± 0.14% (V). The pH values of the beverage were 4.25 ± 0.04 and 4.22 ± 0.04 and viscosity values were 23.1 ± 3.2 and 25.8 ± 6.5 mPas, for pomegranate and vanilla samples, respectively. Intrinsic stability of the prototypes was maintained for at least 8 weeks. The new manufacturing technology for these prototypes may have potential for commercialization of symbiotic carbonated milk-based beverages.

Key Words: symbiotic, carbonation, beverage

T105 Development of symbiotic milk candy. J. McCarthy*, Z. Zhang, and M. Guo, *University of Vermont*, *Burlington*.

Milk candies made from dried milk are a popular item in Asian countries, but are uncommon in the United States. The objectives of this study were to develop a technology for making powdered milk based candy and analyze its chemical composition. With fortifications of probiotic bacteria as well as the prebiotic compound inulin, a new symbiotic milk candy was developed. A base powder mix was formulated using a combination of skim milk powder, whole milk powder, sugar, maltodextrin and inulin, along with antioxidants and probiotics (*L. acidophilus, L. rhamnosus, L. casei,* and *Bifidobacterium* ssp.) followed by thorough mixing. The mix was then pressed into hexagon tablets using the Colton 204 Rotary Tablet Press. Three trials of the prototype were prepared, and triplicates of each of the trials were analyzed for chemical composition using AOAC standard methods for content of protein, fat, total solids and ash. Carbohydrate content was determined by difference. Results were as follows: protein: 17.87 ± 0.19%; fat: 2.44 ± 0.07%; total solids: 96.93 ± 0.24%; moisture: 3.07 ± 0.24%; ash: 3.31 ± 0.47%; carbohydrates: 73.31 ± 0.37%. Each tablet weighed approximately 2 g and contained 150 mg of inulin and at least 10^9 probiotic cells. Results showed that this product is low in fat content and rich in high quality protein and may be a good vehicle for delivery of both prebiotics and probiotics.

Key Words: milk candy, symbiotic, milk powder

T106 Physicochemical properties of whey protein-based safe paper glue. J. Wang, J. Cheng*, and M. Guo, *University of Vermont*, *Burlington*.

Commercial paper glue products on the market may contain toxic organic compounds harmful to people and bad for the environment. To develop safe paper glues, whey protein-based glue prototypes were formulated using polymerized whey proteins (PWP) and other ingredients. Bonding strength, one of main indexes for glue products, was evaluated, along with the physicochemical properties of the prototypes compared with a commercial control sample. Reconstituted whey protein isolate (WPI) solution (10%, pH 7.0) was polymerized at 75°C for 15 min. The polymerized whey protein (PWP) was combined with PVA, (20%, w/w), emulsifier (propylene glycol) and antibacterial agent (1,2-benzisothiazolin-3-one). The best ratio of PWP solution to PVA solution was about 1.7 to 1.0 with 0.5% propylene glycol and 0.2% 1,2-benzisothiazolin-3-one. The experimental and control glues were sealed in plastic containers and held in an environment controlled chamber (23°C, 50% RH) for 6 mo to determine the bonding strength and physical properties and to evaluate the shelf life. Three trials of the glue prototype were carried out and 3 replicates from each trial were taken for chemical analysis. The bonding strength of the glue was evaluated according to a modified ASTM procedure (D1002–05) using an Instron Universal Testing Machine. Physicochemical properties, including viscosity as well as total solids, ash and protein content, were analyzed using AOAC standard methods. The bonding strength of the glue was 221.5 ± 5.06 N. Viscosity was 675.6 ± 34.6 mPa.s; total solids was 14.38 ± 0.04; ash was 0.27 ± 0.02%; and protein was 9.15 ± 0.07%. The bonding strength and viscosity of both whey protein-based safe paper glue and the control sample remained steady during 6-mo storage.

Key Words: paper glue, whey protein, physicochemical property

T107 Forage yield and quality assessment of tall fescue varieties. D. J. R. Cherney*[1], J. H. Cherney[1], and D. Parsons[2], [1]*Cornell University*, *Ithaca, NY,* [2]*University of Tasmania*, *Hobart, Tasmania, Australia*.

Tall fescue (*Festuca arundinacea* Schreb.) varieties available has increased dramatically in the past few years, and comparisons of varieties for yield and quality are needed. Our objective was to evaluate a method to compare yield and digestibility of entries cut on the same spring day by adjusting yield and digestibility to the same NDF level. Bias occurs if varieties are harvested either on the same day or at the same maturity stage on different days. A system is needed to compare relative yield and forage quality of a group of varieties at the optimum harvest date for each variety, based on total fiber content. This was accomplished by determining the linear rate of change of yield and quality over time. Five separate environments from 2003 to 2009, each with from 3 to 18 tall fescue varieties and 2 to 6 replicates, were sampled for yield and quality using a quadrat (0.06 m or larger) and clippers. Experimental design was an RCBD with a split plot feature, with varieties as the main plot and sampling dates as the sub plots. Sites were located in Chazy, Freeville, and Ithaca, NY. Each trial had at least 5 different spring sampling dates separated by 2 to 4 d between mid-May to early June. Rates of daily change were determined using regression analysis, and analysis of covariance was used to determine if slopes were equal. Rates of change per day of yield and quality were different ($P < 0.05$) across environments, but varieties within a given environment did not differ ($P > 0.05$) in NDF, in vitro NDFD, or yield rate of change per day. Across environments NDF concentration increased from 8 to 12 g/kg/day, while digestible fiber decreased from 7 to 12 g/kg/day. Rate of change in CP was very consistent, decreasing an average of 5.6 g/kg/day over all environments. Rate of change in DM yield was relatively consistent within each environment, but varied from 115 to 275 kg/ha/day across environments. Based on our results, it is possible to sample representative varieties during a period of linear change starting in mid-May and use this information to adjust yield and quality of all entries in a variety trial to their individual optimum harvest dates based on NDF content.

Key Words: tall fescue, digestibility

T108 Yield and chemical composition of forage soybeans relative to seeding rate and stage of harvest. B. G. Buller*, W. A. Storer, D. D. Kee, M. M. Fennel, M. A. Idlett, W. B. Brumbaugh, and F. M. LeMieux, *McNeese State University*, *Lake Charles, LA*.

Two experiments were conducted to evaluate a glyphosate resistant forage soybean (Big Fellow RR) in an effort to identify an alternative high protein forage for cattle producers along the Gulf Coast. The aim of this study was to identify the seeding rate and harvesting stage that optimized forage yield and chemical composition of this soybean. "Big Fellow RR" soybeans were evaluated at different seeding rates and harvesting dates at 2 locations (Lake Charles and Kinder, LA). Soybeans were planted in May of 2009. Both experiments were designed in a complete randomized block arrangement. Seeding rate ranged from 148,000 to 445,000 seeds per hectare. Stand counts, stalk diameter, plant height, and growth stage were evaluated at least twice monthly. Harvesting was conducted from August to mid October to determine responses in yield and chemical composition parameters. Seeding rate did not affect ($P > 0.1$) survival rate or yield in dry matter per hectare. Conversely, individual plant population, height, weight, stalk diameter, and CP were greater ($P < 0.05$), while ADF and NDF were lower ($P < 0.05$) in the lowest population. Percentages of starch, oil, and dry matter, across all seeding rates, increased ($P < 0.05$) between d 102 (R2) and 130 (R5). Dry Matter yield increased ($P < 0.05$) with time. These results indicate, contrary to popular opinion with producers, lower seeding rates may optimize forage cost efficiency and chemical composition. Conversely, higher seeding rates would aid in reducing stalk diameter. This study aided in clarification of ideal seeding rate, harvesting date and established the potential for production of forage soybeans along the Gulf Coast.

Key Words: soybean, forage, seeding rate

T109 Chemical constituents of *Cynodon* spp. varieties. C. L. Gordin, E. R. de Oliveira*, L. L. Freitas, F. W. Pedroso, R. H. de Tonissi e Buschinelli de Goes, B. Lempp, S. F. Luna, W. S. Prado, L. H. X. da Silva, C. W. S. Gavilan, and A. M. de Araújo Gabriel, *Universidade Federal da Grande Dourados*, *Dourados, MS, Brasil*.

The chemical composition of 3 *Cynodon* spp. varieties (Tifton 68, Tifton 85, and Jiggs), in different harvesting ages, were evaluated. The experiment was carried of December 2008 to February 2010, at the animal science sector of Dourados Federal University. Dry Matter, CP, NDF, and ADF determinations were processed at UFGD's Animal Nutrition laboratory. The experimental design consisted of random blocks with treatments organized in a split-plot arrangement that comprised 3 varieties (plots) and 4 harvesting ages (subplots) (28, 48, 63, and 79 d), with 4 replicates. The data were evaluated by the Scott-Knott's test at 5% probability using the SAS statistical package. Analysis was conducted on whole plant (T), leaf (F), and stem (C) fractions for each variety. There was difference ($P < 0.05$) for varieties, for NDF, ADF and CP in whole plant, NDF, ADF in leafs and CP in stem. Jiggs presents for whole plant averages of 77.02 ± 4.3, 36.40 ± 3.1 and 10.7% ± 2.6, for NDF, ADF and CP, respectively. NDF and ADF for Jiggs leaves were 78.4% ± 7.9 and 35.5% ± 6.0 and CP of stem was 8.2% ± 2.4. These data demonstrate that the greater values for fiber and lesser values for protein by Jiggs justify the highest value found for Dry Matter of whole plant (91.38%), this can be explained by age of harvesting and age of varieties. As for harvesting age, Jiggs variety showed a leaf ADF increase 30.20%, as it increase the harvesting times, with an average of 40.77% at 79 d. This may have contributed to increase ADF in whole plant for Jiggs. As we increase the fiber content of whole plant was reduced by 30% in crude protein. There were no differences ($P > 0.05$) for the other *Cynodon* varieties evaluated, with presents averages 72.9, 35.5, 13.1%, for NDF, ADF and CP in whole plant, 71.6 and 31.4 for NDF and ADF in leafs . CP stem in Tifton 85 and Tifton 68, was 10.6%. The harvest age does not alter chemical compositions of these *Cynodon* varieties. Jiggs variety presents lower nutritional values in relation to the contents found in Tifton 85 and Tifton 68.

Key Words: Jiggs, nutrients, Tifton

T110 Chemical composition evaluation of different *Cynodon dactylon*. F. W. Pedroso, E. R. de Oliveira*, L. L. Freitas, C. L. Gordin, R. H. de Tonissi e Buschinelli de Goes, B. Lempp, S. F. Luna, W. S. Prado, L. V. Moura, F. P. Monção, A. M. de Araújo Gabriel, and C. W. S. Gavilan, *Universidade Federal da Grande Dourados*, *Dourados, MS, Brasil*.

The aimed of this study was to determine which genotype and harvesting age among *Cynodon dactylon* would show the best chemical characteristics as parameters for feeding ruminant animals in the state of Mato Grosso do Sul, Brazil. The experiment was conducted at Agrarian Science College of Dourados Federal University, from August 2009 to January 2010. A random block design was used and treatments were arranged in a split-plot scheme with 3 genotypes (Tifton 68, Tifton 85, and Russell) representing plots, at 4 harvesting frequencies (28, 48, 63, and 79 d) as subplots, with 4 replicates. Evaluations were done after a uniform cut and the materials collected for the laboratory were processed as DM, NDF, ADF, and CP analyses. The data were evaluated by the Scott Knott's test at 5% probability using the SAS statistical package. The following variables were analyzed: entire plant (T), leaf (F), and stem (C), within each genotype. There was no difference ($P < 0.05$) for harvesting frequencies. There was no difference ($P > 0.05$) for leaf and stem DM, where Tifton 85 and Russell presents averages of 91.60; 91.66; 91.39; and 91.27%, respectively. There was a difference ($P < 0.05$) for NDF and ADF, for whole plant and leaf. Russell presents a higher values, with averages 80.41 and 37,26% for NDF and ADF, in whole plant, respectively; for leafs the averages was 82.65 and 34.02%, for NDF and ADF, respectively. The others genotypes present averages of NDF of 72.9 and 71.6, for whole plant and leaf, respectively; and 35.1 and 31.4% of ADF for whole plant and leafs. Russell variety presents higher fiber contents, it is suggested that Tifton 85 and Tifton 68 allow a better use of these nutrients. All the *Cynodon dactylon* evaluated can be used in ruminant feeding

Key Words: forage, genotype, nutrients

T111 Chemical composition of three grasses of *Cynodon dactylon*. L. L. Freitas, E. R. de Oliveira*, F. W. Pedroso, C. L. Gordin, R. H. de Tonissi e Buschinelli de Goes, B. Lempp, S. F. Luna, W. S. Prado, F. P. Monção, L. V. Moura, and A. M. de Araújo Gabriel, *Universidade Federal da Grande Dourados*, *Dourados, MS, Brasil*.

This experiment aimed to identify which *Cynodon dactylon* varieties would have the best harvesting intervals to produce the best chemical characteristics as a reference for use in ruminant feeding. The experiment was conducted at the animal nutrition laboratory located at Agrarian Science College, of Dourados Federal University, in Mato Grosso do Sul state, located at latitude: 22°14′S, and longitude: 54°49′W, between August 2009 and January 2010. In the initial period, the experiment was installed in the field: 3 varieties of *Cynodon dactylon* were planted (Tifton 85, Tifton 68, and Vaqueiro), with 4 replicates for each variety. Forage was harvested at 28, 48, 63, and 79-d harvest intervals. The materials collected were taken to UFGD's animal nutrition laboratory and were analyzed for DM, NDF, ADF, and CP analyses. A random block design was adopted, with treatments organized as a split-plot arrangement. The averages were evaluated by the Scott Knott′s test at 5% probability using the SAS statistical package. Analyses were conducted on whole plant (T), leaf (F), and stem (C) for each variety. There was effect ($P < 0.05$) for NDFC, ADFT, and CPF, for varieties. Vaqueiro variety presents averages of 85.31; 35.66; and 17.03%, for NDFC, ADFT, and CPF, respectively. Tifton 85 and Tifton 68, presents values of 77.31, 35.53, 14.76% and 77.23, 34.69 and 15.6% for NDFT, NDFC, ADFT, and CPF. For NDFT occurred variety x harvest intervals interaction, where NDFT from vaqueiro variety increased after 63 d of harvesting with average of 87.50%, 17% higher at 28 d of harvest, T-85 and T-68, does not change the NDFT when increases the harvesting days, which averages of 71.6 and 74.5%, respectively. These values are consistent with physiological growth of forages. All varieties, decrease CPF with harvesting days ($P < 0.05$). Vaqueiro in 28 d of harvest presents average of 21.97%, 28% higher in relation of values 79 d of harvest. T-85 and T-68 presents greatest CPF in 28 d of harvest, with values of 18.8 and 19.9%. Vaqueiro variety had the best response for chemical composition in relation to the other varieties, and responded to harvest date differently that T-85 and T-68.

Key Words: forage, Vaqueiro, Tifton

T112 Nutrient composition of tropical forages collected from intensively managed rotational grazing systems. J. C. Lopes*[1], R. B. Reis[2], A. L. Miller[1], and D. K. Combs[1], [1]*University of Wisconsin*, *Madison*, [2]*Universidade Federal de Minas Gerais*, *Belo Horizonte, Brazil*.

Tropical grasses are the primary forages grown for pasture in most regions of Brazil. They are generally characterized as high-yielding, low-quality forages for high producing livestock. This study was conducted to characterize the nutritive value and fiber digestibility of 5 tropical grasses that were produced under intensive rotational grazing management in the west of the southeastern region of Brazil. Samples of *Brachiaria brizanta* (cv. Braquiarão, cv. Marandu, cv. MG-5); *Cynodon dactylon* (cv. Coast-cross, cv. Tifton-85); *Cynodon nlemfuensis* (cv. Tifton-68); *Panicum maximum* (cv. Colonião, cv. Mombaça, cv. Tanzânia), and *Pennisetum purpureum* (cv. Cameron, cv. Napier) were collected from paddocks after less than 30 d of re-growth. Cutting height of each specie was in accordance with the recommendations using 95% of sward canopy light interception as the criterion. Data were analyzed as a split-plot in time using SAS Proc Mixed. For in vitro NDFD (IVNDFD) analysis, each sample were analyzed 3 times and digested, in duplicates, for 24, 30, and 48 h. CP, NDF and ADF ranged from 11 to 25%; 47 to 74% and 28 to 43% of dry matter, respectively. Means of 24, 30 and 48 h, in vitro NDF digestibility, were 35 ± 5, 44 ± 6, and 59 ± 5% of NDF, respectively across the forages. When averaged across 24, 30 and 48 h incubations times, IVNDF digestibility was greater for *Cynodon nlemfuensis* and *Brachiaria brizanta* than *Panicum maximum*, *Pennisetum purpureum*, and *Cynodon dactylon* (50 ± 10, 48 ± 11, 46 ± 11, 45 ± 12, and 42 ± 10% of NDF, respectively). There were no specie by incubation time interactions for IVNDFD ($P > 0.21$), which suggests that between 24 and 48 h, rates of IVNDFD disappearance were similar among forages. These results illustrate that when harvested early, tropical forages from intensively managed pastures can be relatively high in crude protein, low in fiber, and high in fiber digestibility.

Key Words: tropical grasses, NDF digestion, in vitro

T113 In vitro nutritional evaluation of spiny and spineless *Opuntia* cladodes. J. A. Santos-Haliscak[1], E. Gutiérrez-Ornelas*[1,4], M. A. Cerrillo-Soto[2,4], H. Bernal-Barragán[2,4], and O. La-O[3,4], [1]*Universidad Autónoma de Nuevo León*, *San Nicolás de los Garza, Nuevo León, México*, [2]*Universidad Juárez del Estado de Durango*, *Durango, Dgo., México*, [3]*Instituto de Ciencia Animal*, *La Habana, Cuba*, [4]*Red Internacional de Nutrición y Alimentación en Rumiantes*, *San Nicolás de los Garza, Nuevo León, México*.

The objective of this study was to evaluate nutritional properties of 3 spiny (SO) and 3 spineless (SLO) *Opuntia ficus-indica* varieties using in vitro gas production (GP), in vitro true DM digestibility (IVTDMD; DAISY[II]), and chemical composition techniques. Four field blocks with 10 Cactus cladodes of each variety were planted on September of 2006 at a planting distance of 0.5 m between plants and 2.0 m among varieties. Total cladodes produced from 3 plants in each experimental unit were collected on November of 2007. Samples were chopped, dried on 60°C oven and ground to pass 1 mm screen. Chemical composition analysis

included CP, NDF, lignin, ash and EE. Twenty-four *Opuntia* samples (200 mg DM) and one standard sample of alfalfa were incubated, by triplicate, in 100-mL calibrated glass syringes with rumen fluid obtained from 3 sheep fed alfalfa hay and concentrate (75:25). Gas volume was recorded at 0, 3, 6, 9, 12, 24, 48, 72 and 96h post-inoculation and data fitted to the model $P = a + b (1 - e^{-ct})$. The soluble fraction (a), the gas produced from the slowly degradable fraction (b) and the constant rate of GP (c) were estimated using PROC NLIN (SAS), and metabolizable energy (ME, Mcal kg^{-1} DM) was calculated in accordance to the following equation: $ME = (2.20 + 0.136GP_{24h} + 0.057CP + 0.0029EE2)/4.184$. Data were analyzed using a randomized block design, testing the effect of SO vs. SLO with orthogonal contrasts. There were no differences ($P > 0.05$) among *Opuntia* varieties for CP (8.5% ± 0.61), NDF (27.0% ± 2.1), lignin (4.0% ± 0.38) and ME (2.04 Mcal ± 0.07). Spineless cactus cladodes were higher ($P < 0.05$) than SO in ash (30.4 vs. 27.6% ± 0.88), IVTDMD (90.6 vs. 80.1% ± 1.1) and GP parameters a (13.4 vs. 9.3% ± 0.50) and b (61.0 vs. 53.9% ± 2.1), but SO were higher ($P < 0.05$) than SLO in their rate constant for GP c (7.7 vs. 4.8% h^{-1} ± 0.44) and EE (0.94 vs. 0.29% ± 0.048). Alfalfa forage standard had similar or lower GP kinetic values than both *Opuntia* groups. Except by the rate constant, SLO cladodes had better digestion kinetic values than SO varieties but CP and ME values were similar.

Key Words: *Opuntia*, fermentation parameters, gas production

T114 Simple sequence repeats markers on the characterization of *Lolium* and *Dactylis* accessions. C. J. Aguirre-Robert[1], B. Alarcón-Zúñiga*[1], M. R. Venegas-Ordóñez[1], O. Hernández-Mendo[2], S. S. González-Muñoz[2], and J. Burgueño-Ferreira[2], [1]*Colegio de Postgraduados*, *Montecillo, Edo. de México, México*, [2]*Universidad Autónoma Chapingo*, *Chapingo, Edo. de México, México*.

The objective of this study was to carry out an agronomic and molecular evaluation of 8 accessions of *Lolium* [Ansyl France, New Zealand, Uruguay, Netherland Barenza, USA Manhattan II (UMII), Canada Uri (CU4n), Australia Wimmera 62 and France Itaque]; and 3 of *Dactylis* [Canada Hercules, USA Potomac (UP) and USA Napier], in the Mexican Highlands. To evaluate morphological traits the experimental design was randomized complete blocks with a split-plot arrangement; data were analyzed using PROC MIXED and means compared with SLICE LSMEANS ($P \leq 0.05$). Ansyl France surpassed ($P \leq 0.05$) for plant height, dry weight, leaf dry weight, and stem weight per plant; CU4n for % of leaf and stem; UP for % and dry weight of dead material per plant; and UMII for number of stems. For the molecular evaluation, DNA was extracted (modified CTBA method), then PCR, amplification and electrophoresis. To determine population structure and genetic similarity among accesions, as well as the association between loci and morphological traits, data were subjected to cluster analysis (UPGMA), PROC PLS and Nei's unbiased genetic estimators (Pop Gen 32). Out of the 13 SSR-loci, 59 alleles were identified (4.5 alleles per locus). Besides, the UPGMA analysis showed 3 groups: per species (*D. glomerata*), per ploidy level (*L. hybridum* and *L. perenne*) and per genus (*Lolium*). This means that SSRs discriminated the genotypes per species, ploidy level and genus. The relationship between genetic distances of the 13 SSR-loci and the morphological characters, estimated by PMS biplots, indicated that SSR-loci expressed up to 14.3% of phenotypic variation of morphological traits among accessions. Therefore, it may be concluded that morphological traits and genetic distances from SSR-loci may be used for selecting genotypes with the best characteristics to establish a breeding program based on genetic and phenotypic characters, for *Lolium* and *Dactylis*.

Key Words: *Lolium*, *Dactylis*, molecular evaluation

T115 Correlations among shearing force and chemical compositions of wheat stems. Z. Yang, Z. Wang*, W. Yang, S. Jiang, and G. Zhang, *Shandong Agricultural University*, *Tai-an, Shandong, China*.

The objectives of this study were to investigate the relationship between shearing force and chemical compositions of wheat stems. Shearing force, a fracturing property of plant stem, is an important indictor of forage value. Three varieties (YanNong21; JiMai22; ShanNong15), which were plants from different plots, were collected, and each was divided into 4 treatments (150 replicate stems per treatment) by the diameter. After seed harvesting, each stem was cut into 3 16 cm segments for measuring stem diameter and shearing force of top, middle and bottom segments of stem. The top segment was measured from the stem apex, the bottom from the harvest base and the middle segment extended 8 cm above and below the midpoint of the stem. Each segment was sheared at the approximate midpoint ensuring that the location was between 2 nodes to prevent any influence of nodes on shearing force. Shearing forces of the 3 segments were averaged as the stem shearing force. Shearing force was measured with a C-LM3 meat shear made by the Mechanics Research Center of Dongbei Agricultural University and commonly used to measure tenderness of meat tissue. Range of shearing force was 0- 25.0 kg and deformation speed was 5 mm per second. Stems that had been measured for chemical compositions were analyzed by the SAS system, including dry matter (DM), neutral detergent fiber (NDF), acid detergent fiber (ADF), crude protein (CP), ether extract (EE), crude ash (CA), organic matter (OM), Lignin and cellulose. There was a positive relationship between DM and shearing force (r = 0.65), and the similar relationship for NDF (r = 0.85) and ADF (r = 0.90). Correlations were not found between shearing force and other chemical components such as CP (r = −0.19), EE (r = −0.36), CA (r = −0.29), OM (r = 0.54), Lignin (r = 0.26) and cellulose (r = 0.54). Shearing force was a direct indicator for estimating forage the chemical compositions, it can be used to predict forage value of wheat stems. Future research should evaluate correlation between shearing force and digestibility of DM, NDF or ADF.

Key Words: wheat stems, shearing force, chemical compositions

T116 Adaptation of *Brassica* spp. and fodder radishes as late season forages in the high desert region of Oregon. C. L. Engel*, B. A. Charlton, R. J. Roseberg, and R. A. Bentley, *Oregon State University, Klamath Basin Research and Extension Center*, *Klamath Falls*.

The objective of this study was to evaluate the yield potential and viability of winter triticale (TRT; n = 1), *Brassica* spp. (BRS; n = 6), and radish (RAD; n = 3) varieties, as late season forages. In 2009 3 planting dates (PD1, 2 and 3; July 30, Aug.14, & Aug. 28, respectively) were analyzed with 2 harvest dates (HD; approximately 60 and 90 d after planting) per PD (4 replications per variety). Plots were arranged in a randomized complete block design with a split plot. Varieties included: winter triticale (TRT; trical102); dwarf Siberian kale, Winfred (WIN, hybrid); purple top white globe turnip; Hunter (hybrid); New York turnip; pulsar rape (PR); graza radish; colonel radish (CR); and Terranova radish. Plots were seeded with a modified Great Plains drill at 4.5, 7.9, and 112.3 kg pure live seed/hectare (ha; for BRS, RAD, and TRT; respectively) into glyphosate treated small grain stubble. Plots were fertigated with 67.3 kg nitrogen and 22.4 kg sulfur/ha after plants reached the 2-leaf stage and were irrigated through Oct.15. Across all PD, TRT was the lowest yielding variety (3.70 ± 0.56, 2.51 ± 0.29, and 1.44 ± 0.49 t dry matter (DM)/ha; PD1, 2, and 3, respectively). The variety with the greatest yield differed by PD (WIN 7.49 ± 0.47, PR 5.31 ± 0.29, WIN 4.48 ± 0.43 t DM/ha; for PD 1, 2, and 3, respectively). For both PD 1 and 2, CR, BRS hybrids and PR yielded more than turnip and RAD variet-

ies ($P \leq 0.05$), but by PD 3 all BRS varieties yielded more than RAD varieties ($P \leq 0.05$), with turnip varieties tending to have higher yields among the BRS group. The 60 d HD yielded less ($P < 0.01$) than the 90 d HD for PD 1 and 3, only (5.31 vs. 6.30 ± 0.20 and 2.65 vs. 4.04 ± 0.19 t DM/ha; for 60 vs.90 d HD, PD 1 and 3; respectively). No PD × HD interaction occurred ($P \geq 0.16$). Both BRS and RAD produced good late season yields, and seem well-suited to extend the grazing season. For earlier PD, differences between varieties were as large as differences between species, but by PD3 the BRAS varieties produced greater yields than other species.

Key Words: *Brassica* spp., forage, fall

T117 Effects of age of regrowth and geographical location on forage protein and carbohydrate fractions, silicon content, and their impact on IVOMD of four tropical grasses. K. A. K. Lee*[1], J. R. Carpenter[1], B. W. Mathews[2], M. S. Thorne[1], and L. E. Sollenberger[3], [1]*CTAHR, University of Hawaii at Manoa*, *Honolulu,* [2]*CAFNRM, University of Hawaii at Hilo*, *Hilo,* [3]*Universtiy of Florida*, *Gainesville*.

In Hawaii, Kikuyugrass (KG) grown at higher elevations is lower in NDF and higher in IVOMD and CP than KG at the same age of regrowth in lower elevation sites with warmer climates. The impact of elevation on forage nutritive value may be confounded in part by differences in soil silicon (Si) between sites. The objectives of this study were to determine the effects of age of regrowth and geographical location on the nutrient composition, IVOMD, and silicon content of 4 tropical pasture grasses *Pennisetum clandestinum, Digitaria decumbens, Pennisetum purpureum*, and *Pennisetum americanum* × *Pennisetum purpureum*. Grasses were cultivated (3 plots each) at 2 different geographical locations and harvested repeatedly at 4, 8, and 12 weeks of regrowth. Grass samples were weighed and dried at 50°C in a forced draft oven then ground by a Wiley mill (1-mm mesh stainless steel screen). Nutrient analysis of forages was determined by Near Infrared Reflectance Spectroscopy (NIRs) and sub-samples analyzed for silicon (ICPES following sample preparation by the NaOH fusion and melt dissolution procedure), and 48 h IVOMD digestibility (2-stage technique of Moore and Mott). The ranges in percent CP, protein solubility, NDF, ADF, lignin, IVOMD, and silicon (ug/g) and digestion rate (%/hr) across the 4 grasses (for both locations and the 3 ages of regrowth) were 5.3–22.4, 17–54, 52.1–74.5, 31.8–49.2, 1.3–7.8, 39.6–75.4, 407–6703, and 2.65–10.81, respectively. There were differences ($P < 0.05$) between grass varieties, geographical locations, and ages of regrowth for the various nutrient components, IVOMD, and silicon content. IVOMD was positively correlated with CP (+0.730), and negatively correlated with NDF (−0.552) and ADF (−0.747), and NDF was negatively correlated with CP (−0.789). Silicon differed ($P < 0.01$) with geographical location and grasses varied ($P < 0.01$) in silicon level within location. These research results indicate that one must be cautious in using tropical grass data from other regions and growing conditions.

Key Words: tropical grasses, nutrient composition, silicon content

T118 Effect of time from rumen fluid collection to sample inoculation on estimates of in vitro NDF digestibility. J. C. Lopes*[1], R. B. Reis[2], and D. K. Combs[1], [1]*University of Wisconsin*, *Madison*, [2]*Universidade Federal de Minas Gerais*, *Belo Horizonte, Brazil*.

Run to run variability of in vitro NDF digestibility (IVNDFD) measures are reduced when forages are inoculated with a primed rumen inoculum that was held in a sealed flask until it reaches a pre-determined gas pressure. The time for the inoculum to reach this predetermined pressure is variable, ranging from 85 to 325 min. The objective of this study was to determine if the time variation to reach the predetermined gas pressure affects estimates of IVNDFD. An alfalfa silage was dried (60°C), ground (1 mm), and weighed (0.5 g DM) into Ankom F57 fiber bags. Rumen fluid was collected from 2 rumen-cannulated cows and strained through cheesecloth. Rumen fluid (250 mL), mixed with Van Soest buffer (250 mL), reducing solution (40 mL), and carbohydrate/nitrogen nutrient primer (1.25 mg/mL of rumen fluid) was fermented in sealed 1000 mL Erlenmeyer flasks until pressure corresponding to 0.3 mL of gas production/mL of inoculum was attained. Time from inoculum collection to the pre-determined gas pressure was recorded. The alfalfa samples were then inoculated with the standardized inoculum and digested, in duplicate, for 24, 30 or 48 h. Residual neutral detergent fiber was analyzed with a forage fiber analyzer, and NDFD determined. The procedure was repeated 16 times. Data were analyzed as randomized complete block with replication and unequal error variance using SAS Proc Mixed. Alfalfa silage sample was the experimental unit, fermentation time and residual error were random effects, and time point and repetition were fixed effects. IVNDFD estimates differed due to time of incubation (25, 34 and 43% of NDF, for 24, 30 or 48 h, respectively: $P < 0.01$) but did not differ ($P > 0.05$) due to time for inoculum to reach predetermined gas pressure. Residual variance of IVNDFD estimates at each time point did not differ ($P > 0.26$). These results suggest that the time required for the inoculum reach the pre-determined pressure varied widely from run to run but this had no effect on estimates of IVNDFD at 24, 30 or 48 h.

Key Words: NDF digestibility, forage fiber, in vitro

T119 Time course evaluation of NDF digestibility of hay crop silage and lignin as a predictor of indigestible fiber. R. Ward[1] and R. A. Patton*[2], [1]*Cumberland Valley Analytical Services*, *Maugansville, MD*, [2]*Nittany Dairy Nutrition*, *Mifflinburg, PA*.

An investigation was undertaken to determine appropriate incubation times for determination of IVNDFD of hay crop silages and to define lignin based equations that might predict NDF digestibility (NDFd) with high accuracy. Twenty-one hay crop silages were selected from Cumberland Valley Analytical Services samples to represent a range of lignin as a percentage of NDF (LigNDF). This data set included these silages: 3 temperate grass, 5 legume, 6 mixed mainly grass (MMG), 3 mixed mainly legume (MML), and 4 small grain silages. Three LigNDF groups (high, medium and low) were formed with a mean of 17.7%, 13.2% and 7.2% lignin as % NDF. In vitro digestibility was determined at 4, 12, 18, 24, 30, 48, 96, and 120 h in flasks by the method of Tilley and Terry. Differences among lignin groups and forage types were assessed using Proc mixed of SAS. Regression equations for IVNDFD were developed with Proc reg of SAS using stepwise elimination. Although differences among lignin groups were significant ($P < 0.01$), groups were not homogenous with respect to forage types. Forage type was also highly significant ($P < 0.01$). Hourly digestion rates for various forages were: small grain 1.06%, grass 0.97%, MMG 0.68%, MML 0.57% and legume 0.47% ($P < 0.01$). Across all forage types, NDFd was linear between 24 and 96 h. Incubation for 120 h was sufficient to remove digestible NDF. Indigestible NDF (INDF) as % of NDF was 10.3% for small grain, 17.6% for grass, 16.2% for MMG, 20.2% MML, and 23.6% for legume ($P < 0.05$). Overall, LigNDF was less well correlated (= 4.555 + (1.027 * LigNDF), $R^2 = 0.66$) with INDF than was lignin as % DM (= 1.409 +(2.838 * lignin %DM), $R^2 = 0.81$). However, the best equation for predicting 24 h IVNDFD included LigNDF (= 61.065 - (2.873*LigNDF) + (0.858 * CP%) + (0.48331 * NFC), $R^2 = 0.92$. These data suggest that equations for NDFd might be more accurate if based on forage type, that there is little evidence for earlier NDF

digestibility time points providing increased sensitivity for evaluation of NDF digestibility, and that NIR may offer rapid, accurate assessment of NDFd in hay crop silages.

Key Words: hay crop silage, in vitro NDFd

T120 Effect of a nutrient solution on the chemical composition and in vitro fermentation parameters of wheat hydroponic forage. H. Bernal-Barragán[2,5], R. Luevano-Escobedo[1], A. Elias-Iglesias[4,5], E. Gutiérrez-Ornelas[2,5], A. Estrada-Angulo[3,5], M. Guerrero-Cervantes[1,5], M. A. Cerrillo-Soto[1,5], and A. S. Juárez-Reyes*[1,5], [1]*Universidad Juárez del Estado de Durango*, *Durango, Durango, México*, [2]*Universidad Autónoma de Nuevo León*, *Monterrey, Nuevo León, México*, [3]*Universidad Autónoma de Sinaloa*, *Culicán, Sinaloa, México*, [4]*Instituto de Ciencia Animal*, *La Habana, Cuba*, [5]*Red Internacional de Nutrición y Alimentación en Rumiantes*, *Durango, Durango, México*.

A study was conducted to evaluate the chemical composition and the in vitro fermentation parameters of wheat (*Triticum aestivum* L.) hydroponic forage (WHF). Treatments consisted in utilizing either water or an organic nutrient solution containing 1.5% N, 1.0% P and 1.0% K during the process of pre-germination. Seed were soaked for 24 h in one of each solution, drained and allowed to rest for another 24 h. Germinated seeds (800 g) were then distributed in 40 × 40 cm plastic trays in triplicate and placed in a 5 × 4 m green house. The hydroponic forage was harvested at 8, 10, 12 and 14 d after germination. Samples of each day were composite, dried and milled and further analyzed for CP, NDF and ADF. The in vitro fermentation profile was estimated by incubating 200 mg DM of the hydroponic samples in 100 mL calibrated glass syringes. Gas production was registered at 0,3,6, 9,12,24,48, 72 and 96h and the data fitted to the model $P = a+b\ (1\text{-}e^{-ct})$, where *a* is the gas produced from the soluble fraction of feed, *b* is the gas produced from the slowly degradable fraction and ***c*** the constant rate of gas production. The ME content was estimated from in vitro gas production at 24 h. In vitro true dry matter digestibility (IVTDMD) was determined following the Daisy^{II} procedure. Data were analyzed according to a completely randomized design with factorial arrangement of treatments 2 × 4. The nutritive solution did not affect (*P > 0.05*) the studied variables, except for the ADF and IVTDMD where an interaction between factors were registered (*P < 0.05*). Digestibility of wheat treated with nutritive solution remained above 70% until d 12, but those treated with water were below 70% from d 10 on. Differences in CP (%), NDF (%), gas parameters *a* (ml/200 mg DM), *b* (ml/200 mg DM), ME (Mcal kg^{-1} DM) and biomass yield (kg) were registered among harvesting days. An increment (*P = 0.06*) was also registered in the constant rate *c* (% h^{-1}). This study indicated that the utilization of a nutrient solution on wheat seeds did not affect the nutritive value of wheat hydroponic forage.

Table 1. Nutritive value, in vitro fermentation profile and biomass yield of wheat hydroponic forage

	Harvesting days						
	8	10	12	14	SEM	Mean	Sig
CP	14	15	16	18	0,7	16	**
NDF	48	52	55	58	1,0	53	**
a	9	6	4	1	1.0	5	**
b	56	54	51	50	1.0	53	**
c	0.065	0.063	0.053	0.057	0.003	0.060	NS
ME	2.4	2.3	2.1	2.0	0.07	2.2	**
Biomass yield	3.3	3.2	3.8	3.9	0.09	3.5	**

Sig = significance; **(P < 0.01); Mean = overall mean of both treatments.

Key Words: wheat hydroponic forage, in vitro gas production, metabolizable energy

T121 Assessing digestibility of shredded *Juniperus monosperma* treated with 5% alkylation or 3% ammoniation. C. A. Roof*, S. H. Cox, and S. L. Lodge-Ivey, *New Mexico State University*, *Las Cruces*.

Encroaching shrubs such as *Juniperus monosperma* (JM) typically are managed via mechanical removal or treatment with herbicides. *Juniperus monosperma* leaves have a moderate nutritive value (6.0% CP, 71.7% NDF, DM basis) and shredding whole juniper shrubs may represent a potential drought feed. Traditional supplemental feeds such as hay or grain may be unavailable or cost-prohibitive during episodes of drought, and producers may prefer a less expensive alternative. Limited data exists regarding the use of shredded juniper as a drought feed resource. Therefore, the objective of the current study was to evaluate in vitro organic matter digestibility (IVOMD) of shredded JM. Using a completely randomized experimental design, approximately 100 g of JM plus enough water to equalize dry matter at 40% was added to glass jars with sealable lids. Treatments were 1) JM only (C), 2) JM plus ammonia sulfate and excess calcium oxide for reaction giving 3% ammoniation (DM basis; N) and 3) JM plus calcium hydroxide to provide 5% alkylation (DM basis; A). After treatments were added to JM, jars were covered with aluminum foil, sealed and incubated in an anaerobic glove box (approximately 90% CO2 and 10% H2 atmosphere) for 30 d. After incubation, treated JM was freeze-dried and ground to pass a 2mm screen. The resulting material was used to determine 96 h IVOMD. Ruminal fluid used was donated from a ruminally canulated cow (approximately 600 kg) maintained on sudan hay (11.3% CP, 66% NDF, DM basis). Data were analyzed using Proc GLM. In vitro organic matter digestibility for each treatment was (10.1, 12.1, 11.9 ± 0.41, A, C, N, respectively) and was influenced by treatment (*P* < 0.001). Alkylation decreased digestibility by 16.5% when compared with control while control and ammoniation did not differ(*P* = 0.82). Shredded JM includes not only leaf material but woody components resulting in low IVOMD. Although treatments of 5% alkylation or 3% ammoniation did not benefit overall JM digestibility, selection of the more desirable fractions, such as leaves and bark, by the animal could improve digestibility values.

Key Words: *Juniperus monosperma*, alkylation, ammoniation

T122 Yield and quality of grasses in three different dairy regions of El Salvador. E. E. Corea Guillén*[1], J. M. Flores Tensos[1], L. B. Leyton Barrientos[1], J. F. Alvarado Parameño[1], G. O. Castillo Benedetto[1], J. M. Castro Montoya[1], and J. A. Elizondo-Salazar[2], [1]*Departamento de Zootecnia, Facultad de Ciencias Agronómicas*, *Universidad de El Salvador, El Salvador*, [2]*Estación Experimental Alfredo Volio Mata, Facultad de Ciencias Agroalimentarias*, *Universidad de Costa Rica, Costa Rica*.

Grasses are a very important feed resource for dairy cattle in El Salvador as well as in all Central America. However, they are extremely variable in terms of yield and quality which depend on age at which they are grazed and geographical area in which they are grown. Thus many producers do not know what grasses to grow in a specific area of the country and at what age they should be grazed. For these reasons, a study was conducted to establish the grass that produces the highest yield and quality in the dairy regions of La Paz, Sonsonate and Chalatenango. Star grass (*Cynodon plectostachius*), Swazi grass (*Digitaria zwazilandensis*), and Pangola grass (*Digitaria decumbens*) were tested.

Grasses were sampled at 21, 28, and 35 d of regrowth to estimate yield per grazing period and for determination of DM yield, DM, CP, NDF, and ADF concentration. The experiment was arranged in a split-split-plot design with dairy regions as main plots, grass type as split-plots, and age of regrowth as split-split-plots. Variables were analyzed using the GLM procedure of SAS 9.1. Separation of means was done using the Duncan's multiple comparison procedure. There were differences ($P < 0.01$) between regions, grass type and age of grazing for all variables studied. The findings of the study suggest that even though there was great variability between regions, grasses, and days of regrowth; Star grass produced the highest yield and presented a higher nutritional value when compared with the other grasses.

Table 1. Yield and quality of grasses in three regions of El Salvador

	Available DM, kg/ha	DM, %	CP, %	NDF, %	ADF, %
Region					
La Paz	1469.8^{b}	20.5^{a}	8.7^{a}	69.5^{a}	38.7^{a}
Sonsonate	1717.8^{ab}	17.4^{b}	12.7^{a}	67.2^{b}	38.5^{ab}
Chalatenango	1928.3^{a}	20.5^{a}	10.0^{b}	67.9^{b}	39.6^{b}
Grass					
Star grass	2239.8^{a}	21.3^{a}	12.0^{a}	71.3^{a}	37.6^{b}
Swazi	1562.1^{b}	19.8^{a}	9.2^{b}	66.4^{b}	38.1^{b}
Pangola	1314.0^{b}	17.4^{b}	10.1^{b}	66.9^{b}	39.6^{a}
Regrowth					
21 d	1037.3^{c}	17.4^{b}	11.5^{a}	66.6^{b}	36.6^{b}
28 d	1668.7^{b}	18.6^{b}	10.5^{a}	68.5^{a}	38.8^{a}
35 d	2409.9^{a}	22.4^{a}	9.4^{b}	69.5^{a}	39.4^{a}

a-cP < 0.01, comparing least squares means.

Key Words: grasses, grazing, forage

T123 Effect of fertilization with swine wastewater on fermentative characteristics and losses of corn silage. M. T. Cangani, R. A. Oliveira, A. C. Ruggieri*, E. Urbinati, and F. C. Basso, *Unesp/FCAV*, *Jaboticabal, São Paulo, Brasil*.

The objective of this trial was to study in no-tillage system, the effect of sowing and covering fertilization with swine wastewater on fermentative characteristics and losses of corn silage. The experimental design was randomized blocks with 5 treatments and 4 replications. The treatments were: T1 - control without sowing and covering fertilization, T2 - chemical fertilization (urea, simple superphosphate and potassium chloride), T3 - raw swine wastewater, T4 - swine wastewater treated in anaerobic system (2 upflow anaerobic sludge blanket (UASB) reactors in series) and T5 - swine wastewater from aerobic post-treatment (sequencing batch reactor (SBR)). The chopped material was ensiled in plastic buckets (7 L) with sand and screen to determine the effluent losses (EL). The buckets were weighed, sealed and stored at room temperature. After 60 d of fermentation the silos were weighed to quantify the gas losses (GL), opened, spoiled silage discarded and the remainder was homogenized and sampled to determine dry matter (DM), pH and ammonia nitrogen (NH_3/TN). Statistical included ANOVA and Tukey's test ($P < 0.05$). The control silage showed lower gas losses, but did not differ significantly from other treatments ($P < 0.05$). The corn silages produced with swine wastewater treated in UASB reactors (T4) showed lower effluent losses ($P < 0.05$). The DM content not differ significantly among treatments T2, T3, T4 and T5 ($P < 0.05$). The treatment T5 showed the lowest NH_3/TN content ($P < 0.05$). The pH value did not differ significantly among treatments ($P < 0.05$). The corn silages produced with swine wastewater treated in the UASB reactors and pos-treated in aerobic SBR showed lower EL and NH3/TN, and the DM was similar that used chemical fertilization.

Table 1. Fermentative characteristics and losses of corn silage

Treatments	GL	EL	DM %	NH_3/TN	pH
T1	8.72	9.02 a	33.35 a	3.65 a	4.03
T2	12.22	6.20 ab	31.00 ab	3.18 ab	4.08
T3	13.81	6.36 ab	29.74 b	3.20 ab	4.03
T4	9.86	3.28 b	28.67 b	2.80 b	4.11
T5	9.44	5.96 ab	29.99 b	1.95 c	4.03
CV %	40.58	27.44	4.94	12.17	2.05

Means followed by equal letters do not differ by Tukey test (P > 0.05).

Key Words: effluent losses, gas losses, no-tillage system

T124 Tannery sludge as a nutrient source for the tropical grass *Brachiaria brizantha*. C. H. B. Miranda*[1,2], [1]*Embrapa Labex USA*, *Lincoln, NE*, [2]*Embrapa Beef Cattle*, *Campo Grande, MS, Brazil*.

A field study was conducted to determine the potential value of tannery sludge as nutrient source for *Brachiaria brizantha* cv. Marandu. Five different rates (0, 1.65, 3.3, 6.6 and 13.2 Mg/ha) of air-dried (final moisture of 40%) and ground (2 mm sieve) sludge were applied to a pasture established in a Red Latosol soil in Campo Grande, Brazil. Sludge was from a tannery plant that recycles water and Cr during the first processing stages. Its nutrient content was (%) 13.3 Ca, 2.9 N, 0.52 P, 0.1 K, 4.6 Na, and 0.38 Cr. A control treatment with chemical fertilizer (2 Mg/ha of Ca, and 100 kg/ha of N, P and K, respectively) was also included. Treatments were distributed in a completely randomized block design, with 5 replications (a field plot 5m x4 m wide), and applied after cutting and removing the cut biomass. Re-growth material was cut 10 cm above ground 45, 90, 270 and 360 d later and analyzed for total dry mass production, plant quality (IVDMD, ADF, ADL, NDF, crude protein and lignin), and P, K, Ca, Mg, S, and Cr contents. Soil samples (0 to 20 cm depth) were collected before sludge application, and also a year later, and they were analyzed for Ca, P, K, pH and conductivity. Overall, forage yield was significantly higher ($P < 0.05$) in the rates of 6.6 and 13.2 Mg/ha of sludge (2.4 and 3.1 Mg/ha, respectively) than in the control without sludge amendment (1.6 Mg/ha), but significantly ower ($P > 0.05$) than that produced in the chemical fertilizer treatment (3.6 Mg/ha). There was increase in soil Ca contents in these sludge treatments (0.75 and 1.05 cmol/dm^3, respectively) compared with the control soil (0.4 cmol/dm^3), but not of P (average 0.49 mg/dm^3) or K content (average 0.08 cmol/dm^3). No significant differences ($P > 0.05$) in plant Cr content nor of soil conductivity were observed. Thus, it can be concluded that tannery sludge can be a good source of Ca, but it is a poor source of P and K. Further monitoring of Cr chemistry in the plant and in the soil is needed to assure the use of these sludge materials.

Key Words: agrindustrial residues, plant nutrition, forage

T125 Absorption and utilization of nitrogen by *Panicum maximum* cv. Massai. C. H. B. Miranda*[1,2], [1]*Embrapa Labex USA*, *Lincoln, NE*, [2]*Embrapa Beef Cattle*, *Campo Grande, MS, Brazil*.

An experiment was conducted to determine the response of *Panicum maximum* cv. Massai, a tropical forage grass, to increasing levels of N fertilizer and harvest date. This is a new variety, suitable for cattle, horses and sheep, that shows some quality constraints, which may be alleviated with proper N management. Treatments consisted of 4 N rates (0, 50, 100

and 200 kg N/ha), supplied as ammonium nitrate, and 5 harvest dates (21, 28, 35, 42, and 49 d after planting - DAP). A set of 20 replications was prepared for each treatment, distributed in a complete factorial experimental design, with 4 replications per treatment. Each replication was a pot with 4 kg of a Quartz-sandy soil, typical of the Brazilian Cerrados (savannah-like area), base of the beef cattle industry in the country. Nitrogen rates were applied a week before the transplanting of 4 seedlings per pot. The experiment was conducted in a greenhouse. Soil moisture was kept constant at 80% of soil field capacity throughout the experimental period. At every harvest date 4 replications per treatment were collected, and roots and above ground dry mass was separated, dried at 72°C for 72 h, weighed, and grounded, being analyzed for N content using Near Infrared Spectroscopy. ANOVA of the experimental results showed that there were significant effects ($P < 0.01$) of N rates, harvest date, and their interaction, for above-ground and roots dry mass and N accumulation. Plant yield within the harvests dates followed a polynomial quadratic pattern, with N uptake increasing up to 42 DAP, and dry matter accumulation increasing up to 49 DAP. On average, the efficiency of N utilization was around 4 mg of dry mass per mg of N taken per day. Further evaluations on plant quality are necessary to conclude which would be the best combination of N rate and harvest date for this forage grass.

Key Words: plant nutrition, tropical grasses, forage

T126 Comparisons among predictive equations and NIR for determination of in vitro indigestible NDF of corn silages. R. Ward*[1], S. Weaver[1], and R. A. Patton[2], [1]*Cumberland Valley Analytical Services*, *Maugansville, MD*, [2]*Nittany Dairy Nutrition*, *Mifflinburg, PA*.

An investigation was undertaken to assess the accuracy of NIR or equations based on analyzed nutrient content to predict in vitro indigestible NDF (INDF). A data set of 115 corn silages with indigestible NDF determined by 120 h Tilley and Terry incubations was developed. For application of equations based on forage type, silages were classified as BMR (n = 18, mean lignin = 2.06% DM), MED (n = 62, mean lignin = 2.81), and HI (n = 25, mean lignin = 3.51). Using this data, chemically determined INDF was compared against equations developed from a smaller data set by Proc Reg of SAS using the stepwise selection. Predictive equations were based on all corn silage types (general equation), individual corn silage type as well as calculation of INDF as lignin*2.4. The Mean Square Predicted Error statistic of Bibby and Toutenburg was used to compare predictions with observed values. The general equation was INDF = 2.065 + (1.378 * soluble protein %DM)- (0.352*NDF %DM) + (6.128 * lignin %DM), $R^2 = 0.98$. For BMR, the equation was INDF = (28.985 - (6.272 * fat %DM), $R^2 = 0.99$; MED was INDF = (1.838*ADF) - 36.688, $R^2 = 0.99$; and HI was INDF = 12.285 - (1.550 * Ash %DM),$R^2 = 0.99$. Forcing equations based on lignin and/or lignified NDF content resulted in no significant equations for BMR or HI corn silage. However, a general equation was better than feed type specific equations. Residual analysis indicated that as lignin content increases, feed type specific and lignin*2.4 equations become less accurate, while the general equation continues to perform satisfactorily. We conclude that NIR is a better predictor of INDF than equations and that for corn silages, a general equation is better than feed specific equations.

Table 1.

Model	Mean	Std Dev	RMSPE	% Mean	Bias	Error Due To Regression	Random
Observed	12.55	2.12	—	—	—	—	—
NIR	12.50	1.93	0.83	6.6	0.4	0.1	99.5
Feed Specific	7.80	4.06	6.71	53.4	50.1	40.1	9.8
General	10.90	3.30	3.25	25.9	25.8	44.0	30.2
Lignin*2.4	6.97	1.32	5.75	45.8	94.3	0.3	5.4

Key Words: corn silage, NIR, INDF

T127 Nitrogen lixiviation and uptake by forage maize with different fertilization and previous soil use. R. D. Améndola-Massiotti*[1], I. Cach-Gómez[1], M. E. Álvarez-Sánchez[1], J. A. Burgueño-Ferreira[2], and I. López-Cruz[1], [1]*Universidad Autónoma Chapingo*, *Chapingo, México*, [2]*Colegio de Postgraduados*, *Montecillo, México*.

In crop rotations of forage maize (*Zea mays*) and pastures, nitrogen (N) content of the soil declines during the maize crop. The present study was carried out at Chapingo (central temperate Mexico). The aim was to estimate the effect of 3 N rates (NF) in combination with 3 previous soil uses (SU, representing possible phases in the rotation) on the amount of N harvested with a forage maize crop and lost by lixiviation during that crop. Nine treatments were evaluated, combining NF: 0 (N0), 100 (N100) and 200 (N200) kg N/ha and SU: 3.5 years of permanent *Medicago sativa* and *Dactylis glomerata* pasture (P); 3.0 years of permanent pasture and 6.0 mo of annual *Avena sativa* and *Lolium multiflorum* pasture (PA); and 2.5 years of permanent pasture, 6.0 mo of forage maize crop and 6.0 mo of annual pasture (PMA). A randomized complete block split-plot design with 3 replicates was used; SU was assigned to whole units and NF to sub-units of 54 m^2. Response variables were N-uptake by the crop, N lixiviation (not measured at N0 treatments) and total N content of the soil at 2 depths, 0–30 and 30–60 cm. Analysis was performed using a mixed model and means were compared using orthogonal contrasts. The NF had a linear effect ($P < 0.05$) on N-uptake (274 ± 15 kg N/ha at N0, 44.9% lower than at N200) and lixiviation (98 ± 19 kg N/ha at N100, 73% lower than at N200); SU did not affect ($P > 0.05$) those variables. The N content in the top soil layer decreased ($P < 0.05$) with increasing time of annual crops (5461, 5095 and 4685 kg N/ha for P, PA and PMA), and it was higher ($P < 0.05$) in the 0–30 layer (5080 kg N/ha) than in the 30–60 layer (3437 kg N/ha). Average N content of soil decreased ($P < 0.05$) in 775 kg N/ha during the maize crop, due to N harvest, lixiviation and not measured gaseous losses. It is concluded that efficient N management is needed to reduce N losses during the forage maize phase of the rotation.

Key Words: pastures, alfalfa, soil nitrogen

T128 Biological nitrogen fixation in the tropical forage legume Stylo. C. H. B. Miranda*[1,2], J. R. Verzignassi[2], and C. D. Fernandes[2], [1]*Embrapa Labex USA*, *Lincoln, NE*, [2]*Embrapa Beef Cattle*, *Campo Grande, MS, Brazil*.

The forage legume *Stylosanthes* spp. is an excellent forage legume alternative for tropical areas because of its adaptation to acidic, low fertility soils, and, especially, because of its biological nitrogen fixation (BNF) potential. We compared dry mass production, total N content, and BNF of 4 field grown advanced genotypes of both *S. capitata* and *S. guianensis* taken from a breeding program being conducted at

Embrapa Beef Cattle, in Brazil, with the objective of selecting materials that represent increased BNF potential through symbiosis with native soil N-fixing bacteria. BNF was evaluated by comparison of their ^{15}N isotope natural abundance content and that of 5 non-fixing plants species naturally growing among them (^{15}N isotope dilution technique). Genotypes were planted in a randomized block experimental design, with 4 replications, in a Dark Red Latosol, without inoculation with N-fixing bacteria. Three hundred kg/ha of 0–20–20 NPK were applied at planting and re-applied a year latter, after a full harvest. Evaluation of second year biomass production, harvested at seed grain filling stage, indicated that genotypes of *S. capitata* produced ($P < 0.05$) more dry biomass (ranging from 14 to 16 Mg/ha, average 14.9 Mg/ha) than those of *S. guianensis* (9.8 to 13.1 Mg/ha, average 11.5 Mg/ha). They also showed larger ($P < 0.05$) N content (average 256 kg/ha, compared with 238 kg/ha), from which an average 65% (or 167 kg of N/ha) was originated from BNF, compared with 33% in *S. guianensis* (or 85 kg/ha). Such BNF may result in a significant contribution to quality improvement and maintenance of mixed tropical pastures, either by direct contribution as feed or as organic material that would add N to the soil. We conclude that *S. capitata* genotypes have high BNF potential and should be prioritized in a new variety selection program.

Key Words: pasture sustainability, plant biomass, plant nutrition

T129 Yield and quality of two tropical leguminous trees in the establishment year. E. Cortes-Diaz*, F. Amador-Solano, G. T. Gonzalez-Bonilla, J. L. Zaragoza-Ramirez, and P. Martinez-Hernandez, *Animal Science Department, University of Chapingo*, *Texcoco, Mexico*.

Leguminous trees planted into tropical grass-pastures can increase forage yield and quality offered to grazing sheep. The aim of the study was to determine forage yield and quality of *Leucaena leucocephala* cv. Cunningham (improved and introduced tree species) and *L. collinsii* (native tree species) in the establishment year and forage yield of the associated grass (*Brachiaria brizantha* cv. Libertad).Treatments were arranged in a 2 × 3 factorial: 2 leguminous trees, and 3 densities: 5000 (high), 3333 (medium) and 2500 (low) plants/ha; in a completely random design with 3 replications, experimental unit was a 256 m2 plot. Tree seeds were grown in a nursery for 4 mo, then transplanted in early summer (rainy season) into a year-before established grass pasture, planting was in rows 2 m apart and with 1, 1.5 and 2 m between plants within a row to achieve high, medium and low densities, respectively. At the time of planting grass was cut to a 5 cm stubble. Three harvests to determine yield and quality were done before the onset of dormancy season, these were at 47, 83 and 206 d after transplant and after each harvest ewe-lambs grazed all plots to leave a 5 cm grass stubble. Season yields and mean crude protein concentrations were analyzed. Statistical analysis was with a model for a factorial arrangement and 3 replications. Grass yield was 4909 kg DM/ha and similar ($P > 0.05$) across factors. *L. collinsii* gave 36 and 4.9 kg DM and CP/ha, respectively which were 2.6 and 1.8 times higher ($P < 0.05$) than in *L. leucocephala*, this last species showed 20.9% CP, 6 percent units higher ($P < 0.05$) than *L. collinsii*. It was concluded that in the establishment year tree density has no effect on any component while tree forage yield and quality can be different between species.

Key Words: *Leucaena leucocephala*, *Leucaena collinsii*, fodder trees

T130 Sequence similarities of genes from the lignin biosynthesis pathway in tropical grasses, maize and rice. D. M. Gerônimo, N. S. Oliveira, A. B. S. Machado, and L. F. P. Silva*, *Universidade de São Paulo*, *Pirassununga, SP, Brazil*.

Rapid decline in cell wall digestibility, due to lignifications, hinders efficient use of warm-season grasses. The objective was to partially sequence transcripts of the main enzymes involved in monolignol synthesis to determine similarity among tropical grasses, and other with more advanced genomic resources (maize and rice). Total RNA was isolated from bermudagrasss (*Cynodon dactylon* L. Pers. cv. Coastcross-1), and palisade grass (*Brachiaria brizantha* A. Rich. cv. Marandu) and treated with DNase 1. Degenerated oligonucleotide primers for glyceraldehyde-3-phosphate dehydrogenase (GAPDH), 4-coumarate-CoA ligase (4CL), cinnamate-4-hydroxylase (C4H), cinnamoyl-CoA-reductase (CCR), caffeic acid O-methyltransferase (COMT), and phenylalanine ammonia lyase (PAL) were designed based on conserved regions of maize, rice and guineagrass. Treated RNA was reverse transcribed and amplified with PCR, and PCR products were purified and sequenced in both directions. Quality and alignment of sequences were obtained using Phred and Cap3 softwares. Obtained sequences were compared using the BLAST program. There was a high degree of similarity between all grasses. Palisade grass and bermudagrass had overall nucleotide sequence similarity with maize of 94.2 and 93.8, respectively; and aminoacid sequence similarity of 96 and 88%, respectively. Comparing with rice sequence, palisade grass and bermudagrass had overall sequence similarity of 87.4 and 87.2, respectively; and aminoacid sequence similarity of 88 and 90.7%, respectively. Both tropical grasses had higher nucleotide and aminoacid sequence similarity with maize than with rice, indicating that maize genomic resources could be used for gene expression studies in these tropical grasses.

Table 1. Similarity among nucleotide and aminoacid sequence of tropical grasses, maize and rice

		Nucleotide, %		Aminoacid, %	
Grasses	Genes	Maize	Rice	Maize	Rice
Palisade grass	GAPDH	91	88	92	90
	4CL	—	—	—	—
	C4H	96	91	98	88
	CCR	95	77	96	81
	COMT	96	90	100	89
	PAL	93	91	94	92
Bermuda grass	GAPDH	91	87	96	92
	4CL	93	89	95	91
	C4H	94	89	93	86
	CCR	94	76	96	80
	COMT	96	90	98	95
	PAL	95	92	98	100

Key Words: *Brachiaria brizantha*, *Cynodon dactylon*, DNA sequencing

T131 Ovine and caprine in vitro digestibility of *Peganum harmala*. L. N. Tracey*, L. B. Abbott, J. Browne-Silva, and S. L. Lodge-Ivey, *New Mexico State University*, *Las Cruces*.

The possibility of using small ruminants to reduce African rue (*Peganum harmala*; AR) on New Mexico rangelands is being evaluated. African rue is known to be toxic to guinea pigs, cattle and sheep; however, toxicity has not been documented in goats. The objective of this study was to examine the IVDMD and rumen fermentation of AR by sheep and goats in vitro. A completely randomized experimental design with a 2 × 4 factorial arrangement of treatments was used. Factors included ruminal fluid donated from sheep vs goats and 4 levels of AR:Sudan hay (0:100, 25:75, 50:50, 100:0; n = 8; DM basis) as substrate for a 48-h

Tilley-Terry in vitro digestion trial. Significant treatment (trt) by species interactions were observed for IVDMD and 48-h VFA concentrations ($P < 0.05$). Increasing levels of AR increased IVDMD for both sheep and goats ($P = 0.005$). However, when 50:50 was added goat IVDMD was 5.56% greater than sheep ($P = 0.03$). Sheep IVDMD was 5.72% greater than goat when 100:0 was digested ($P = 0.01$). Total VFA production varied by trt and species ($P < 0.001$) with sheep 0:100 and goat 25:75 resulting in the greatest total VFA production (198.5 and 192.3 mM, respectively). Digest of 100:0 resulted in the least total VFA with goat being the lowest at 131.1 mM. Acetate levels were highest in goat digests of 100:0 which was 23.0% greater than the lowest concentration (sheep 50:50). Propionate concentrations differed in both species except in the 50:50 concentration ($P = 0.76$). The acetate:propionate ratio differed in both species at each AR concentration ($P < 0.05$) with the greatest variation existing at 100:0 digest where A:P ratio was 48.4% higher in the goat digest than in sheep. Overall increase in digestibility with increasing AR concentration and VFA results suggest that rumen microbial activity is undiminished at 50:50 or less AR in small ruminants. Additional in vivo research is needed to determine the potential to control AR using targeted grazing with small ruminants.

Key Words: *Peganum harmala*, ovine, caprine

T132 Chemical composition and in vitro ruminal fermentation activity of three Mexican browse species during dry season. D. López, R. Rojo*, A. Z. M. Salem, J. L. Tinoco, J. F. Vázquez, B. Albarrán, F. González, and D. Cardoso, *Centro Universitario UAEM-Temascaltepec*, *Temascaltepec, Estado de México, México*.

Browse foliages from *Pithecellobium dulce*, *Heliocarpus velutinus* and *Guazuma ulmifolia* natives to the subtropical region of southern Mexico, were harvested during the dry season to determine chemical composition and some parameters of ruminal fermentation using ruminal inoculum of goats. Crude protein, NDFom, ADFom, in vitro gas production after 24 (GP_{24}), 48 (GP_{48}) and 96h (GP_{96}) of fermentation, IVDMD and IVOMD were determined while ME was estimated. Data were analyzed using the general lineal model (GLM) procedure in SAS for a completely randomized design and differences among means by Tukey test. Crude protein (*P. dulce*: 222.10, *H. velutinus*: 154.30 and *G. ulmifolia*: 147.76 g/kg) values were different among browse species ($P < 0.01$). *P. dulce* had the lowest NDFom: 435.22; and ADFom: 305.79), *H. velutinus* showed intermediate values (NDFom: 455.80 and ADFom: 323.57) and *G. ulmifolia* had the highest values (NDFom: 478.06 and ADFom: 368.46) g/kg. In vitro gas production, IVDMD, IVOMD and ME values varied among browse species ($P < 0.001$) (Table 1). *P. dulce* has the highest potential as a feed protein source in small ruminants during the dry period.

Table 1. In vitro ruminal fermentation parameters (g/kg DM) of some browse tree leaves

Parameters	*P. dulce*	*H. velutinus*	*G. ulmifolia*	SEM	*P*-value
GP_{24}	90.2[a]	69.5[b]	34.2[c]	8.2	<0.01
GP_{48}	153.3[a]	129.3[b]	81.0[c]	10.7	<0.01
GP_{96}	184.3[a]	156.8[b]	124.6[c]	8.6	<0.01
IVDMD	526.0[a]	528.5[ba]	460.2[b]	11.6	<0.04
IVOMD	559.9[a]	534.9[a]	464.6[c]	14.4	<0.01
ME (MJ/kg DM	9.60[a]	7.81[b]	5.37[c]	0.62	<0.01

Means in the same row with different superscripts differ (P <0.05). (GP) Gas production after 24, 48 and 96 h of fermentation (mL/g DM).

Key Words: browse species, chemical composition, ruminal fermentation

T133 Effect of forage species on ruminal fermentation in continuous culture. K. J. Soder*[1], M. A. Sanderson[1], and G. E. Brink[2], [1]*USDA-ARS, University Park, PA*, [2]*US Dairy Forage Research Center, Madison, WI*.

The objective of this experiment was to evaluate the effects of forage grass species on ruminal fermentation using a dual-flow continuous culture fermenter system. Four grass species [reed canarygrass (RCG, *Phalaris arundinacea* L.); quackgrass (QG, *Elytrigia repens*); orchardgrass (OG, *Dactylis glomerata* L.); and meadow fescue (MF, *Festuca pratensis* Hud.)] were compared in a 4 × 4 Latin square design. Four 10-d periods were conducted, using the first 7 d as adaptation and the last 3 d for sampling. Fermenters (1120–1140 mL in volume) were fed 11.25 g forage DM 4 times daily at 0700, 1030, 1430 and 2030 h. A corn-based supplement (8.7% CP, 10.6% NDF) was fed (15 g DM) twice daily at 0700 and 1430 h. Solids retention time was set at 24 h. The pH was measured at each feeding time. Fermenter effluent were collected at 1430 h on d 8 to 10 and subsampled for analyses of VFA, ammonia, and DM content. Fermenter contents were harvested on d 10 for analyses of DM and bacterial production. Apparent DM, OM, and NDF digestibilities were not affected ($P > 0.05$) by forage species, averaging 39.2, 42.6 and 77.0%, respectively, across all forage species. Apparent ADF digestibility was least ($P < 0.05$) for QG (53.5%). The pH was not affected ($P > 0.05$) by forage species, averaging 6.21 across all forage species. Total and individual VFA production and acetate to propionate ratio (A:P) were not affected ($P > 0.05$) by forage species with the exceptions of isobutyrate, which was greatest ($P < 0.05$) for OG, and isovalerate, which was least ($P < 0.05$) for MF. Ammonia production was greatest ($P < 0.05$) for QG and least for MF. Total N and ammonia flows (expressed as g/d) were greatest ($P < 0.05$) for QG and least for MF. Efficiency of bacterial protein synthesis (gN/kd DM truly digested) was greatest ($P < 0.05$) for RCG and QG. The impact of individual forage species on ruminal fermentation is critical to gaining a better understanding of digestive and ingestive behavior for improved pasture management recommendations.

Key Words: canopy structure, digestibility, forage species

T134 Yield, chemical composition and ruminal degradability of winter wheat grown under organic and conventional management. I. Mateos[1], M. J. Ranilla[1,2], A. Diaz[1], C. Palacios[1], C. Saro[1,2], M. L. Tejido[1,2], and M. D. Carro*[1,2], [1]*1Dept. Producción Animal, Universidad de León*, *24007 León, Spain*, [2]*Instituto de Ganadería de Montaña (CSIC-ULE)*, *Finca Marzanas, 24346 Grulleros, León, Spain*.

The objective of this study was to investigate differences in yield and nutritive value of organically and conventionally grown winter wheat crops. Each cultivation system was carried out in 3 plots bordering each other to assure similar soil properties. Whole-plant (WP) yield was determined in May 2009, and grain and straw yields were determined at maturity in July 2009. Samples were dried and chemical composition and in vitro dry matter digestibility were determined. Samples (500 mg) of each substrate were incubated with 50 mL of buffered rumen fluid at 39°C, and gas production was measured at 3, 6, 9, 12, 16, 21, 26, 31, 36, 48, 60, 72, 96, 120 and 144 h to estimate fermentation kinetics. Mean yield in conventional plots was 3.12, 1.28 and 1.06 t DM/ ha for WP, grain and straw, respectively. Organic cultivation decreased the yield of WP, grain and straw to 74, 57 and 76% of that in the conventional cultivation, respectively ($P > 0.24$). No differences ($P > 0.05$) in organic matter, neutral detergent fiber and acid detergent fiber content of WP or grain were detected between cultivation systems, but crude protein content was lower ($P < 0.01$) in organic compared with conventional cultivars (6.69 vs. 5.23% for WP, and 12.10 vs. 8.56% for grain). No

differences ($P > 0.05$) between cultivars were detected in chemical composition of straw. Organic and conventionally grown crops did not differ ($P > 0.11$) in their in vitro dry matter digestibility (43.6 vs. 45.2% for WP, 26.3 vs. 24.8% for straw and 79.6 vs. 78.2% for grains). The cultivation method did not affect ($P > 0.26$) either the potential gas production or the average production rate (calculated as mL of gas/h). The results indicate that organic cultivation reduced crop yield and protein content in WP and wheat grains, but no effects were observed on ruminal degradation.

Key Words: organic cultivation, winter wheat, gas production

T135 Comparison of nonlinear functions for describing the growth curve of Nile tilapia *Oreochromis niloticus* var. *chitralada* in a commercial production cycle. D. Rodriguez[1], C. Ariza-Nieto[2], A. Munoz[1], and G. Afanador*[1,2], [1]*Universidad Nacional de Colombia*, *Bogota, Colombia*, [2]*CORPOICA*, *Bogota, Colombia*.

Mathematical models in fish nutrition have proven indispensable in estimating growth and feed requirements. The aim of this study was to make a statistical comparison of the mathematical growth models in Nile tilapia. The data set used for this analysis was taken from a study that evaluated the effects of oregano essential oils (OEO) supplementation in Nile tilapia, *Oreochromis niloticus* (L.) (males) raised form 10 to 550 g of weight. Six nonlinear mathematical functions were compared: Gompertz, Logistic, Richard, Janoschek, Michaelis-Menden, and Bertalanffy which were fitted to the data using the NLIN procedure of SAS. Gauss-Newton method was used through this statistical procedure and the maximum number of iterations to converge was 11. A quantitative approach of statistical analysis was used to evaluate model adequacy and the residual variation for each prediction equation was partitioned into 3 components using means square prediction error (MSPE), analysis for comparing accuracy among models. The Gompertz, Richards and Janoscheck were shown to be the most appropriate models for *Oreochromis niloticus* (4597, 4591 and 4589 MSPE values, respectively). Parameters that allowed comparisons between general rates of body weight change (both absolute and relative) as derived by Gompertz model were: average lifetime absolute growth rate (AGR, 2.395 g/day), average lifetime absolute maturing rate, (AMR, 0.00278) and average lifetime relative growth rate (RGR, 0.0151 g/day).

Key Words: nonlinear functions, Nile tilapia, AGR, AMR, RGR

T136 In vivo measurement of body composition of chickens using quantitative magnetic resonance (QMR). A. D. Mitchell*[1], R. W. Rosebrough[1], G. Taicher[2], and I. Kovner[2], [1]*USDA-ARS*, *Beltsville, MD*, [2]*Echo Medical Systems*, *Houston, TX*.

QMR is a nuclear magnetic resonance based method for measuring the fat, lean and water content of the total body of the live animal. The purpose of this study was to evaluate the use of QMR for measuring the body composition of chickens while comparing QMR results to those obtained by dual x-ray absorptiometry (DXA) and chemical analysis (CA). A total of 144 birds, were scanned live (non-anesthetized) by QMR, killed, and then scanned by DXA. The birds were Ross 708 broiler chickens and ranged in weight from 768 to 2230 g. In addition, 32 of the carcasses were chemically analyzed for total body lipid, water and ash content. For the entire group of birds, the QMR and DXA measurements of total body water and total body lean mass were in good agreement, with no significant difference (1149 ± 202g vs. 1169 ± 183g and 1395 ± 246g vs. 1354 ± 226g, respectively, $P > 0.05$) and highly correlated ($R^2 = 0.96$ and 0.96, respectively). However, the QMR measurement of total body fat was significantly lower ($P < 0.05$) than that measured by DXA (94 ± 44g vs. 190 ± 43g, respectively) and poorly correlated ($R^2 = 0.40$). Compared with CA, QMR underestimated the percentage of total body fat by 37% while DXA overestimated the percentage of fat by 22% (9.7 ± 3.6 by CA vs. 6.1 ± 4.3 by QMR and 11.8 ± 3.0 by DXA, $P < 0.05$). Both QMR and DXA measurements of percentage total body fat were highly correlated with the CA measurement ($R^2 = 0.96$ and 0.82, respectively). Both QMR and DXA estimates of total body water were close to the CA measurement (1153 ± 232g by CA vs. 1199 ± 239g by QMR and 1202 ± 218g by DXA, $P > 0.05$), with R^2 values of 0.81 and 0.82, respectively. In conclusion, the results of this study demonstrate that QMR is a potentially useful method for measuring the body composition of chickens. Major advantages of this method are that no anesthesia is required and no other measurements are needed for the data input or analysis.

Key Words: chickens, body composition, quantitative magnetic resonance

T137 Estimation of direct and maternal heritability of body weights in Iranian native chickens using a multivariate animal model. H. Farhangfar*[1], M. E. Navidizadeh[2], and S. M. Hosseini[1], [1]*Birjand University*, *Birjand, Iran*, [2]*Agricultural Jihad Organisation*, *Mashhad, Iran*.

The main objective of this research was to estimate direct and maternal heritability of body weights in Iranian native chickens. Generally, heritability is a key component for predicting breeding value of animals and few research have been so far undertaken in this respect for native chickens of Iran. To estimate genetic and environmental variance and covariance components for body weight traits, a multivariate animal model was applied. The traits were body weight at ages of 1 (W1) and 56 (W56) days. The data were provided by the breeding center of native chickens located in Khorasan Razavi province of Iran. The total number of records was 18,253 collected over 3 generations from 18,253 male and female chicks representing 315 sires and 2,141 dams. The average W1 and W56 were 33.8 g (SD = 3.27 gr) and 557 g (SD = 95.30 g), respectively. In the multivariate animal model, combined contemporary fixed effect of generation, hatch and sex (GHS), random effects of direct additive genetic, maternal additive genetic and maternal permanent were included. REML estimates of (co)variance components were obtained by DMU package. For W1, direct additive genetic, maternal additive genetic, maternal permanent environment and residual variance components were found to be 1.79, 0.68, 4.64 and 3.16 g^2, respectively. The corresponding figures for W56 were 2383, 823, 685 and 3553 g^2, respectively. Covariance components between direct and maternal additive genetic effects were −0.91 and −1398.8 g for W1 and W56, respectively. Direct heritabilities of W1 and W56 were 0.2 ($P < 0.05$) and 0.39 ($P < 0.05$), respectively. Maternal heritabilities of W1 and W56 were found to be 0.07 and 0.14, respectively. Correlation between direct and maternal additive genetic effects was −0.82 for W1 while it was approximately −1 for W56. The results also indicated that there is a significant additive genetic variation in the Iranian native chickens for W56 suggesting that genetic selection could be successfully practiced.

Key Words: Iranian native chicken, genetic parameters, body weight

T138 Maniçoba hay effects on the gastrointestinal tract of free-range birds. P. E. N. Givisiez*, G. S. G. Bach, J. H. V. Silva, F. G. P. Costa, C. J. B. Oliveira, and R. C. Lima Neto, *Universidade Federal da Paraiba*, *Areia, PB, Brazil*.

This study evaluated the effect of partial substitution of the diet by maniçoba hay (*Manihot pseudoglaziovii*) on gastrointestinal (GIT) morphology of free-range birds at 73 d of age. Eighty-four Paraiso Pedres birds were randomly distributed into 3 treatments and 4 repetitions of 7 birds each. Corn-soybean meal diet was substituted by maniçoba hay at 0, 10 and 20%. At 73 d of age, 2 birds per repetition were slaughtered and liver, gizzard, intestine and its segments were weighed and intestinal and segment lengths were measured. Weight and length were expressed

as percentages of the live weight (%PV). Fragments of duodenum and jejunum were collected from each bird and routinely processed for histological analysis. Villus height and crypt depth were assessed using a image analysis software and the villus:crypt ratio was calculated. Data were submitted to ANOVA in a completely randomized design, with 3 treatments and 8 repetitions for macroscopic parameters and different number of repetitions for microscopic parameters. Means were compared by Tukey's test at 5% probability. There were no significant differences ($P < 0.05$) between treatments for macroscopic results, except for the relative weight of gizzard, which increased in the treatments with maniçoba hay (1.82; 2.42 and 2.46% for 0, 10 and 20%, respectively). In the duodenum, villus height increased ($P < 0.05$) when 10% maniçoba was fed (789.18; 1110.3 and 698.90 μm for 0, 10 and 20%) and crypt depth decreased ($P < 0.05$) with 20% maniçoba (65.07; 68.7 and 44.71 μm for 0, 10 and 20%), but villus: crypt ratio was not affected ($P < 0.05$). No differences were seen in the jejunum. The increase in dietary fiber probably caused more extrusion of epithelial cells. Considering that high energy is necessary for GIT maintenance and that the inclusion of maniçoba hay decreases AME and AMEn, apparently recovery was possible in the 10% treatment, but not in the 20%. Maniçoba hay may be used up to the level of 10% without compromising the epithelium of duodenum and jejunum.

Key Words: free-range birds, intestinal morphology, dietary fiber

T139 Study on probiotic characteristics of three isolates of lactic acid bacteria in in vitro and in vivo condition in broilers. S. Ghyamyipour[1], S. Rahimi*[1], M. A. Karimi Torshizi[1], and N. Mojgani[2], [1]*Tarbiat Modares University*, *Tehran, Tehran, Iran*, [2]*Razi Vaccin and Serum Production Research Institute*, *Karaj, Tehran, Iran*.

The effect of administration of 3 lactic acid bacteria isolates on broiler performance and carcass characteristics were investigated. This study was done in 2 phases. In first phase the microbiological characteristics of these 3 isolates such as tolerance to low pH, growth in presence of bile salts, tolerance to some commercial antibiotics, hydrophobicity, ability to inhibit the growth of some pathogenic bacteria and their ability to release the hydrolase enzyme of bile salt were examined. Data from first phase indicated that the isolated bacteria were identified as lactobacilli. In the second phase, to determine whether probiotics improve broiler growth and carcass characteristics, 3 lactic acid bacterial isolates were added to drinking water. Day old chicks (n = 320) were distributed to 4 experimental groups with 4 replicates with 20 chicks in a completely randomized design. Control group (C) did not receive any probiotic culture in drinking water; groups A, B and D received one of the 3 lactic acid bacterial cultures at a concentration of 10.6 log cfu/mL in drinking water from 9 to 49 d of age. Data were analyzed by Duncan's multiple range test (SAS, 1990). Administration of B culture resulted the greater BW gain compared with the other groups on d 49 ($P < 0.05$). Lactic acid bacteria did not influence the feed intake, weight and length of internal organs and carcass characteristics of chicks and blood factors except spleen weight, jejunum length and total carcass weight.

Key Words: lactic acid bacteria, performance, carcass

T140 Utilization of yeast extract and bacitracin for early intestinal maturation by broiler chicks obtained from breeder hens of different ages. Y. O. Fasina*, R. Thanissery, and S. J. Thomas, *Auburn University*, *Auburn, AL*.

The intestine of the newly hatched chick is immature at hatch and hatchlings from young breeder hens (YHC) typically demonstrate reduced livability compared with those from old breeder hens (OHC). Supplementing yeast extract (YE) into the diet may enhance intestinal development and growth of broiler chicks because, YE contains nucleotides that are essential for cellular functions and are also immunomodulatory. A 14-d experiment was conducted with day-old chicks from young (26–27 week old) and old (58 to 59 week old) breeder hens. Chicks (384) were randomly assigned to 8 dietary treatments. Treatment 1 (YH) consisted of YHC fed corn-soybean meal (SBM) diet without bacitracin methylene disalicylate (BMD) or YE added. Treatment 2 (YHB) consisted of YHC fed corn-SBM basal into which BMD was added at 0.055g/kg. Treatment 3 (YHE) consisted of YHC fed corn-SBM basal into which YE was added at 0.075% level. Treatment 4 (YHED) consisted of YHC fed corn-SBM basal into which YE was added at 0.15% level. Treatments 5 (OH), 6 (OHB), 7 (OHE), and 8 (OHED) consisted of OHC fed diets similar to those given to YHC in treatments 1, 2, 3, and 4, respectively. Intestinal jejunal tissue samples were analyzed for alkaline phosphatase (ALP) activity as an indicator of intestinal maturation on d 4 and 13 of experiment. Results showed that among YHC treatments, intestinal ALP activity was higher in YHB, YHE, and YHED treatments ($P < 0.05$; 1.85 to 2.61 IU/mg protein) compared with YH (1.06 IU/mg protein) on d 4 of experiment. Among OHC treatments, only OHB (2.14 IU/mg protein) had higher ALP activity than OH (0.89 IU/mg protein; $P < 0.05$). By d 13, ALP activity became similar for all treatments ($P > 0.05$). It was concluded that YE supplemented at 0.075% level of the diet performed similarly to BMD in enhancing early intestinal maturation in YHC, but had no effect in OHC.

Key Words: yeast extract, alkaline phosphatase activity, broiler chick intestine

T141 Growth and organogenesis of progeny chicks from dams fed different sources of trace minerals. Q. J. Sun*, S. Y. An, and Y. M. Guo, *State Key Lab of Animal Nutrition, College of Animal Science & Technology, China Agricultural University*, *Beijing, China*.

A study was conducted to evaluate growth and organogenesis of progeny chicks from broiler breeders fed diets supplemented with different sources of trace minerals. A total of 120 Cobb 48 broiler breeder females aged 31 wk were given 3 diets with organic or inorganic trace minerals at equal levels. The control (CON) was the basal diet supplemented with a combination of inorganic minerals ($CuSO_4$, $ZnSO_4$, $MnSO_4$ and Na_2SeO_3 separately, i.e., Cu 8 mg/kg, Zn 50 mg/kg, Mn 60 mg/kg and Se 0.3 mg/kg of diet). The second treatment (ZM) was basal diet supplemented with a combination of inorganic Cu, Mn and Se, and organic Zn from Mintrex-Zn. The third treatment (MIX) was basal diet supplemented with a combination of Mintrex-Cu Zn Mn (Novus Intl., USA) and yeast-selenium from Sel-Plex (Alltech Inc., USA). Diets were formulated based on NRC (1994). Trace minerals in basal diets were Cu 4.6 mg, Mn 30 mg and Zn 47 mg/kg diet based on actual analysis. All diets were iso-energetic, iso-nitrogenous and iso-methionine. After 8 wk, eggs laid during 39wk of age were incubated. Hatched chicks were raised for evaluation of growth performance and development of organs respectively. Broilers were fed with a common commercial ration with inorganic minerals (Cu 8 mg, Zn 50 mg, Mn 60 mg and Se 0.3 mg/kg diet). Results showed that minerals sources in broiler breeder hens diets did not influence the feed intake of their progeny. Supplementation of ZM and MIX in the diet increased body weight (BW) ($P = 0.121$), and decreased feed/gain ($P < 0.05$) of the chicks. No difference was observed in development of heart, however the liver weight (LW) and its relative weight (LW/BW) on d 1 and bursa weight (BAW) on d 11 were increased with ZM and decreased with MIX (LW, $P < 0.05$; LW/BW, $P < 0.10$; BAW, $P = 0.056$). Relative weight of bursa on d 11 was increased when breeders fed ZM ($P < 0.05$). On d 21, chicks fed

inorganic minerals obtained the greatest spleen weight (SW) and its relative weight (RSW) (SW, $P < 0.05$; RSW, $P < 0.10$). In conclusion, organic sources of minerals improved progeny growth performance and affected organogenesis.

Key Words: broiler breeder, progeny, mineral

T142 Effect of dietary probiotic and prebiotic on bone characteristic of Ross broiler chickens. H. Ziaie[1], G. H. Hadarbadi*[1], A. Zeinali[2], M. A. Karimi Torshizi[4], M. Bashtani[3], and H. Farhangfar[3], [1]*Agriculture and Natural Resources Research Center*, *Birjand, South Khorasan, Iran*, [2]*Ferdowsi University*, *Mashhad, Iran*, [3]*Birjand University*, *Birjand, South Khorasan, Iran*, [4]*Tarbiat Moddares University*, *Tehran, Iran*.

Weak bones result in breaking during processing and lower meat grade. Also, weak legs often result in reduced feed intake thus affecting weight gain and feed conversion ratio. Therefore, the objective of the present study was to determine the effect of dietary probiotic and prebiotic on bone characteristic and Breaking Strength of Ross broiler chickens. In this study, 240 day-old male broiler chickens (Ross strain) were allocated to 4 treatments in pens (120 × 100 × 90 cm) with 4 replicates (15 birds / pen) in a block completely randomized design. Experimental diets were fed: T1 = Control diet based corn and soybean meal without supplementation, T2 = Control diet + antibiotic (Virginiamycin) 15 ppm, T3 = Control diet + probiotic (commercial mixture of lactobacillus, Protexin) 150g/ton diet and T4 = Control diet + prebiotic (commercial mixture, Immnuwall) 450g/ton diet).). At the end of the experiment (42 d), 2 birds from each replicate were randomly selected and killed to evaluate the tibia bone characteristic (modulus of elasticity, yield stress and percentage of ash, calcium and phosphorous). Bone breaking strength analysis was conducted using an Instron Materials Tester (Model 4411, Instron Corp., Canton, MA) with Automated Materials Test System software version 8.09. The results of the present study indicated that mechanical parameters, ash percentage, Ca and P contents were significantly improved by the supplementation antibiotic and their alternatives ($P < 0.05$) but, the difference between antibiotic diet and treatments 3 and 4 was not significant ($P > 0.05$). In finally, with the prophylactic use of antibiotic (as growth promoters) in animal feeds probiotic and prebiotic resulted in increase resistance to stress fracture of broiler bones and as a suitable replacement can be proposed.

Key Words: broiler, antibiotic alternative, bone characteristic

T143 Improved hatchability and post-hatch performance in turkey poults receiving iodinated casein in ovo. W. G. Bottje*[1], A. Wolfenden[1], L. Ding[2], M. Morgan[1], N. Pumford[1], R. Wolfenden[1], G. Duncan[3], T. Smith[3], T. Slagel[3], K. Lassiter[1], and B. Hargis[1], [1]*Dept. of Poultry Science, Center of Excellence for Poultry Science, Univ. of Arkansas*, *Fayetteville,* [2]*Dept. of Animal Nutrition, College of Animal Science and Technology, China Agriculture University*, *Beijing, China*, [3]*Cargill Turkey Division*, *Springdale, AR*.

Iodinated casein has been shown to have thyroid hormone-like properties, and thyroid hormone has been shown to improve turkey embryo hatchability. Thus, studies were conducted to investigate the effect of iodinated casein injected in ovo at 25 d of incubation on hatchability, hatch weight, and growth (6 or 7 d post-hatch) in turkey poults. Two experiments were conducted with a commercial turkey hatchery using a commercial egg injection system. In Exp. 1, 3900 turkey eggs (1300 per group) were injected at 25 d of incubation with 200 µL of solution containing either 10 mg/mL of gentamicin (Control) or ones containing 75 µg/mL or 375 µg/mL of iodinated casein (IC75 and IC375, respectively) in a dextrin solution mixture of maltodextrin and potato starch dextrin (~28%). Two hundred poults each from the Control, IC75 and IC375 groups were neck tagged, placed in a commercial turkey house within a single brooder ring, and weighed 7 d later. In Exp. 2, 5200 eggs (2600 per group) were injected with the Control or the IC75 solution. A total of 600 poults (300 per group) were neck-tagged and placed in a single brooder ring in a commercial house and weighed on d 6 post-hatch. Eggs in Exp. 1 and 2 were obtained from hen flocks that were 33 and 5 wk into the laying cycle, respectively. In Exp. 1, the IC75 injection resulted in a 1.8% increase ($P = 0.03$) in hatch weight and numerically higher hatchability and 7 d BW compared with Controls. In Exp. 2, the IC75 treatment resulted in a 2.4% increase in hatchability ($P = 0.01$), a 4.3% increase in hatch weight ($P < 0.001$), and a 1.8% increase in 6 d poult weights ($P < 0.03$) compared with Controls. The results of this study indicate that a solution containing 75 µg/mL iodinated casein in a dextrin solution injected into turkey eggs at 25 d of incubation may be used to improve hatchability and early poult weights in commercial turkey production.

Key Words: poult hatchability, iodinated casein, in ovo injection

T144 Effect of daily lithium chloride (LiCl) administration on bone quality and strength in growing broiler chickens. B. M. Harvey*[1], M. Eschbach[2], E. Ackell[1], S. Kotha[2], M. Darre[1], N. Francis[1], D. J. Adams[3], R. Ramanathan[1], R. Mancini[1], and K. E. Govoni[1], [1]*Department of Animal Science, University of Connecticut*, *Storrs,* [2]*Department of Mechanical Engineering, University of Connecticut*, *Storrs,* [3]*Orthopedic Surgery, University of Connecticut Health Center*, *Farmington*.

Bone fractures and deformities are a serious problem for the broiler industry; therefore, identification of mechanisms to improve bone quality and strength would be beneficial. The wnt/β-catenin pathway plays a critical role in the bone formation process and this pathway can be stimulated by oral LiCl supplementation in mice. We hypothesized that oral supplementation of LiCl would increase bone strength and quality in broiler chickens. 144 broilers were divided into LiCl, control (C) and pair-fed (PF) groups. Beginning at 1 or 3 weeks (wk) of age, chickens were administered LiCl (20 mg/kg BW) or water daily by oral gavage. At 6 wk of age, chickens were killed and blood, bone and muscle samples were collected. A 24h LiCl (20 mg/kg BW) challenge determined that serum LiCl increased within 2h and cleared the system within 24h, thus demonstrating the effectiveness of our oral gavage to deliver LiCl. We did not observe any differences in BW ($P \geq 0.53$) or feed intake ($P \geq 0.19$) between all treatment groups, demonstrating that LiCl treatment did not negatively affect growth in these broilers. To evaluate bone composition, we performed morphometric analysis on the tibiae of C and LiCl groups using microCT imaging. We did not observe a difference in cortical or trabecular bone volume, trabecular thickness, number, or spacing ($P \geq 0.52$). To determine bone strength, we performed 3-point bending on the femora and tibiae of C and LiCl birds from the 1 wk group. We did not measure a difference in bone length or ultimate load ($P \geq 0.60$). However, we did observe a 23% reduction in stiffness ($P = 0.02$) in the femora and 34% reduction in fracture energy ($P = 0.11$) in the tibiae of the LiCl treated birds, thus suggesting reduced bone quality in the LiCl birds. We did not observe any effect of LiCl treatment on pectoralis muscle color or lipid oxidation ($P > 0.05$). In conclusion, LiCl treatment in broilers did not affect growth or meat quality. Surprisingly, we measured a reduction in bone stiffness with LiCl treatment which may be due to the dose of LiCl utilized or a species difference in response to LiCl treatment on bone formation.

Key Words: poultry, bone, broiler

T145 The bi-allelic expression of *delta-like 1 homolog* (*Dlk1*) in avian species. S. Shin* and K. Lee, *The Ohio State University*, *Columbus*.

Delta-like 1 homolog (*Dlk1*) is known as an important gene in the regulation of adipose and muscle differentiation and development. This gene is also known as an imprinted gene usually expressed only from the paternal allele in mammals. To determine the properties of the *Dlk1* genes of the avian species, *Dlk1* genes for chicken, quail and turkey were cloned and characterized for cDNA and amino acid sequences, alternative splicing, and genetic distances from other species. In addition, the structure of genomic DNA containing the cluster of genes including *Dlk1* was investigated in the chicken and compared with the human. The allelic expression pattern of the avian *Dlk1* gene was also determined here. The coding sequences of the quail and turkey *Dlk1* were the same as chicken *Dlk1* in their numbers of nucleotides (1,161 bp) and amino acids (386 a.a.). The similarities in DNA and amino acid sequence were more than 96% among the poultry species. The chicken and turkey *Dlk1* were closer than the quail in the phylogenetic analysis. The domains, such as one signal sequence, 6 *epidermal growth factor* (*EGF*)-like domains and a transmembrane domain were predicted in DLK1. There was no alternative splicing of *Dlk1* transcripts as in the chicken. Like in mammals, *Yy1*, *Wars*, *Wdr25*, *Begain*, *Dlk1*, *Dio3*, and *Ppp2r5c* were found as a syntenic gene cluster in chicken genome. However, *Meg3*, *Rtl1*, and *Meg8* genes located between *Dlk1* and *Dio3* were not found in the cluster of the chicken genome. There were several single nucleotide polymorphisms (SNPs) in the fifth exon of *Dlk1* genes in chickens and quail, and the heterozygous SNPs of *Dlk1* transcripts were observed in the adipose and muscle, indicating the bi-allelic expression of *Dlk1* in the avian species. The data confirmed avian *Dlk1* is not imprinted in poultry and might be regulated in a different manner from mammals.

Key Words: avian Dlk1, genomic imprinting, biallelic expression

T146 Expression of myosin heavy chain isoforms during muscle development in Leghorns and broilers. A. Lee*, Y. Suh, and K. Lee, *The Ohio State University*, *Columbus*.

Myosin heavy chain (MyHC), one of the major components in the contractile machinery of skeletal muscle fibers is found in several isoforms during myogenesis. During chicken development embryonic, neonatal, and adult MyHC isoforms are expressed. Broiler chickens have been selected for fast and large muscle growth while Leghorn chickens have been selected for egg laying capabilities. This has led to an obvious difference in muscle growth and development with broilers being much larger than Leghorns. The objective of this study was to determine if differences in muscle growth and development of Leghorns and broilers are associated with differences in temporal expression of MyHC isoforms in skeletal muscle between the 2 breeds. Pectoralis major muscle was collected from Leghorns and broilers at embryonic d 15, and 17 and d 1, 5, 11, 20, 27, and 33 d post hatch with n = 3 samples per time point and breed. Western blotting using 3 monoclonal antibodies (EB165, 2E9, and AB8) was performed to compare the expression patterns of embryonic/adult, neonatal, and adult isoforms of MyHC, respectively, for all time points in both Leghorn and broiler chickens. Pectoralis major tissue from broiler chickens expressed the adult MyHC isoform as early as d20 whereas the Leghorn chickens began expressing the adult isoform later. Both broiler and Leghorn chickens began expressing the neonatal MyHC isoform on d5 however Leghorn chickens expressed the neonatal isoform much longer than broilers. Leghorn chickens had sustained expression of the neonatal MyHC isoform through d27 whereas in broiler chickens the neonatal isoform was not expressed at d20. The differences in the expression of both adult and neonatal MyHC isoforms in broilers and Leghorns are consistent with the faster maturation and growth of broilers relative to Leghorns. Further study of other MyHC isoforms is needed to determine their association with differences in muscle growth and development of broiler and Leghorn chickens.

Key Words: muscle development, myosin heavy chain, chicken

T147 Growth of internal organs in quail embryo (*Coturnix japonica*) as a function of age. K. L. Arora*, *Fort Valley State University*, *Fort Valley, GA*.

The Japanese quail embryo is a very valuable model for experimental studies in developmental biology, toxicology, virology, teratology, endocrinology and drug testing. Various reports in the literature have focused on embryonic growth, weight, and developmental defects as a function of age. However, it is important to know the progressive changes in the growth of different organs which make up the total organism for complete pathological analysis. Eggs of uniform size and weight (10–11g) were collected, between 3 to 6 p.m., from 56d old birds weighing 130–135g. The birds were housed in cages under 14L: 10D lighting system and fed commercial turkey starter. Eggs were incubated at 37.8°C and 65–70 R.H. At the end of 10, 12, 14, and 16 d of incubation, a group of 15 eggs each were removed from the incubator and opened into Petri-dishes containing lukewarm saline solution. The embryos which were devoid of extra-embryonic tissues and spare yolk, were washed again, blotted with paper towel, organs dissected and removed and weighed individually using analytical balance. Day old chicks were killed with CO_2 and handled in a similar fashion. The following organs were collected: brain, liver, heart, gizzard, proventriculus, lungs, eyes and kidneys. Embryonic mass increased rapidly from 1.44 ± 0.01g at d 10 to 5.38 ± 0.14g at d 16, the time to hatch ($P < 0.01$). By d16, the embryonic mass had reached 91.7%, liver 88.2% heart 98%, kidney 100%, brain 100%, gizzards 89.6%, proventriculus 87.6%, lungs 95.2% and eyes 99.4% of the weight of day-old chick (100%). The embryonic growth accelerated during d10 and 12 and d14 and 16 with the organs growing at different rates ($P < 0.01$). The larger and faster growing organs in order of growth were: eyes, brain, gizzard and liver. The smaller and slower growing organs were ranked similarly in order of growth: proventriculus, heart, lungs and kidneys. The importance of the relationship between the growth of internal organs, age and stage of development will be discussed.

Key Words: Japanese quail, internal organ, embryo

T148 Growth after an innate immune challenge is different between broiler strains. L. Xu*[1], M. deBeer[2], M. Einstein[1], A. Schinckel[1], and T. J. Applegate[1], [1]*Purdue University*, *W. Lafayette, IN,* [2]*Aviagen, Inc.*, *Huntsville, AL*.

The acute phase response (APR) is defined as the early set of innate immune reactions induced by unfamiliar infectious agents or tissue injury. Lipopolysaccharide (LPS)-induced APR is associated with depressed growth and appetite loss. However, the question remains if there is a difference in the recovery after an APR between broiler strains. Therefore, a 40d feeding study was conducted with 2 broiler strains that were challenged between 7 to14 d with LPS. The experiment was designed with 3 treatments per strain (n = 8 cages/treatment; 6 birds/cage) starting at 7 d of age: an unchallenged positive control, LPS-challenged negative control (LPS-NC), and an unchallenged treatment that was pair-fed to LPS-NC. The LPS was injected i.p. Four times at 48-h intervals (1 mg/kg of BW). Body weight was recorded individually at 7, 14, 27, and 40 d of age. The LPS challenge depressed BW gain from 7 to 14 d of age by 10% and 12% for strains 1 and 2,

respectively. However, 67 and 74% of growth depression for strains 1 and 2, respectively, was attributable to factors other than feed intake reduction when compared with the pair-fed treatment. No BW differences between strains were apparent at the end of the challenge period (14 d; $P > 0.05$); whereas Strain 1 was 5.4% heavier (153.9 g) at 40 d of age ($P < 0.0001$). When 7 to 14 d of age BW gain was used as a covariate, average daily gain was affected by treatment within strain 1 but not strain 2. In other words, birds given the LPS treatment for strain 1 demonstrated compensatory growth; whereas those for strain 2 did not. Additionally, the coefficient of variation for 40d BW of strain 1 was 1.3% versus that for strain 2 which was 1.6%. Thus, growth recovery after an APR is different between broiler strains.

Key Words: broiler strain, innate immune response, lipopolysaccharide

T149 Influence of gender and initial body weight uniformity on growth performance and carcass quality of pigs slaughtered at 130 kg BW. L. Cámara*[1], M. P. Serrano[1], D. G. Valencia[2], A. Fuentetaja[3], and G. G. Mateos[1], [1]*Universidad Politécnica de Madrid*, *Madrid, Spain*, [2]*Nutral S.A.*, *Madrid, Spain*, [3]*Copese S.A.*, *segovia, Spain*.

A trial was conducted to study the influence of gender (castrated female, CF vs. castrated male, CM) and initial pen uniformity (BW ± SD, 7.5 ± 0.6 kg vs. 7.5 ± 1.2 kg BW) on performance and carcass quality of crossbreds pigs resulting from Landrace * Duroc × Large White dams mated to Duroc sires pig. Males were castrated at 5 ± 2.0 d of age (2.5 ± 0.57 kg BW) and females at 69 ± 2.6 d of age (22.3 ± 0.83 kg BW). Each treatment was replicated 4 times and the experimental unit was a pen with 30 piglets from 7.5 to 27.3 kg BW and a pen with 14 pigs from 27.1 to 130.4 kg BW for productive traits. For carcass quality traits, 10 carcasses of the same pen constituted the experimental unit. From 7.5 to 27.3 kg BW, CF had lower ADFI ($P < 0.05$) and ADG ($P < 0.001$) and poorer FCR ($P < 0.001$) than CM. Also in this period, uniform pigs tended to be less efficient than less uniform pigs ($P < 0.10$). From 27.1 to 130.4 kg BW, CF tended to eat less feed and to have better FCR than CM but pen uniformity did not affect performance. Castrated females had more ($P < 0.05$) fat thickness at P_2 and tended to have more ($P < 0.10$) fat at *gluteus medius* muscle than CM. Trimmed shoulder yield ($P < 0.001$) and trimmed primal cut yield ($P < 0.01$) were higher for CM than for CF. Gender did not affect carcass, ham, and loin yields or shrink loss. Pen uniformity had little effect on carcass quality; the only effect detected was that uniform pigs tended to have more trimmed primal cut yield than the less uniform pigs. It is concluded that castrated females, had higher carcass fat content than castrated males. Therefore, castrated females are a good alternative to castrated males for the production of pigs destined to the dry-cured industry. On the other hand, the distribution of the pigs to improve pen uniformity does not provide any advantage in growth performance or carcass quality.

Key Words: castration and gender, heavy pig productivity and quality, uniformity

T150 Sow and litter productivity as affected by sow age. L. Cámara[1], M. P. Serrano*[1], D. G. Valencia[2], A. Fuentetaja[3], and G. G. Mateos[1], [1]*Universidad Politécnica de Madrid*, *Madrid, Spain*, [2]*Nutral S.A.*, *Madrid, Spain*, [3]*Copese S.A.*, *Segovia, Spain*.

A total of 180 sows (crossbred of Landrace × Duroc × Large White) was used to study the effect of parity (primiparous, PRI, vs. multiparous in the 3rd and 4th reproductive cycle, MUL) on productive performance and posterior fertility. Each treatment was replicated 5 times and the experimental unit was a room with 16 sows housed individually. Feed and water intake were controlled daily and BW and backfat at P_2 were measured at farrowing and at weaning. Total number of piglets born alive, death, and mummified, and piglet mortality during lactation were recorded per litter. Also, piglet body weight was recorded at birth, and at 3, 14, 21, and at 28 d of age. In addition, the interval weaning to first estrous and the percentage of sows that did not make next farrowing were recorded. Multiparous sows ate more feed (5.64 vs. 4.25 kg/d; $P < 0.001$) and drank more water (28.63 vs. 23.07 l/d; $P < 0.05$) than PRI sows but feed:water ratio was not affected. Body weight change from farrowing to weaning was similar for both groups. Multiparous sows had more piglets born alive (11.4 vs. 10.2; $P < 0.05$) than PRI sows. Piglets from MUL sows were heavier ($P < 0.05$) at birth (1.73 vs. 1.53 kg), 3 (2.14 vs. 1.89 kg; $P < 0.01$), 14 (4.73 vs. 4.26 kg), 21 (6.45 vs. 5.84 kg), and 28 (8.61 vs. 7.58 kg) days of age than piglets from PRI sows. Consequently, from 1 to 28 d of age, piglets from MUL sows had higher ADG than piglets from PRI sows (260 vs. 229 g/d; $P < 0.05$). Mortality of piglets during lactation and of sows between farrowings was not affected by sow parity. The interval weaning to positive gestation was similar for both groups of sows. Sow parity did not affect the number of piglets born alive or death in the following parity. It is concluded that multiparous sows had higher voluntary feed intake and produce more piglets per litter, which are heavier, than primiparous sows.

Key Words: multiparous, primiparous, piglet productivity

T151 Effects of L-arginine supplementation to suckling piglets on plasma metabolites and skeletal muscle properties at weaning. D. Loesel*, S. Goers, and C. Rehfeldt, *Leibniz Institute for Farm Animal Biology (FBN)*, *Dummerstorf, Germany*.

Piglets of low birth weight exhibit a lower total number of skeletal myofibers at birth and throughout life compared with piglets of middle and heavy birth weight, which is associated with impaired (lean) growth, carcass and meat quality at market weight. To investigate, whether L-arginine is effective in stimulating the early postnatal increase in the number of myofibers, piglets of low birth weight (≤1.22 kg) from 5 German Landrace sows received 0.48 g L-arginine-HCl/kg body weight/day (n = 12) or an isonitrogenous amount of L-alanine (control; n = 12) from d 7 to 28 of age. Piglets were weaned and slaughtered at d 28 of age. Supplementation with arginine or alanine increased blood plasma concentrations of arginine and alanine, respectively ($P < 0.001$). Live weight gain, final body weight, and body composition by dissection and chemical analysis were not affected by arginine, except for a reduction in relative liver weight ($P = 0.05$). Plasma concentrations of glucose and free fatty acids remained unchanged, whereas urea concentration tended to be smaller in response to arginine supplementation ($P = 0.12$). The total number of semitendinosus (ST) myofibers was not affected by treatment ($P = 0.80$). Likewise, fiber area and metabolic fiber type composition by red, intermediate, and white fibers were not influenced. Protein and DNA concentrations remained unchanged, whereas total DNA amount tended to be greater in ST muscle of arginine-supplemented piglets ($P = 0.12$). Specific activities of CK ($P < 0.01$) and LDH ($P = 0.05$) increased 1.06-fold and 1.08-fold, respectively, in response to arginine, whereas ICDH activity was unchanged. The results suggest that arginine slightly stimulated muscle differentiation and metabolic maturation, but not muscle protein accretion and myofiber formation. It remains to be investigated whether modifications in the dosage or period of arginine supplementation would be more efficient in affecting skeletal muscle growth and metabolism of suckling piglets.

Key Words: body composition, enzyme, pig

T152 Finishing growth and carcass characteristics following reciprocal embryo transfer between Meishan and White crossbred pigs. J. R. Miles*, J. L. Vallet, B. F. Freking, J. J. Ford, S. D. Shackelford, and T. L. Wheeler, *USDA-ARS, US Meat Animal Research Center*, *Clay Center, NE*.

Crossbreeding studies between Meishan (MS) and contemporary White crossbred (WC) pigs have shown that increased lean, finishing growth of WC pigs is affected by the direct genotype of the piglet. The objective of the current study was to determine the contributions of the piglet and maternal genotypes and their interactions on finishing growth and carcass characteristics following reciprocal embryo transfers between MS and WC gilts. Twenty-five pregnancies were produced in 2 farrowing seasons that represented all piglet and maternal genotype combinations; MS × MS (n = 4 litters), WC × WC (n = 7 litters), MS × WC (n = 7 litters), and WC × MS (n = 7 litters). Starting at d 105 of age, gilts (n = 50) and barrows (n = 40) were weighed and backfat was recorded every 3 weeks. At d 165 of age, pigs were slaughtered and hot carcass weights were recorded. Within 3 d of slaughter, leaf fat was weighed and loin eye color, marbling, and area were determined. All data were analyzed using MIXED model procedures. There were piglet breed effects ($P < 0.01$) for body weight. As a result, average daily gain during grow-finish was greater ($P < 0.001$) in WC pigs. In contrast, average back fat measurements were greater ($P < 0.001$) in MS pigs. At slaughter, a piglet breed effect ($P < 0.001$) was observed in hot carcass weight in favor of WC pigs. Conversely, there was a direct breed effect ($P < 0.05$) of leaf fat weight in favor of MS pigs. No significant genotypic effects were observed for loin eye marbling between the breeds. However, loin eye color was darker ($P < 0.01$) in the MS pig. Furthermore, there was a piglet breed effect ($P < 0.001$) for loin eye area in favor of WC pigs. This study detected no significant interactions between the piglet and maternal genotypes of MS and WC pigs on finishing growth and carcass characteristics, and supports crossbreeding studies illustrating that differences in finishing growth are attributed to the genotype of the piglet.

Key Words: finishing growth, carcass characteristics, pigs

T153 Cytokine gene expression patterns of milk from healthy bovine mammary glands in late and early lactation. D. F. R. Bruno*[1], R. G. S. Bruno[3], P. V. Rossitto[2], J. S. Cullor[2], and J. L. Stott[2], [1]*Texas Veterinary Medical Diagnostic Laboratory*, *Amarillo,*[2]*University of California Davis*, *Davis,* [3]*Texas AgriLife Research and Extension*, *Amarillo*.

Cytokines mediate and regulate the immune system and have been studied as an alternative non-antibiotic therapy to treat and prevent mastitis in dairy cows, mainly in critical times as dry-off and early postpartum. The aim was to compare natural levels of expression of 9 cytokines on late lactation (dry-off) and early lactation (first week postpartum) in milk cells from healthy cow mammary glands. Transcriptional levels of expression of interleukin (IL)2Rα, IL4, IL6, IL8, IL10, IL17, interferon (IFN)γ, inducible nitric oxide synthase (iNOS) and tumor necrosis factor (TNF)α were evaluated in both periods by real time PCR. Milk samples from 10 Holstein cows were collected aseptically from 2 quarters/cow at dry-off and again at first week postpartum. Only quarters with somatic cell count ≤200,000 and absence of bacteria in both time points were considered for this study. Significance was defined as $P < 0.10$. Transcripts from IL2Rα, IL8, IL10, IFNγ, iNOS and TNFα were detected in both periods. IL2Rα and IL6 ($P < 0.10$), and IL8 and IL10 ($P < 0.04$) were upregulated in late lactation in comparison with the levels in early lactation. In late lactation, there was a positive correlation of proinflammatory cytokines IL6 and TNFα with anti-inflammatory cytokine IL10, and chemokine IL8 ($P < 0.10$). However, a negative correlation was observed between the proinflammatory cytokine IL17 with IL6 and IL8 ($P < 0.10$). In early lactation, fewer cytokines were correlated. A positive correlation among IL8 and TNFα and IL2Rα was observed. Similar to late lactation, there was a positive correlation between IL6 and IL10, and between TNFα and IL8, which was also correlated to the regulatory mediator iNOS ($P < 0.10$). In conclusion, cytokine mRNA profiles between late and early lactation showed differences, which can be attributed to dramatic changes the mammary gland is subjected to during these 2 stages of lactation. Positive correlation and upregulation of proinflammatory and anti-inflammatory cytokines account for an efficiency of the mammary gland immune system at late lactation and could be used as markers for health control of the udder.

Key Words: cytokine expression, lactation, RT PCR

T154 Intra- and inter-dairy heifer variation of cellular neutrophil functions. L. E. Hulbert*[1,2], L. R. Schwertner[1], J. A. Carroll[2], and M. A. Ballou[1], [1]*Department of Animal and Food Sciences, Texas Tech University*, *Lubbock,* [2]*Livestock Issues Research Unit, USDA-ARS*, *Lubbock, TX*.

Immune competence of dairy cattle is difficult to determine as a healthy immune system requires the resolution of pathogen invasion without excessive host-tissue damage. Neutrophil phagocytosis (PG) is important for eliminating pathogens, but PG induces an oxidative burst (OB), which helps destroy the pathogen but also can damage the neutrophil and surrounding tissue. Neutrophil adhesion molecule L-selectin (L) mediates neutrophil rolling in the periphery, allowing for "surveillance" of pathogens, while its counterpart, β-integrin (β), allows for neutrophil anchoring to epithelial cells and migration into tissue from the periphery. The objectives of these studies were to examine inter-heifer variation (Exp.1, n = 36, 13–16 mo. of age) as well as intra-heifer variation (Exp. 2, n = 12, days = 3) of neutrophil functions. Phagocytosis and OB were determined by 2-color flow cytometry using propidium iodide labeled enterotoxigenic *E. coli* and the oxidation of dihydrorhodamine, respectively. Adhesion molecule expressions were also determined using flow cytometry and expressed as the mean fluorescence intensities. In Exp. 1, neutrophil PG and OB were highly correlated ($R^2 = 0.50$), while adhesion molecules L and β were moderately correlated ($R^2 = 0.39$). Inter-heifer coefficients of variation (CV) were low for PG (19.9%) and β (18.5%), but high for OB (51.1%) and L (38.0%). In Exp. 2, there were day effects ($P \leq 0.01$) for PG, OB and β, but not L ($P \geq 0.10$). Neutrophil PG intra-heifer CV was the least among all immune parameters (11.0%) while OB was the most variable at 22.43%. Adhesion intra-heifer CVs were 17.6% for β and 16.1% for L. These data indicate that neutrophil migration into tissue and subsequent phagocytosis of *E. coli* were more similar between Holstein heifers than either the oxidative killing or surveillance potential. Therefore, the OB and L expression are more likely to contribute to individual heifer variation in immune competence.

Key Words: bovine, granulocytes, immunology

T155 Comparison of the proliferative response of CD8 memory T cells from experimentally and naturally infected cattle shows the response to live *Mycobacterium avium* ssp. *paratuberculosis* stronger than the response to Johnin purified protein derivative (JPPD). H. M. Rihan*[1], G. S. Abdellrazeq[2], M. J. Hamilton[3], A. J. Allen[3], K. T. Park[3], and W. C. Davis[3], [1]*Mansoura University*, *Egypt*, [2]*Alexandria University*, *Egypt*, [3]*Washington State University*, *Pullman*.

Johnin purified protein derivative (JPPD) is the antigen most frequently used to study the T-cell response to *Mycobacterium avium* ssp. *paratuberculosis* (MAP). It has been assumed the response to this antigen can be used to characterize the CD4 and CD8 T cell responses to MAP in experimentally and naturally infected animals. Comparison of the response to PPD and live MAP, however, has revealed a clear difference, especially in the CD8 T cell response. Flow cytometric analysis of the proliferative response of PBMC from experimentally infected calves to JPPD and MAP showed the CD8 memory T cell response to JPPD was low during the first 3 mo post infection. In contrast, the response to MAP was strong and similar to the response of CD4 memory T cells. A comparable difference in the response to JPPD and MAP was observed in PBMC from cows at the late stage of infection. The findings show that further investigation of the mechanisms of immunopathogenesis of paratuberculosis must include a comparison of the response to JPPD and live MAP.

Key Words: *Mycobacterium avium* ssp. *paratuberculosis*, Johnin purified protein derivative, CD8 memory T cell

T156 Tumor necrosis factor-α concentrations from whole blood cultures correlate with isolated peripheral blood mononuclear cell cultures. L. E. Hulbert*[1,2], J. A. Carroll[2], and M. A. Ballou[1], [1]*Department of Animal and Food Sciences, Texas Tech University*, *Lubbock,* [2]*Livestock Issues Research Unit, USDA-ARS*, *Lubbock, TX*.

Many cellular immune assays are impractical because they require labor-intensive isolation of cells from their natural environment. The objectives of this study were to determine the relationship between cell culture supernatant tumor necrosis factor (TNF)-α from isolated peripheral blood mononuclear cells (PBMC) and whole blood (WB) when stimulated with lipopolysaccharide (LPS from *E. coli* O111:B4; 1 and 10 μg/mL for WB; 0.01 and 1 μg/mL for PBMC). Thirty-six dairy heifers (12–16 mo. age) free from any signs of disease were analyzed in

the study. The PBMCs were isolated using a percoll gradient, washed twice with PBS, counted using a hemacytometer, then resuspended to 2 × 10^6 cells/mL in a cell culture RPMI medium with 1% antibiotics, 10% autologous plasma and 5 ng/mL of recombinant bovine interferon-γ. In the WB assay, 200 μL of whole blood were added to 800 μL of RPMI with 1% antibiotics. Samples were incubated with their respective LPS doses for 24-h before supernatants were collected and analyzed for TNF-α using a commercially available sandwich ELISA. Mean TNF-α concentrations from PBMC and WB were moderately correlated (R^2 = 0.40). There were strong correlations between the low and high doses of LPS within each assay (R^2 = 0.67 and 0.87, for isolated PBMC and WB, respectively). The WB data were not correlated with either the number of leukocytes or the percentages of neutrophils (R^2 = 0.15). Inter-heifer coefficients of variation (CV) for the PBMC and WB data were 39.5% and 57.6%, respectively. In another experiment, using samples from 12 Holstein heifers from 3 consecutive days determined that the intra-heifer CVs for PBMC and WB data were 25.33% and 26.51%, respectively. These data indicate the WB assay may serve as a simple but effective ex vivo assay for evaluating bovine pro-inflammatory cytokine synthesis and secretion potential. Additionally, these data elucidate a large population variation, but if a heifer has a reduced response relative to the population at lower LPS concentrations then she will have a reduced response at a higher LPS concentrations, and vice versa.

Key Words: bovine, innate immunity, immune competence

T157 Effect of a *Bacillus*-based direct-fed microbial on cytokine gene expression in the IEC-6 rat intestinal epithelial cell line. C. A. Wehnes*, K. N. Novak, M. Duersteler, E. Davis, and A. H. Smith, *Danisco USA, Inc.*, *Waukesha, WI*.

Enhanced immune maturation was observed in a previous study where calves were treated with a 3-strain *Bacillus*-based direct-fed microbial (DFM). The objective of this study was to examine the immunomodulatory effects of the combination of bacilli strains in an intestinal epithelial cell line. Treatments were vegetative or sporulated bacilli, applied at 1 × 10^7 cfu per well, compared with untreated rat IEC-6 cells (3 × 10^5 cells per well). Expression of interleukin (IL)-1, IL-6, IL-10, tumor necrosis factor-α (TNF-α), and macrophage-inflammatory protein-2 (MIP-2) was analyzed by quantitative PCR and expressed relative to untreated IEC-6 cells. Sporulated bacilli increased IL-6 and MIP-2 gene expression compared with control cells; whereas, vegetative bacilli increased IL-10 gene expression (Table 1). To determine whether the bacilli would affect inflammation caused by LPS, IEC-6 cells were co-incubated with bacilli and 10 ng LPS per well. LPS increased IL-6, TNF-α, and MIP-2 gene expression compared with control cells (Table 1). Vegetative bacilli reduced ($P \leq 0.05$) elevated TNF-α gene expression caused by LPS 4-fold; whereas, sporulated bacilli did not ($P > 0.05$). These data demonstrate that cytokine gene expression differs depending on whether bacilli are vegetative or sporulated in both the presence and absence of LPS stimulation; furthermore, expression of inflammatory cytokines induced by LPS was reduced by vegetative bacilli, but not by spores.

Table 1. Fold change in gene expression, relative to unstimulated cells, of various cytokines in a rat intestinal cell line (IEC-6) exposed to vegetative or sporulated bacilli with or without lipopolysaccharide (LPS) to stimulate inflammation

Bacilli	None	Spores	Spores	Vegetative	Vegetative
LPS	+	–	+	–	+
IL-1B	1.0	–0.5	3.1	1.9	1.0
IL-6	3.3*	3.4*	5.8*	2.4	2.6
IL-10	2.9	1.7	1.5	5.5*	3.3
TNF-α	25.5*	17.7	35.9*	8.3	7.4
MIP-2	43.1*	42.2*	73.0*	9.7	21.4

*Means are significantly different to untreated control cells ($P \leq 0.05$).

Key Words: probiotic, immunity, DFM

T158 Post-weaning intestinal mucin dynamics is influenced by cereal grain type and commensal microbiota. G. Malik*, M. D. Drew, and A. G. Van Kessel, *University of Saskatchewan*, *Saskatoon, SK, Canada*.

Mechanisms by which diet composition and commensal microbiota influence post-weaning intestinal mucin dynamics were studied using conventional and gnotobiotic pigs in a 2x2 factorial design. Caesarean-section derived germ-free pigs (n = 16) were reared in HEPA-filtered isolator units (4 pigs/unit) and fed sterilized sow colostrum (120 mL/pig) followed by infant formula (2:1; formula: water) ad libitum. Conventional (CON) pigs (n = 32) were vaginally delivered and sow-reared. At 14 d of age all pigs were weaned to diets formulated to meet nutrient requirements using corn or wheat/barley. At 24 d of age, pigs were killed and tissue collected at 75% (cranial to caudal) of small intestinal (SI) length. Contamination of germ-free pigs resulted in monoassociation with *Enterococcus faecium*. Acidic, neutral and total numbers of goblet cells were determined in villi and crypts using stained formalin-fixed tissue cross-sections taken at 75% of SI length. Expression of membrane associated mucin genes Muc 1, Muc 13 and secreted type Muc 2 was also determined. Data were analyzed as a 2x2 ANOVA using GLM procedure (GLM, SPSS software v. 12.0, SPSS Inc., Chicago IL, USA) with main effects of cereal grain (corn vs. wheat/barley) and microbial status (conventional vs. monoassociated) plus interactions as sources of variation. Monoassociation reduced ($P < 0.01$) neutral, acidic and total goblet cells in crypts and neutral goblet cell in villi and mucin gene expression. Monoassociation tended to increase ($P < 0.01$) acidic mucin cells in the villi. Interactive effects were observed only as trends ($P < 0.1$) such that Muc 2 expression was lower only in monoassociated pigs fed wheat-barley. In conclusion, as expected, monoassociation markedly influenced intestinal physiology. Limited effects of cereal grain type were observed.

Key Words: microbiota, mucin, swine

T159 Mannan oligosaccharide (MOS) modulates ileal gene expression in pigs experimentally infected with porcine reproductive and respiratory syndrome virus (PRRSV). T. M. Che*[1], R. W. Johnson[1], K. W. Kelley[1], W. G. Van Alstine[2], K. A. Dawson[3], C. A. Moran[3], and J. E. Pettigrew[1], [1]*University of Illinois*, *Urbana,* [2]*Purdue University*, *West Lafayette, IN,* [3]*Alltech Biotechnology Center*, *Nicholasville, KY*.

The objective of this study was to investigate ileal gene expression in control- or mannan oligosaccharide (MOS) (Bio-Mos)-fed pigs with or without porcine reproductive and respiratory syndrome virus (PRRSV) at d 14 postinfection (PI). Weaned pigs (3 wk old) fed 0% or 0.2% MOS

diets were intranasally inoculated with PRRSV or medium at 5 wk old. Total RNA was extracted from ileal tissue including Peyer's patches. Double-stranded cDNA was amplified, labeled, and further hybridized to the Affymetrix GeneChip Porcine Genome Array consisting of 23,937 probe sets representing 20,201 genes. Microarray data were analyzed in R using packages from the Bioconductor project. The MOS x PRRSV interaction and PRRSV main effect were not significant. Therefore, gene expression data from control-fed pigs and MOS-fed pigs were pooled (4 pigs/dietary treatment) for statistical analysis using the LIMMA package. Dietary MOS affected ($P < 0.05$) the expression of thousands of non-immune probe sets (1151 up and 1571 down). Using a 2-fold change difference and *P*-value cutoff of <0.05, we identified that MOS increased the expression of 134 non-immune genes and reduced the expression of 25 non-immune genes. The greatest mRNA upregulation was observed in many important genes involved in absorption of lipid, glucose, and glutamate, cellular protection from endogenous or external proteolysis, and d-amino acid oxidation. With respect to immune genes, MOS altered ($P < 0.05$) the expression of 23 immune probe sets (16 up and 7 down). Using a 2-fold change difference and P-value cutoff of <0.05, MOS upregulated 8 genes and downregulated 5 genes. The greatest increases were seen in genes encoding antimicrobial peptide, intestinal lymphocyte recruiting chemokine, and complement component 5. In short, PRRSV infection did not affect the ileal gene expression at d 14 PI, but feeding MOS to pigs may be beneficial by enhancing intestinal uptake of nutrients and mucosal defense against enteric infection.

Key Words: ileal gene expression, mannan oligosaccharide, nursery pigs

T160 Differential gene expression in subcutaneous and visceral adipose depots in response to lipopolysaccharide in the Sinclair minipig. S. L. Booker*, C. J. Kojima, J. S. Gouffon, and N. Moustaid-Moussa, *The University of Tennessee*, *Knoxville*.

The goal of this study was to elucidate depot-specific differences in transcriptome response of adipose tissue to a pro-inflammatory challenge. Eight intact male Sinclair minipigs (8 mo of age; 32.3 ± 1.9 kg) were non-surgically cannulated and challenged with 15 μg/kg lipopolysaccharide (LPS; n = 4) or saline (n = 4) delivered IM. Blood was collected every 20 min from −60 to +240 min relative to LPS administration. The following day, pigs received a second IM injection of 5 μg/kg LPS or saline, and were killed 2 h post-injection. Tissues including visceral fat (VF) and subcutaneous fat (SQF) were collected, and RNA was isolated for transcriptome analysis (Affymetrix). Only transcripts for which expression differed between treatments by 2-fold or greater with $P < 0.05$ were noted. In SQF, 541 transcripts were downregulated and 1,117 transcripts were upregulated by LPS relative to saline. Upregulated SQF genes included members of the NFκB inflammation cascade: TLR4 (toll-like receptor 4), TICAM2 (toll-like receptor adaptor molecule 2), TLR9 (toll-like receptor 9), and MIF (macrophage migration inhibitory factor). In VF, only 9 transcripts were downregulated and 7 upregulated by LPS relative to saline. Thrombospondin (THBS1) and adiponectin (ADIPOQ) were upregulated in VF, while in SQF, THBS1 was downregulated and ADIPOQ was not affected by LPS. When transcriptomes from SQF and VF of LPS-treated animals were compared, differentially regulated genes mapped to 3 main pathways: the aryl hydrocarbon receptor (AhR) and transforming growth factor β (TGFβ) signaling pathways (both of which are involved in the inflammatory process), and Type 2 Diabetes (T2D). Genes belonging to the AhR and T2D-related pathways were overall upregulated in VF relative to SQF; genes in the TGFβ pathway were downregulated in VF relative to SQF. These results indicate that both SQF and VF depots are metabolically active but are differentially responsive to an immune challenge. Finally, these data further support the role of visceral adipose in inflammatory processes often associated with metabolic disorders.

Key Words: pig, inflammation, adipose

T161 A comparative analysis of galectin-11 gene expression in ruminants. N. Mikiashvili, M. Worku*, and H. Muktar, *North Carolina Agricultural and Technical State University*, *Greensboro*.

The objective of this study was to assess the expression of galectin-11 in neutrophils isolated from cow and goat blood. Galectin-11 isolated form sheep infected with *Haemonchus contortus* is a member of a family of proteins that consists of β-galactoside binding lectins. Host galectins have been shown to be active participants in the recruitment of cells to sites of inflammation and modulating the effector function of inflammatory cells such as the neutrophil. For example they can serve as negative regulators of lipopolysaccharide (LPS) function, to protect the host from endotoxic shock. The role of galectins in the inflammatory response in ruminants has not been defined. A comparative analysis was conducted to determine expression of galectin-11 in neutrophils and to assess the impact of LPS exposure. Three clinically healthy Holstein Friesian cows and 3 Boer goats pasturing at the North Carolina A&T State University farm were used. Blood was collected from the jugular vein in anticoagulant. Neutrophils were isolated from blood samples by differential centrifugation and hypotonic lysis of red blood cells. Isolated neutrophils in PBS were treated with 10 or 100 ng *E. coli* LPS for 15 or 30 min. Total RNA and DNA isolated using Tri-reagent method. Reverse transcriptase PCR was performed using Oligo (dT) primers. Quantitative one step real time PCR was performed with the intercalating dye SYBR Green. Expression level in target samples was calculated using relative quantification with normalization to a reference gene. Amplified products were run on a 2.5% agarose gel with PCR markers. Primers for GAPDH were used as amplification controls and for calculation with Pfaf method. Neutrophils isolated from cow and goat blood expressed galectin-11. Dose of LPS had an effect on overall transcription in neutrophils as indicated by increased RNA concentration. Control (untreated) and LPS treated samples showed expression of target galectin mRNA transcripts. Our study on ruminant neutrophils may help further understanding of the role of galectins in the inflammatory response following host-pathogen interactions.

Key Words: galectin, neutrophil, ruminant

T162 Analysis of a transient receptor potential channel 3 *(Trpc3)* gene in myotonic goats: A potential model for human cerebellar ataxia. M. M. Corley and J. E. Caviness*, *Virginia State University*, *Petersburg*.

Cerebellar ataxia (CA) is a progressive neurological disorder, manifested by poor coordination of the arms and legs, increased difficulty walking or paralysis, slurred speech, depleted hearing and cold feet. Cerebellar ataxia is caused by the degeneration of Purkinje cells of the cerebellum. More than 50 different inherited forms of CA are known, and evidence suggests common pathological pathways (transcriptional regulation, calcium homeostasis) trigger degeneration of Purkinje cells. Myotonia congenita (MC) is an inherited neuromuscular disorder characterized by the inability of muscles to quickly relax after a voluntary contraction. Mutations in calcium cycling genes have been reported to contribute to the myotonic state. It has been shown that a point mutation in a transient receptor potential channel (Trcp) gene that regulates calcium stores, *Trpc3* causes abnormal Purkinje cell development and CA in moonwalker mice. Although genes in the TRPC family have been linked

to MC, the myotonic goat has not been evaluated as a model for CA, nor has the *Trpc3* gene been isolated in goats. Therefore the objective of this study was to identify and characterize the *Trpc3* gene in the myotonic goat. Total RNA was isolated from whole blood samples and purified. Reverse transcriptase polymerase chain reaction (RT-PCR) was performed using cross species primers designed from the human, bovine, and mouse *Trpc3* gene alignment. The RT-PCR product was visualized via agarose gel electrophoresis. The expected 213 bp RT-PCR product was observed, indicating successful amplification of the goat *Trpc3* cDNA. The RT-PCR product was purified and sequenced. The goat *Trpc3* gene showed 95% and 91% sequence homology to the bovine and human *Trpc3* genes, respectively. Identification and analysis of the myotonic goat *Trpc3* gene will provide insight into the etiology of CA in humans and its relationship to MC.

Key Words: myotonic goat, cerebellar, TRPC3

T163 Simultaneous detection and quantitation of anthelmintic resistance and *Haemonchus contortus* infection in grazing goats. M. M. Corley and A. A. Saeed*, *Virginia State University*, *Petersburg*.

The most prominent factor currently limiting meat goat producers is the blood sucking nematode *Haemonchus contortus*. This gastrointestinal parasite costs the global livestock industry billions of dollars per annum in lost production and drug costs. Resistance to all the major anthelmintic classes is now common worldwide, often leading to failure of treatment and control. Standard methods of gastrointestinal nematode infection (GIN) load are fecal egg counts (FEC), FAMACHA eye color chart score (FAM), and packed cell volume (PCV). Thus far, these detection methods provide the presence of GIN infection, but cannot predict whether the animals will be resistant to the administered anthelmintic after standard method detection. In *Haemonchus contortus*, a single nucleotide polymorphism (SNP) of the β-tubulin gene (TTC to TAC), causing a phenylalanine to tyrosine amino acid substitution, has been shown to be involved in many cases of resistance. This study was conducted to demonstrate simultaneous quantitation of *Haemonchus contortus* load and detection of its resistance to benzimidazole based anthelmintics. Goats exhibiting natural resistance or susceptibility to *Haemonchus contortus* infection were selected based on the standard methods described above. Total RNA and genomic DNA were extracted from stool samples and subjected to both genomic DNA PCR and RT-PCR using primers designed to target the *Haemonchus contortus* β-tubulin 1 gene SNP. Pearson Correlation coefficient analysis showed that there was a negative correlation between FAM and PCV ($P < 0.05$), β-tubulin DNA and a very low positive correlation with FEC ($P < 0.05$). The PCV showed strong negative correlation with FAM ($P < 0.05$), FEC ($P < 0.05$) and β-tubulin DNA ($P < 0.05$). These results demonstrate that the opportunity to detect *Haemonchus contortus* infection by standard methods and at the same time determine whether the animal will be resistant to anthelmintic treatment by DNA detection and quantitation will aid in saving the global livestock industry billions of dollars.

Key Words: *Haemonchus contortus*, anthelmintic resistance, DNA quantitation

Meat Science and Muscle Biology: Fresh Meat Quality of Ruminants, Nonruminants and Poultry

T164 Brazilian commercial cuts yield of crossbred beef bulls slaughtered at different body masses. R. Mello*[1], A. C. de Queiroz[2], F. D. de Resende[3], M. H. de Faria[3], P. V. R. Paulino[2], and G. R. Siqueira[3], [1]*Universidade Federal de Santa Maria*, *Santa Maria, RS, Brazil*, [2]*Universidade Federal de Viçosa*, *Viçosa, MG, Brazil*, [3]*Agência Paulista de Tecnologia dos Agronegócios*, *Colina, SP, Brazil*.

The aim of the present experiment was to study the effects of genetic groups and slaughter end points on commercial meat cuts yield. Thirty-six young (20 mo) bulls, 18 crossbred F1 Red Angus × Nellore (1/2 RA 1/2 N) and 18 F1 Blonde D'Aquitaine × Nellore (1/2 BA 1/2 N) were used. The young bulls were feedlot finished and slaughtered at 480, 520 and 560 kg of shrunk body weight (SBW). A completely randomized experimental design of a 2 × 3 (2 genetic groups × 3 slaughter weights) factorial arrangement with 6 replicates was used. The pistola from right side of each carcass was dissected into crude and trimmed cuts and trimmed fat for predicted commercial cuts yield. Data were analyzed with SAS software using initial SBW as a covariate. The table below shows the least squares means of dependent variables. The 1/2 BA 1/2 N young bulls had a higher relative yield (% of pistola) of trimmed top sirloin butt than 1/2 RA 1/2 N young bulls. As the slaughter weight increased, the crude loin and top sirloin cap, and trimmed cube roll, strip loin, and top sirloin cap increased; however the trimmed fat from loin and top sirloin butt increased also. Besides, the interaction between GG and SW was significant ($P > 0.05$) for trimmed fat from tenderloin (data not shown), where the 1/2 BA 1/2 N had increase of trimmed as the slaughter weight increased, while the 1/2 RA 1/2 N outcome was virtually unchanged. Thereby, crossbred F1 Blonde D'Aquitaine × Nellore young bulls and heavier animals produced more saleable meat than F1 Red Angus × Nellore and lighter animals.

Table 1. Least squares means

	Genetic Group (GG)		Slaughter Weight (SW)		
	½ RA ½ N	½ BA ½ N	480	520	560
Crude cuts					
Loin	13.5	13.4	12.1^{b}	14.2^{a}	14.0^{a}
Top sirloin cap	2.5	2.5	2.1^{b}	2.7^{a}	2.6^{a}
Trimmed cuts					
Cube roll	3.7	3.6	3.2^{b}	3.5^{b}	4.1^{a}
Strip loin	6.7	6.8	6.2^{b}	7.3^{a}	6.6^{b}
Top sirloin butt	4.7^{B}	4.8^{A}	4.8	4.7	4.7
Top sirloin cap	1.8	1.9	1.6^{b}	2.1^{a}	2.0^{a}
Trimmed fat					
Loin	3.1	3.1	2.6^{b}	3.4^{a}	3.3^{a}
Top sirloin butt	1.4	1.4	1.2^{b}	1.5^{a}	1.5^{a}

Within a row, means followed by different capital and small letters differ ($P < 0.05$), respectively, among GG and SW by Tukey test.

Key Words: boneless cuts, breeds, saleable meat

T165 Brazilian primal cuts yield of crossbreed beef cattle slaughtered at different end points. R. Mello*[1], F. D. de Resende[2], A. C. de Queiroz[3], M. H. de Faria[2], F. Maldonado[2], and G. R. Siqueira[2], [1]*Universidade Federal de Santa Maria*, *Santa Maria, RS, Brazil*, [2]*Agência Paulista de Tecnologia dos Agronegócios*, *Colina, SP, Brazil*, [3]*Universidade Federal de Viçosa*, *Viçosa, MG, Brazil*.

The objective in this trial was to assess the basic cuts yield of finished crossbred feedlot beef bulls and slaughtered at different body masses. Thirty 6 young (20 mo) bulls, 18 crossbred F1 Red Angus × Nellore (1/2 RA 1/2 N) and 18 F1 Blonde D'Aquitaine × Nellore (1/2 BA 1/2 N) were used. The young bulls were finished on feedlot and slaughtered at 480, 520 and 560 kg of shrunk body weight (SBW). A completely randomized experimental design in a 2 × 3 (2 genetic groups × 3 slaughter weights) factorial arrangement with 6 replicates was used. Primal cuts were predicted for each carcass using separation (forequarter, thin flank, pistola) on the right side of the carcass. Data were analyzed with SAS software using initial SBW as a covariate. The table below shows the least squares means of Brazilian primal cuts yield. Cuts yield ranged on average from 40.9 to 42.5% of forequarter, 11.2 to 11.9% of thin flank and 45.7 to 47.8% of pistola. There were no effect ($P > 0.05$) of genetic group (GG), slaughter weight (SW) and its interaction (GG × SW) on relative yield (%) of the primal cuts. Thus, finishing of crossbred F1 Blonde D'Aquitaine or Red Angus versus Nellore young bulls on feedlot and slaughter at 480, 520 and 560 kg produced carcasses with the same primal cuts yield.

Table 1. Least squares means

	Genetic Group (GG)		Slaughter Weight (SW)		
	½ RA ½ N	½ BA ½ N	480	520	560
Forequarter, %	41.7	41.1	41.3	40.9	42.0
Thin flank, %	11.7	11.5	11.4	11.6	11.8
Pistola, %	46.6	47.4	47.3	47.5	46.2

Key Words: bone-in cuts, feedlot, young bulls

T166 Portions of high value cuts in carcasses of different beef cattle in the Czech Republic. J. Riha*[1], J. Bezdicek[1], M. Homola[2], E. Vacatko[2], and J. Subrt[3], [1]*Agrovyzkum Rapotin Ltd.*, *Vikyrovice, Czech Republic*, [2]*Research Institute for Cattle Breeding, Ltd.*, *Vikyrovice, Czech Republic*, [3]*Mendel University in Brno*, *Brno, Czech Republic*.

The aim of this study was to assess the effect of breed on highly valued parts of carcasses. The study was carried out with 45 Blonde d'Aquitaine, 40 Piemontese, 48 Hereford and 52 Galloway bulls. After slaughter, the following cuts were evaluated: round, strip loin, tender loin and shoulder blade (boneless). The age of slaughtered animals, and their corresponding BW ranged from 312 to 699 d and 395.2 to 811.9 kg, respectively. Highly valued meat was weighed (in kg) and presented in percent of carcass halfbodies (HC). General regression models (GRM) design with breed as fixed categorical and slaughter age and BW as fixed continuous effects were used for statistical analysis. Coefficients of determination calculated for each model ranged from 0.173 (strip loin) to 0.587 (tender loin). According to the model, round percentage was reduced (*$P < 0.05$; **$P < 0.001$) in the following ascending order: Piemontese (22.82%) > Blonde d'Aquitaine (20.85%) > **Hereford (17.64%) > Galloway (16.85%). For strip loin, tender loin and boneless shoulder blade the order was Blonde d'Aquitaine (4.41%) > Piemontese (4.36%) > Galloway (4.08%) > *Hereford (3.58%); Piemontese (1.83%) > Blonde d'Aquitaine (1.69%) > **Galloway (1.32%) > **Hereford (1.71%) and Piemontese (8.59%) > Blonde d'Aquitaine (8.01%) > *Galloway (7.38%) > **Hereford (6.51%), respectively. The highest percentage of cut with regard to weight and age of bulls was found for Piemontese bulls. From this screening study, it is evident that Piemontese and Blond d'Aquitaine bulls (which however have also more subtle

constitution) have a higher portion of valued cuts than extensively kept ones (Hereford and Galloway) with regard to model correction of weight and age. Selected designed models (e.g., for tender loin) seem to be suitable for prediction of high value cuts portion with usage of the described effects.

Key Words: beef cattle, high value cuts, prediction of cutting parts using GRM

T167 Predicting retail product yield of Nellore bulls using live animal measurements. S. L. Silva*[1,3], R. C. Gomes[1], J. U. Tarouco[2], M. N. Bonin[1], P. R. Leme[1], and J. B. S. Ferraz[1], [1]*Universidade de Sao Paulo (FZEA)*, *Pirassununga, SP, Brazil*, [2]*Universidade Federal do Rio Grande do Sul*, *Porto Alegre, RS, Brazil*, [3]*FAPESP*, *Sao Paulo, SP, Brazil*.

Information regarding retail product yield (RPY) for beef cattle is of great importance for genetic evaluation programs based on carcass merit. Equations using carcass or live animal measurements to predict RPY have been developed mainly based on steers data with little information about its use for young bulls that are mostly used in genetic evaluation programs. Therefore, the aim of this work was to evaluate the accuracy of RPY estimates in young Nellore bulls obtained by using an equation originally developed in our laboratory based on data of Nellore steers. Thirty-eight Nellore young bulls (23 mo old) finished in feedlot (485 ± 37kg of shrunk body weight (SBW) at slaughter) were ultrasound scanned for 12th-rib Longissimus muscle area (ULMA) and backfat thickness (UBFT), and rump fat (URF) determinations, within 3–5 d prior slaughter. The left side of each carcass was deboned into retail cuts according to Brazilian standards, with the excess of fat trimmed to approximately 5 mm. Predicted retail product weight (RPW, kg = –36.28367 + 0.36485*SBW – 0.74324*ULMA; $R^2 = 0.93$; SEP = 7.36) and percentage (RPP, % = 70.38312 – 0.00716*SBW + 0.07257*ULMA – 0.10939*UBFT – 0.15077*URF; $R^2 = 0.34$; SEP = 1.24) were calculated and compared with actual RPW and RPP. The averages of actual and predicted RPW and RPP averaged 196.6kg and 192.4kg, and 71.7% and 70.8%, respectively. Prediction equations underestimated both RPW (bias = –4.2kg) and RPP (bias = –0.91%). Coefficients of determination between predicted and observed RPW and RPP were 0.77 and 0.44, respectively. These results suggest that prediction equations developed from steers can be used with similar accuracy to predict RPY in Nellore bulls. Further studies including a greater number of RPY data in young bulls are necessary to verify the accuracy of these models and their usefulness for use in genetic evaluation programs.

Key Words: beef, ultrasound, zebu

T168 Mixed model analysis of non-linearity between cooking loss and aging time plus other effects. A. Dufek*[1], J. Subrt[2], J. Simeonovova[2], and M. Homola[3], [1]*Research Institute for Cattle Breeding, Ltd.*, *Vikyrovice, Czech Republic*, [2]*Mendel University in Brno*, *Brno, Czech Republic*, [3]*Agriresearch Rapotin Ltd.*, *Vikyrovice, Czech Republic*.

We used the package nlme in the R software for description and statistical analysis of non-linear relationship between cooking loss and aging time. The relationship was described by the asymptotic regression model "cooking loss = Asym+(R0-Asym) exp[-exp(lrc)Time]" with 3 physically meaningful parameters: R0 = the response at slaughter time, lrc = logarithm of the rate constant and Asym = a response that approaches a horizontal asymptote. After the basic model was formed, we put random effects into the model at nested levels: i) subject (animal), ii) subjects within sires and iii) sires within years. Age, fattening system (extensive vs. intensive), length of hind quarter, weight of carcass, ratio between length of fore and hind quarter, weight proportion of the LM in the carcass and status (bulls, steers) were put into the model as fixed effects. We selected the effects to test the hypotheses from the aspects of beef production and anatomy since the LM is of high value as well as important for constitution. The LM was divided into 4 samples and individually vacuum packed. One of the samples was analyzed 48 h post-mortem. The other 3 samples were stored at 2–4°C for 16, 30 and 44 d. Cooking loss was determined by weighing the samples before and directly after cooking in a water bath at 70°C for 1 h. Percentage of cooking loss was calculated. Values of the parameters for the basic model including all animals (n = 46) were R0 = 25.33%, lrc = −2.38, Asym = 34.12%. The random effects analyses showed that only the subject affected the Asym and R0 significantly (tested with AIC). Analyses of fixed effects produced following results: higher values for age resulted in higher Asym ($F = 15.15$, $P = 0.0002$) and R0 ($F = 3.59$, $P = 0.06$). Higher values for length of hind quarter resulted in lower Asym ($F = 5.83$, $P = 0.017$). The Asym of extensively fattened animals was 3.88% higher ($F = 5.05$, $P = 0.026$) and the R0 −1.21% lower than for intensively fattened animals. Steers had −2.57% lower Asym than bulls ($F = 3.99$, $P = 0.047$). The results revealed that fattening system, age and length of animals significantly affect cooking loss in aged beef.

Key Words: mixed, non-linear, beef

T169 Epinephrine-induced MMP expression in muscle cells is uncorrelated with AMPK signaling. M. C. Cha and P. P. Purslow*, *University of Guelph*, *Guelph, Ontario, Canada*.

Acute stress at or around the point of slaughter is known to impact on post-mortem development of pH and subsequent meat quality. One signaling pathway involved in the stress response is AMP-activated protein kinase (AMPK), which regulates energy metabolism in muscle and post-mortem glycolysis. Elevated levels of epinephrine (adrenaline) in the circulation are also known to increase matrix metalloproteinase (MMP) expression in muscle. MMPs are proteases (MMPs) that control the degradation of connective tissue. Post-mortem degradation of intramuscluar connective tissue by MMPs could affect sub sequent meat toughness. Using a cell culture model, we have therefore investigated: (1) whether epinephrine increases the expression of MMPs from muscle cells and fibroblasts isolated from muscle, and (2) any relationship changing MMP expression may have to AMPK signaling. Mouse skeletal fibroblasts (NOR-10) and myoblasts (C2C12) in plate culture with DMEM medium were treated with or without 11 nmol/L or 55nmol/L doses of epinephrine for 2 or 6 hours. The intracellular and secreted expression of MMPs was determined by zymography and AMPK expression was examined by immune blotting. Intracellular MMP-3 expression was increased in muscle cells by both the high and low doses of epinephrine at longer (6 hour) treatment times. Intracellular MMP-2 and MMP-13 expression were also amplified by the lower dose, longer time epinephrine treatment in the myoblasts. AMPK expression was elevated only at the shorter treatment time at both epinephrine dose levels and in both cell lines. At the higher epinephrine dose level only and at short incubation times, fibroblasts also show transient expressions of MMP-2 and −13.

The time-course of MMP expression from muscle cells is not well correlated to the time-course of AMPK activity. Fibroblasts respond only to the higher level of epinephrine and on a much shorter timescale, better correlated to AMPK activity.

Key Words: muscle, proteolysis, collagen

T170 Measurement of purge protein composition as an indicator of beef tenderness. B. C. Bowker*, J. S. Eastridge, and E. W. Paroczay, *USDA-ARS*, *Beltsville, MD*.

The objective of this study is to determine if the protein composition of the purge moisture collected from vacuum-packaged beef can be used as a potential indicator of meat tenderness. Frozen beef striploins (n = 12) were each divided into 3 sections which were thawed, vacuum packaged, and aged at refrigerated temperatures. After 0, 7, and 14 d of aging, purge moisture was collected from the vacuum packages and analyzed for protein content using a biuret assay and protein composition using SDS-PAGE. Steaks were also removed at 0, 7, and 14 d of aging for Warner-Bratzler shear force (WBS) determination. With aging from 0 to 14 d, WBS decreased ($P < 0.0001$) from 5.8 to 3.4 kg shear force. Purge losses at d 7 and 14 were 5.8% and 8.4%, respectively. The amount of purge loss between 0 and 14 d was significantly correlated (r = −0.3707) to the decrease in WBS from d 0 to 14. The protein content of the purge moisture collected after 0, 7, and 14 d was similar, however, the protein composition of the purge changed with aging. SDS-PAGE analysis of collected purge samples demonstrated that 10 protein bands increased ($P < 0.05$) in relative abundance with aging and 4 protein bands decreased ($P < 0.01$) with aging. The relative abundance of 5 protein bands, ranging from 65 to > 250 kDa, were negatively correlated to WBS (r = −0.5072 to −0.6759). The relative abundance of the 45 and 38 kDa protein bands were positively correlated to WBS (r = 0.5700 and 0.6215, respectively). Furthermore, the relative abundance of the 45 kDa protein band measured in the purge moisture collected at d 0 was significantly correlated to WBS at d 14 (r = 0.7692). While these data do not indicate a cause and effect relationship between sarcoplasmic proteins and tenderness, the data suggest that purge protein composition may be an indirect indicator of WBS and that the water-soluble protein fraction of beef muscle may be useful in the development of rapid, non-invasive methodologies for predicting beef tenderness.

Key Words: beef tenderness, purge, protein composition

T171 Effect of oxidative stress on collagen turnover by bovine intramuscular fibroblasts. A. C. Archile*[2,1], S. P. Miller[1], I. B. Mandell[1], M. C. Cha[1], and P. P. Purslow[1], [1]*University of Guelph*, *Ontario, Canada*, [2]*University of Zulia*, *Maracaibo, Venezuela*.

Intramuscular collagen is responsible for the background toughness in cattle. Vitamins E and C may increase collagen turnover, but handling of cattle may reduce vitamin concentrations in muscles, impeding the removal of reactive oxygen species (ROS) and leading to what is known as oxidative stress. Fibroblasts synthesize collagen and regulate its turnover by the production of matrix metalloproteinases (MMPs) responsible for collagen degradation. The aim of this work was to study the effect of oxidative stress on the ability of intramuscular fibroblasts to turnover old collagen and synthesize new collagen. Fibroblasts were isolated from *longissimus dorsi* (LD) and *semitendinosus* (ST) muscles from a yearling animal and grown in DMEM, 10% serum, 5% CO_2. Fibroblasts were treated for 24 h with 1) 0.1 or 0.01 mU/mL xanthine oxidase /500 μ*M* xanthine (X/XO), and 2) 0.5 or 5 μ*M* of hydrogen peroxide (H_2O_2). Control group cells received no treatment. MMP-2 activity secreted into the media was analyzed by gelatin zymography. Total collagen synthesis (TC) in cell lysates was measured using the collagen Sircol assay. Analysis included 2-way ANOVA, Fisher's LSD and Pearson bivariate correlation. There was a different pattern in the response of fibroblasts from the 2 muscles to ROS. Concentrations of 0.01 mU/mL X/XO and 5 μ*M* H_2O_2 induced ($P < 0.05$) the activation of MMP-2 in LD cells, while for ST cells no effect was observed for any treatment. No effect was observed in the inactive Pro-MMP-2 precursor levels for any muscle and treatment. In general, ROS slightly lowered TC, more so in LD-derived cells than in ST cells. No relation ($P > 0.05$) between Pro-MMP-2 and TC was found for cells from either muscle, while for LD cells, MMP-2 activity showed a negative correlation ($P < 0.05$) with respect to TC. Oxidative stress may decrease net collagen turnover in intramuscular fibroblasts and this could lead to decreased collagen solubility in some muscles. Thus, oxidative stress is an environmental/dietary factor that might affect meat quality.

Key Words: oxidative stress, collagen turnover, meat quality

T172 Phenotypic differences in MMP activity between fibroblasts from three beef muscles. A. C. Archile*[2,1], M. C. Cha[1], and P. P. Purslow[1], [1]*University of Guelph*, *Ontario, Canada*, [2]*University of Zulia*, *Maracaibo, Venezuela*.

It has been found that muscles from the same beef carcass may respond differently to the same stimulus. This might cause difficulties when looking for a production system to render meat tender. The aim of this work was to study phenotypic differences in the expression of matrix metalloproteinases (MMP) among intramuscular fibroblasts from 3 beef skeletal muscles. To our knowledge intramuscular fibroblasts from beef animals have not previously been characterized. Fibroblasts were isolated from *longissimus dorsi* (LD), *semitendinosus* (ST) and *sternomandibularis* (SMD) muscles from a yearling animal and grown in DMEM + 10% FCS. All cultures were serially sub-cultured and cell behavior studied from passages 1 to 15. Cell lifespan and doubling times were evaluated for each cell line. After reaching 80% confluence, cells were supplied with fresh DMEM for 24 h. Then, media were collected and analyzed for MMP-2 activity by zymography. Data were analyzed by 2-way ANOVA and Fisher's LSD. At all passages, LD-derived cells had the largest ($P < 0.0001$) doubling time in comparison to SMD and ST; cells from these last 2 muscles also differed significantly ($P < 0.001$). Cultures derived from ST displayed longer ($P < 0.05$) lifespan compared with cells from the other muscles. Cells from ST presented higher ($P < 0.0001$) levels of active MMP-2 in comparison to LD and SDM, which were also different ($P < 0.0001$) from each other. No statistical differences ($P > 0.05$) in pro-MMP-2 expression were found between any cell lines; however, the total expression of this enzyme was higher for ST. These results suggest that fibroblasts from different locations are phenotypically different and so may respond differently to the same growth or nutrition stimulus in vivo, causing differences in accumulation and maturity of collagen, and hence its degree of turnover, which may affect meat tenderness. These findings are of significance when selecting a strategy for improving meat tenderness by manipulation of animal growth, as a strategy applied to the whole animal may work for some muscles but not for others.

Key Words: fibroblast heterogeneity, collagen turnover, matrix metalloproteinases

T173 Myofibril fragmentation index of the longissimus muscle of Senepol and Charolais crossbred bulls. L. del Valle-Mercado*, A. Casas, D. Cianzio, M. Pagan, and G. Ortiz-Colón, *University of Puerto Rico*, *Mayaguez, Puerto Rico, United States*.

The objective of this experiment was to determine whether there was a difference in the Myofibril Fragmentation Index (MFI) of longissimus muscle (LM) samples obtained from Senepol (n = 12) and Charolais (n = 14) crossbred bulls. Calves were weaned at 9 mo (266.5 kg) and then raised under grazing conditions until harvest at 22 mo (499.6 kg). From each bull 2 LM subsamples were cut in 1 cm^2 pieces and homogenized using a Polytron PT1600E homogenizer (30,000 rpm) in cold (4°C)

homogenizing buffer (100 m*M* KCl; 7 m*M* KH_2PO_4; 18 m*M* K_2HPO_4 ; 1 m*M* EDTA; 1 m*M* NaN_3 [pH 7.0]). The Biuret reagent assay was use to determine LM homogenates protein concentrations. All muscle homogenates were diluted to a constant protein concentration of 0.5 mg/mL of homogenization buffer. Subsequently, the absorbance of each LM homogenate was determined at a specified wavelength of 540 nm (Thermo Spectronic Genesys). Absorbance results were multiplied by 200 to determine MFI values. The obtained MFI values were different among crossbreds ($P = 0.012$). Senepol crossbred bulls showed MFI values of 43.89 (SE 4.52) while Charolais crossbred bulls showed MFI values of 30.09 (SE 2.77). Because previous studies have associated higher MFI values with more tender meat, our data suggests that Senepol crossbred bulls might have more tender meat than Charolais crossbred bulls.

Key Words: beef tenderness, MFI, Senepol

T174 Effect of brine enhancement and mechanical tenderization on consumer sensory characteristics of cow semimembranosus steaks. J. M. Popowski*, R. B. Cox, T. J. McNamara, and P. Nelson, *University of Minnesota, Twin Cities*, *St. Paul*.

The purpose of this research was to evaluate the effect of brine enhancement by means of mechanical tenderization on an underutilized cut from the dairy cow carcass. Additionally considered was a comparison of enhanced and tenderized dairy cow beef to traditional fed beef. Beef was evaluated from both dairy cull (CUL) carcasses and fed (FED) beef carcasses. Processing treatments included a control (CON) and a brine enhancement by means of mechanical tenderization (BRN) of the semimembranosus muscle. Beef semimembranosus from both CUL and FED beef carcasses were obtained from the University of Minnesota Meat Laboratory and cut into roasts (60 roasts, 5 per each of 3 replications, approximately 1kg each). FED and CUL roasts were then randomly assigned to CON and BRN treatments. BRN roasts were placed in a commercial meat tumbler with 15% (w/w) brine (water and sodium tripolyphosphate) to create an enhanced roast with a phosphate level of 0.2%. Roasts and brine were tumbled for 30 min. BRN and CON roasts were then individually vacuum packaged and allowed to equilibrate at 4°C for 24 h before being cut into steaks (2.54 cm thick), individually vacuum packed, and frozen (−20°C) until further use. Steaks were thawed at 4°C for 36 h and cooked in an electric oven (180°C) to an internal temperature of 71°C. Each cooked steak was then cut into cubes (1cm –1cm – 1 cm). Sensory evaluation was carried out by an untrained consumer panel. One–hundred–12 consumers rated overall liking, flavor liking, texture liking, off-flavor, juiciness, and toughness of sample from all treatments and replications. BRN scores were higher than CON for overall liking ($P < 0.001$), flavor liking ($P = 0.002$), and texture liking ($P < 0.001$) for CUL steaks, but not FED. BRN scores were lower than CON for juiciness ($P = 0.001$) and off-flavor intensity ($P = 0.01$) in CUL steaks, but not FED. Overall liking ($P < 0.001$) and texture ($P < 0.001$) scores were higher for FED steaks compared with CUL. Results indicate there may be potential to market whole-muscle products from the cow round with mechanical tenderization and enhancement.

Key Words: beef, cull, enhancement

T175 Fatty acid composition including *cis*-9, *trans*-11 CLA of cooked ground lamb. G. Davila-El Rassi*[1], V. Banskalieva[1], and M. Brown[2], [1]*R. M. Kerr Food and Agricultural Products Center, Oklahoma State University*, *Stillwater,* [2]*USDA-ARS, Grazinglands Research Laboratory*, *El Reno, OK*.

Little information is available on effect of cooking on health-promoting fatty acids (FA) such as *cis*-9, *trans*-11 conjugated linoleic acid (CLA) and ω-3 polyunsaturated fatty acids (PUFA). The objective of this study was to examine the impact of broiling per se on the FA composition of ground lamb of 2 different muscles with special emphasis on CLA. Samples were prepared from trimmed, ground steaks of m. *Longissimus lumborum* (LL) and m. *Semimembranosus* (SM) from forage-fed Suffolk × Katahdin lambs. Patties were broiled in a conventional oven, at 205°C, for 6.15 min on each side to internal temperature of 71°C. Raw and cooked patties were subjected to proximate and FA analyses. Data were analyzed by mixed model procedures with linear models including fixed effects of treatment (raw vs. cooked, subunit), muscle type (sub-subunit) and treatment by muscle type. After broiling fat content increased from 2.83 to 4.98% ($P < 0.001$), and from 3.89 to 6.04% ($P < 0.001$), respectively for SM and LL patties, whereas no changes in levels of total saturated, monounsaturated and polyunsaturated FA were observed for either muscle type. No treatment differences were found in percent CLA (0.53–0.58%, raw vs. cooked) or CLA as mg/g fat in SM (6.45–6.72, raw vs. cooked) and in LL (6.2–5.9, raw vs. cooked) patties. However, content of CLA as mg/100 g of cooked lamb increased from 18.1 (raw) to 33.2 ($P < 0.01$) and from 24.05 (raw) to 35.8 ($P < 0.001$), respectively for SM and LL patties. Average over muscles, a trend ($P < 0.1$) for lower proportion of vaccenic acid in cooked (1.64%) vs. raw meat (2.15%) was observed. The ratio ω-6 PUFA/ω-3 PUFA slightly increased from 5.7 (raw) to 6.0 (cooked) ($P < 0.01$) and from 5.8 (raw) to 6.1 (cooked) ($P < 0.01$), respectively for SM and LL patties. Results imply that broiling did not cause thermal degradation of CLA levels and that a serving portion (100g) of cooked lamb provides over 34 mg of CLA. Despite the small changes of ω-6 PUFA/ω-3 PUFA ratio broiling could be considered as a method preserving the nutritional value of lamb.

Key Words: lamb, cooking, fatty acids

T176 Effects of maternal metabolizable protein supplementation during late gestation on ovine fetal muscle calpain and calpastatin activities. J. D. Magolski*[1], W. L. Keller[1], T. M. Jeske[1], C. A. Schwartz[1], L. A. Lekatz[1], J. D. Kirsch[1], C. S. Schauer[2], K. A. Vonnahme[1], and K. R. Maddock-Carlin[1], [1]*North Dakota State University*, *Fargo*, [2]*Hettinger Research Experiment Center*, *Hettinger, ND*.

To investigate the effects of maternal supplementation of MP during late gestation on calpain and calpastatin activities in fetal muscle, multiparous ewes (n = 30) were randomized to receive 75% (LOW), 100% (CON), or 125% (HIGH) of MP requirements from d 100 until d 130 of gestation. On d 130, ewes were slaughtered, and fetuses were necropsied. Longissimus thoracis (LT) and semimembranosus (SM) were collected (20 g) and analyzed for calpastatin activity by casein assay and calpain activity by casein zymograms. μ-Calpain autolysis was evaluated by Western blotting. Ewes carried singletons and twins; however, only singletons were analyzed. Calpastatin activity did not differ ($P \geq 0.21$) among treatments. Casein zymograms showed no treatment differences ($P \geq 0.80$) for μ-calpain or m-calpain activities. Autolysis of μ-calpain in the SM was greater in the HIGH group compared with that in the CON group as indicated by smaller percentage of the ($P = 0.01$) 80 kDa band. Calpastatin activity and specific activity were greater ($P < 0.01$) in the LT (4.02 units/mL ± 0.10; 58.48 units/mg ± 1.51) than in the SM (3.31 units/mL ± 0.10; 47.07 units/mg ± 1.51). Additionally, autolysis was occurring at a greater ($P < 0.01$) extent in the SM than in the LT as indicated by the disappearance of the 80 kDa band (21.72 vs. 27.51 ± 1.84) and the accumulation of the 76 kDa autolysis product (46.27 vs. 39.77 ± 1.66). Therefore, maternal supplementation of MP

during late gestation did not affect calpastatin activities in fetal skeletal muscle, but increased μ-calpain autolysis in HIGH compared with CON may indicate differences in protein accretion. However, there were differences in calpain and calpastatin activities between muscles during late gestation with the LT having greater calpastatin activity and less μ-calpain autolysis, possibly indicating a difference in rate of protein accretion between muscles.

Key Words: fetal muscle, metabolizable protein, calpain

T177 Hyperplastic muscle growth occurs from birth to weaning in pigs. J. M. R. López[1], C. Pardo[2], and G. Bee*[2], [1]*Unidad de nutrición animal, Estación Experimental del Zaidín (CSIC)*, *Granada, Spain*, [2]*Agroscope Liebefeld Posieux, Research station ALP*, *Posieux, Switzerland*.

Pig myogenesis is a biphasic phenomenon with the sequential formation of 2 generations of fibers termed primary (P) and secondary (S) fibers. Currently, it is believed that total number of fibers (TNF) is fixed at birth. However, there are indications that at birth between P and S fibers very-small diameter fibers containing embryonic and fetal myosin heavy chain isoforms exist. They represent a different population of myotubes, designated tertiary myotubes and might contribute to hyperplastic growth after birth. The goal of this study was to establish if TNF remains constant from birth to weaning. For the trial 8 pairs of Swiss Large White female littermates with a similar birth weight (1.41 ± 0.113 kg; $P = 0.82$) were used. One piglet of each pair was sacrificed either at birth or at weaning at d 28 of age (BW: 6.93 ± 0.527 kg). Subsequently, internal organs and the semitendinosus (ST) muscles were collected and weighed. Histological analyses were performed on the ST using the mATPase staining procedure after pre-incubation at pH 10.2. This allowed identifying the muscle cross-sectional area, TNF, number of P and S fibers and the S/P ratio of the dark (STD) and the TNF of the light (STL) portion of the ST. Relative to slaughter weight, the spleen and ST were 90 and 26% heavier ($P < 0.01$), respectively, whereas lungs, liver, heart and kidneys were 17, 16, 30 and 24% lighter ($P < 0.06$) at weaning than at birth. From birth to d 28 of age TNF increased in the STD (151020 vs. 235191; $P < 0.01$) but not in the STL (395497 vs. 405836; $P = 0.83$). The increase resulted from both a greater number of P (4597 vs. 6605; $P < 0.01$) and S fibers (146423 vs. 228586; $P < 0.01$) with no changes in the S/P ratio (32 vs. 35; $P = 0.25$). Overall the TNF of the ST was only numerically greater (546517 vs. 641028; $P = 013$) in weaned than newborn piglets. This preliminary data suggest that the TNF of parts of muscles are not fixed at birth. Further studies needs to determine whether the potential of an increase in TNF can be already observed in the muscles of new born pigs and whether the development of these fibers can be stimulated during postnatal growth.

Key Words: muscle development, semitendinosus, pigs

T178 Relationship between average litter weight and intralitter weight variability on myogenesis in newborn piglets. C. Pardo[1,2], M. Kreuzer[2], and G. Bee*[1], [1]*Agroscope Liebefeld Posieux*, *Posieux, Switzerland*, [2]*ETH Zurich, Institute of Plant, Animal and Agroecosystem Sciences (IPAS)*, *Zurich, Switzerland*.

A high variability in total litter birth weight (BtW) has been reported in common litter sizes (10–15 piglets). Limitations in uterine efficiency may affect the development not only of low BtW piglets but also that of the entire litter. The aim of this study was to elucidate the relationship between average litter BtW and intra-litter variability on semitendinosus (ST) development in newborn piglets and postnatal growth from birth to weaning. From multiparous sows, 7 litters with a high (H: > 1.7 kg) and 7 litters with a low (L: < 1.3 kg) average litter BtW were selected. At farrowing 2 females/litter were sacrificed: from H-sows those with the medium (HM) and lowest (HL) BtW and from the L-sows those with the medium (LM) and highest (LH) BtW. The mATPase staining after pre-incubation at pH 4.3 or 10.2 was used to identify muscle cross-sectional area (CSA), total number of fibers (TNF), number of primary and secondary fibers of the dark and light (STL) portion of the ST. ADG during lactation and BW at weaning of the remaining piglets were determined for each gender. Data were analyzed with PROC MIXED using BtW groups as fixed factor. Three contrasts were established: HM vs. LM and LH, respectively, and HL vs. LH. For H- and L-sows the realized average litter weight/piglet was 1.74 and 1.23 kg (13.3 and 14.8 piglets/litter, respectively). Compared with H-sows, female piglets from L-sows grew slower (236 vs. 293 g/d; $P < 0.01$) and were lighter at weaning (8.54 vs. 10.34 kg; $P < 0.04$). At birth HM-piglets were heavier than LM- and LH-piglets (1.73 vs. 1.27 and 1.57 kg; $P < 0.07$) whereas BtW was similar in HL- and LH-progeny (1.42 vs. 1.57 kg; $P < 0.15$). The STL and by that the ST from HM piglets was larger (CSA: STL = 58 vs. 44 mm^2; ST = 85 vs. 67 mm^2; $P \leq 0.05$) and tended to have more TNF (STL = 380 vs. 308 × 10^3; ST = 540 vs. 467 × 10^3; $P < 0.10$) than LM-piglets. In conclusion, low gestation efficiency resulting in a lower total litter weight not only affects the development of low but also of medium BtW offspring. Interestingly, female but not male progeny from L-sows grew slower during lactation than those from H-sows.

Key Words: birth weight variation, myogenesis, litter weight

T179 Influence of genotype and slaughter weight on carcass and meat quality of Iberian pigs. M. Sánchez*[1], J. Viguera[1], M. I. Gracia[1], J. Peinado[1], A. Robina[2], and J. Ruiz[2], [1]*Imasde Agroalimentaria S.L.*, *Madrid, Spain*, [2]*Universidad de Extremadura*, *Cáceres, Spain*.

A total of 48 pigs (50% castrated males and 50% castrated females) were used to evaluate 2 different genotypes: Duroc1 × Iberian (DR1×IBE) and Duroc2 × Iberian (DR2×IBE) and 2 slaughter weights: 145 and 155 kg BW on carcass traits, composition and color of meat, and fatty acid profile of subcutaneous fat. Data were analyzed as a completely randomized design using PROC GLM of SAS. The model included the terminal sire genotype and slaughter weight as main effects. DR1×IBE pigs showed higher backfat thickness than DR2×IBE pigs (52.7 vs. 46.3 mm; $P < 0.05$). However, no ($P > 0.05$) differences between genotypes were found for carcass, ham, shoulder and loin yields, in the composition or the color of meat and the fatty acid profile of the subcutaneous fat. As expected, pigs slaughtered at 155 kg BW had greater backfat thickness (53.7 vs. 45.3 mm; $P < 0.01$) and carcass yield (81.52 vs. 79.80%; $P < 0.01$), but lower ham and shoulder yields (17.95 vs. 19.16% and 11.64 vs. 12.37%, respectively; $P < 0.01$) than pigs slaughtered at 145 kg BW. Loins from heavier pigs tended to have higher redness value (10.05 vs. 9.26; $P = 0.07$) than lighter pigs, but no differences were observed in lightness and yellowness of loin. Finally, the increase in slaughter weight decreased the level of saturated fatty acids (33.78 vs. 32.14%; $P < 0.01$) and increased that of the monounsaturated fatty acids (54.29 vs. 55.68%; $P < 0.01$) in the subcutaneous fat. Our data indicate that an increase in the slaughter weight of Iberian pigs from 145 to 155 kg BW improved carcass yield and positively altered the fatty acid profile toward a more unsaturated subcutaneous fat.

Key Words: Iberian pig, carcass traits, fatty acid profile

T180 Effect of birth parity and sex on carcass traits and meat quality characteristics in crossbred pigs. G. D. Kim*[1], J. Y. Jeong[2], K. Y. Seo[1], E. Y. Jung[1], H. S. Yang[1], and S. T. Joo[1], [1]*Division of Applied*

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The effect of birth parity and sex on carcass traits and meat quality characteristics were studied on crossbred (Landrace × Korean native pig) pigs, with age ranging between 182 and 195 d. 182 males and 158 females of pigs from 3 different birth parities were investigated. The females and third parity pigs grew slower than males and first or second parity pigs. However, there are no significant ($P > 0.05$) differences in carcass weight (kg) among the different sexes and birth parities. Backfat thickness (mm) at 3 points (4th-5th thoracic vertebrae, 11th-12th thoracic vertebrae and vertebrae thoracic-lumber vertebrae) were higher in females (33.8, 29.3, and 27.0mm, respectively) than in males (31.1, 24.8, and 22.6mm, respectively) ($P < 0.01$). The third parity pigs had higher loin eye area (22.10cm2) and lower backfat thickness (30.16mm) at 4th-5th thoracic vertebrae than the others ($P < 0.05$). The males and third parity pigs had higher pH value (5.83) at 24h postmortem ($P < 0.05$). Lightness (L* value) and yellowness (b* value), intramuscular fat content (%), and sarcomere length (Î1/4m) were higher in females than in males, while moisture content (%) was higher in males ($P < 0.05$). Intramuscular fat content (3.41%), redness (a* value, 7.97) and yellowness (b* value, 3.30) were higher in third parity pigs than in the other parities, however, moisture content (73.22%) and drip loss (1.09%) were lower in third parity pigs ($P < 0.05$). The results suggest that females and third parity pigs which exhibited the lowest growth performance, have higher fat content and lower moisture content.

Key Words: birth parity, sex, crossbred pig

T181 Carcass quality of pigs vaccinated against gonadotropin releasing factor compared to surgically castrated males and gilts from two different sire lines. J. I. Morales[1], M. P. Serrano*[2], L. Cámara[2], J. D. Berrocoso[2], J. P. López[1], and G. G. Mateos[1], [1]*Copiso S.A.*, *Soria, Spain*, [2]*Universidad Politécnica de Madrid*, *Madrid, Spain*.

A total of 360 pigs was used to study the influence of gender (immunocastrated males, IM; surgically castrated males, CM; intact females, IF) and terminal sire line (Top York; Tempo) on carcass and meat quality of pigs slaughtered at 125 kg BW. The female line used was Large White × Landrace in all cases. The IM pigs received 2 doses of Improvac (76 and 124 d of age, 7 wk before slaughter). Backfat thickness (BF) was measured the day of slaughter in live pigs, using an ultrasound scanner, and postmortem, using a flexible ruler. Meat samples were taken at m. *Longissimus dorsi* and analyzed by NIR. Treatments were arranged factorially (3 × 2) with 6 replicates (10 pigs/pen) per treatment. The IM pigs had less carcass yield than IF and CM (77.2 vs. 79.1 and 78.7%; $P < 0.001$). Also, IM and IF had less BF than CM ($P < 0.001$) when measured by ultrasound scanner or after slaughter. The correlation coefficient between the in vivo and the postmortem methods was $r = 73\%$ ($P < 0.001$). Fresh (14.8 vs. 14.6 vs. 14.5%) and trimmed (13.2 vs. 13.0 vs. 12.9%) ham yields were higher for IF than for CM with IM being intermediate ($P < 0.05$). Also, IF had higher loin yield than IM and CM ($P < 0.01$). Meat from IM and CM had more intramuscular fat (3.93 and 4.03 vs. 3.52%; $P < 0.01$) than meat from IF. No differences between sire lines were observed for carcass yield, BF or pH_{24}. Crossbreds from Top York presented higher fresh (14.8 vs. 14.5%; $P < 0.05$) and trimmed (13.2 vs. 13.0%; $P < 0.05$) ham yield but lower loin yield ($P < 0.01$) than crossbreds from Tempo. Meat from Tempo crossbreds had more intramuscular fat content than meat from Top York crossbreds (4.01 vs. 3.64%; $P < 0.01$). We conclude that IM and CM present similar values for carcass and meat quality traits. Crossbreds with Top York sire line had better carcass quality but poorer meat quality than crossbreds of Tempo sire line.

Key Words: immunocastration, gender, sire line

T182 The influence of cage housing system and laying hen strain on breast meat quality traits. K. Juurlink*[1], A. McMillan[1], R. Ofori[1], B. Rathgeber[2], and M. Jendral[1], [1]*Nova Scotia Agricultural College*, *Truro, Nova Scotia, Canada*, [2]*Agriculture Agri-Food Canada*, *Truro, Nova Scotia, Canada*.

The influence of cage housing system and laying hen strain on breast meat quality traits was determined for 3 strains of laying hens (Shaver White (SW), Lohmann Lite (LL), Lohmann Brown (LB)) housed in conventional cages, and furnished colony units, and processed under commercial conditions. During the laying period, hens were either housed in conventional battery (CONV) (60 cm × 55 cm) (n = 24 cages per strain; 5 hens per cage) or furnished colony cages (COL) (240 cm × 110 cm) (n = 12; 4 per strain; 40 hens per cage). COL contained a nestbox (60 cm × 55 cm), 3 hardwood, semi-circular perches (240 cm × 5 cm) and a dustbathing facility (60 cm × 20 cm). Hens were slaughtered at 80 weeks and 25 hens per colony cage, and all 5 hens in 9 conventional cages per strain were randomly selected for 17 and 30 min postmortem determination of right breast (pectoralis major) pH and color (lightness (L*), redness (a*) and yellowness), respectively. At 24 h post mortem, left breast (pectoralis major) samples were collected from the same hens to determine shear force values. Data were analyzed using the Mixed model of SAS with significance accepted at $P \leq 0.05$. Breast meat was paler in color in CONV than COL (51.69 vs. 56.72; $P = 0.02$). In Col, LL and LB hens exhibited higher redness values than SH hens (5.99 and 5.12 vs. 2.73; $P = 0.01$). These results suggest that breast meat color may be affected by bird movement in different housing systems, and by genotype.

Key Words: laying hen, furnished cages, meat quality

T183 Effect of ultimate pH on the chemical properties of proteins in turkey breast meat. J. Chan*, D. A. Omana, and M. Betti, *University of Alberta*, *Edmonton, AB, Canada*.

A major challenge facing the turkey industry is the increasing occurrences of pale, soft, exudative (PSE)-like meat. PSE-like meat results in paler color and reduced protein functionality. In contrast, dark, firm, dry (DFD)-like meat results in darker color and shorter shelf life. Hence, the objective of this study was to determine the chemical properties of proteins in turkey breast with different ultimate pH at 24 h postmortem (pH_{24}) so as to improve utilization of these types of meat. Turkey breasts from Hybrid Toms were collected from a local processing plant at 24 h postmortem. Sixteen breasts for each class (pale, normal, dark) were selected based on lightness (L*) values. Further selection of 8 breasts from each class was made based on pH_{24}. Samples were within values: pale (L*>51, pH<5.7), normal (46< L* <51, 5.9< pH <6.0), and dark (L*<46, pH>6.3) and referred to as low, normal, and high pH meat, respectively. Analyses were conducted on fresh minced samples. Data were analyzed using analysis of variance and means were separated using Tukey's HSD. The extent of myosin denaturation was similar as a function of pH_{24} as revealed by Ca^{2+}- ATPase enzyme activity. Total and sarcoplasmic (SP) protein solubility was significantly (P<0.0001) higher in high pH meat. SP protein hydrophobicity (Ho) showed only marginal changes as a function of pH_{24}. However, high pH meat showed significantly (P<0.05) higher myofibrillar protein Ho and reactive sulfhydryl groups compared to low pH meat indicating lesser degree of protein denaturation. The difference in pH_{24} had no significant effect on

total sulfhydryl groups. Protein oxidation was not evident as a function of pH_{24} as shown by carbonyl content. In conclusion, low and normal pH meat showed similar chemical properties whereas high pH meat was found to have higher solubility and hence expected to have better functional properties. Thorough understanding of these properties will assist industry in developing strategies to improve meat quality and protein functionality, thus preventing yield losses.

Key Words: pale, dark, pH, chemical properties, turkey

T184 The effect of turkey breast meat pH on fatty acid profile of polar lipids and susceptibility to oxidation. P. K. Hong*, J. Chan, D. A. Omana, and M. Betti, *University of Alberta*, *Edmonton, AB, Canada*.

High prevalence of PSE-like turkey meat is one of the major challenges for meat processors. However, there are limited studies on the muscle membrane fatty acid content and its oxidative stability in turkey meat with different pH. In this study, fatty acid profile and lipid oxidation level in polar lipid of turkey (Hybrid Tom) breast meat were investigated. Initially, 3 groups (pale, normal & dark) of turkey breasts (16 pieces each) were screened in a local processing plant at 24 h postmortem based on lightness (L*). Eight breasts from each were further selected based on the following criteria: pale (L*>51, pH<5.7), normal (46< L* <51, 5.9< pH <6.0) and dark (L*<46, pH>6.3) and were referred as low (LpH), normal (NpH) and high (HpH) pH meat respectively. All samples were minced and stored at 4°C until use. Total fat was first extracted by the Folch method; polar lipid was separated by silica gel column followed by gas chromatography detection. Lipid oxidation in turkey meat was determined by induced thiobarbituric acid reactive substance (TBARS) values, expressed as nmol malondialdehyde/mg protein (MDA). Data were analyzed using One-way ANOVA test and means were separated by Tukey′s HSD. Results showed that polar lipid from each group differed in the fatty acid composition as they were influenced by meat pH. LpH polar lipid had significantly lower levels of polyunsaturated fatty acids (PUFA) ($P < 0.01$), particularly linoleic acid (C18:2n-6) ($P < 0.001$), total n-3 ($P < 0.05$) and total n-6 fatty acids ($P < 0.05$). For HpH, the highest PUFA level ($P < 0.01$) including total n-3 ($P < 0.05$) and n-6 fatty acids ($P < 0.05$) content were recorded. The TBARS value in LpH meat confirmed that lipid oxidation level was the lowest among the three turkey meat groups (0.17-0.37), followed by HpH (0.24-0.51) and NpH (0.32-0.85). In conclusion, low levels of polyunsaturated fatty acids were found in LpH meat. Our results indicated that different meat pH values are more than a function of short-term antemortem stress.

Key Words: turkey, pH, fatty acid, TBARS, lipid oxidation

T185 Exploring the biochemical basis of dfd in broiler breast and thigh meat. S. Dadgar*[1], H. L. Classen[2], T. G. Crowe[3], and P. J. Shand[1], [1]*Department of Food and Bioproduct Sciences*, [2]*Department of Animal and Poultry Sciences*, [3]*Department of Agricultural and Bioresource Engineering*, *Saskatoon, SK, Canada*.

The effect of acute cold exposure on muscle energy reserve at slaughter and its relation to post-mortem glycolysis and the incidence of dark, firm and dry (DFD) breast and thigh meat was investigated. Male broilers (160) were exposed to temperatures of −9 to −15 (cold-stressed; CS), or +20°C (control) for 3 h before slaughter. Glycolytic potential (GP) and pH of breast and thigh muscles were determined at different times post-mortem from selected birds. Activity of adenosine monophosphate-activated protein kinase (AMPK) in breast meat was assessed at 0 min post-mortem. Color, water binding capacity (WBC) and processing cook yield (PCY) were measured. Data were analyzed using ANOVA option of the GLM procedure of SAS. Classification of breast and thigh meats were based on ultimate pH (pH_u) and lightness (L*): normal breast ($pH_u < 6.1$, L* > 46) and thigh ($pH_u < 6.4$, L* > 44); DFD breast ($pH_u > 6.1$, L* < 46) and thigh ($pH_u > 6.4$, L* < 44). The total AMPK was similar for normal and DFD breast, but phosphorylated AMPK, indicative of its activity, could not be detected. DFD breast meat was darker, higher in pH_u, WBC and PCY ($P < 0.05$ for each), but not ($P > 0.05$) different in initial pH compared with normal meat. DFD thigh meat had higher ($P < 0.05$) initial and ultimate pH, and darker color compared with normal meat. Energy reserve at slaughter (GP) was almost exhausted in DFD (15 μmol/g) compared with normal (76 μmol/g) thigh meat, suggesting lack of substrate availability resulted in DFD thigh meat. However, GP was lower in DFD breast of CS birds (67 μmol/g) compared with DFD meat of control birds (87 μmol/g), which was not significantly ($P < 0.05$) different from normal meat of CS and control birds (92 and 102 μmol/g respectively), indicating that incomplete post-mortem glycolysis may contribute to DFD in breast meat. Thigh and breast meat from CS birds showed a higher incidence of DFD than that of control birds (85 and 42% versus 0 and 20%). GP for breast meat, but not for thigh meat, was time sensitive and showed some fluctuations over time post-mortem. In addition, GP was more highly correlated to changes in meat quality of thigh than breast meat.

Key Words: broilers, meat, energy reserve, DFD, cold

T186 Comparison of four methods that measure hydroxyproline. H. L. Bruce* and A. Chan, *University of Alberta*, *Edmonton, Alberta, Canada*.

Hydroxyproline (HYP) is used to estimate collagen content of meat because it is unique to collagen, a protein associated with toughness. Neuman and Logan (1950)(NL) and Bergman and Loxley (1963)(BL) assays are popular HYP colorimetric methods and the BL assay has been modified by Parekh and Jung (1970)(PJ) and Edwards and O'Brien (1980)(EO) to decrease assay volume. Absorbance variability and stability of the BL, PJ and NL assays were compared in a randomized complete block design blocked by day with assay order randomized and balanced. Assays were performed 9 times using trans-4-HYP (Sigma Chemical Co., Oakville, Ontario) aqueous standards at 2.5, 5, 10, 20 and 40 μg HYP/mL. Absorbance of each standard was assessed 15, 30, 45, 60, 90, 120, 180 and 240 min after an initial 0 min reading using a Jasco V630 spectrometer. EO assay absorbance stability and variability were also compared with those of the BL assay in a second randomized complete block design experiment identical to the first except that each assay was performed 8 times. For each experiment, assay variability was inferred from absorbance standard deviations calculated using PROC UNIVARIATE (SAS Version 9.2, SAS Institute Inc., Cary, North Carolina). Change in color stability was determined using repeated measures within PROC MIXED of the same software ($P < 0.05$). Sources of variations included assay, HYP concentration, time after initial assay reading and their 2- and 3-way interactions. Results showed that assay stability declined with time as HYP concentration increased. All assays except EO were stable for the first 90 min at HYP concentrations less than 10 μg/mL. At 20 μg HYP/mL, absorbance changed at 15, 30, 30 and 120 min for the NL, EO, PJ and BL assays, respectively. At 40 μg HYP/mL, absorbance was stable for 15 min in the BL assay only. The BL assay is most appropriate for high HYP concentration samples or assays with large sample numbers and prolonged measurement times.

Key Words: collagen, meat, hydroxyproline

Nonruminant Nutrition: DDGS

T187 Effect of the inclusion levels of DDGS to the feeds of broilers and glucanase, xylanase and phytase addition to low-energy DDGS-added diets. M. L. Angeles*[1] and S. Gómez[1,2], [1]*INIFAP, Ajuchitlán, Colón, Qro, México*, [2]*FESC-UNAM, Ajuchitlán, Colón, Qro. México*.

Three experiments were carried out to evaluate the growth performance and breast yield of broiler chickens fed diets with increasing levels of DDGS and the additions of different enzymes to compensate the energy reduction in DDGS-added diets. In all the experiments Ross B308 male broilers were individually fed. In Exp. 1, 96 broilers from 21 to 35 d of age were used and assigned to 8 treatments in a factorial combination of 2 diets based either on sorghum (S) or corn (C) and 4 increasing dietary levels of DDGS (0, 5, 10 and 15%). Diets were formulated to meet the nutrient requirements of grower broilers. In Exp. 2, 80 broilers from 35 to 49 d of age were used and assigned to the same treatments used in Experiment 1, but diets were formulated to meet the nutrient requirements of finisher broilers. In Exp. 3, 84 broilers from 32 to 49 d of age were used and assigned to 6 dietary treatments in a factorial combination of 2 cereals: S or C and 3 diets: 1) S or C plus soybean meal (SBM) and 3200 kcal of ME/kg, 2) S or C, SBM, 10% DDGS and 3200 kcal of ME/kg, and 3) S or C, SBM, 10% DDGS but reductions of 100 kcal of ME/kg, 0.12% Ca and 0.12% available P, and added with 200 ppm of phytase (Ronozyme-P [CT]), 175 ppm of glucanase (Ronozyme VP) and 175 ppm of xylanase (Ronozyme WX). In Exp. 1, the feed intake and weight gain were better when 10% DDGS was included in the diet. In Exp. 2, the weight gain, feed conversion and energetic efficiency were improved ($P < 0.01$) at each increment of DDGS in the diet; the best responses were observed for dietary levels of 10 and 15% DDGS. In Exp. 3, there was not any negative effect on the growth performance of broilers fed a low-energy, low-Ca and low-available P diet supplemented with phytase, glucanase and xylanase. In summary, 10% and between 10 and 15% of DDGS can be included in the diet of grower and finisher broilers, respectively, without any negative effect on the growth performance even in low-energy, Ca and P diets added with phytase, glucanase and xylanase enzymes

Key Words: broiler chickens, DDGS, enzymes

T188 High dietary inclusion of dried distillers grains with solubles in broiler rations—Production effects and yields. M. K. Masa'deh* and S. E. Scheideler, *University of Nebraska-Lincoln*, *Lincoln*.

A study was conducted to test the effects of feeding high levels of dried distillers grains with solubles (DDGS) in broiler chicks on body wt, feed intake, feed to gain ratio and parts yield. Ross x Ross broiler chicks were divided into 6 dietary treatments with different inclusion rates of DDGS (0, 10.0, 15.0, 20.0, 25.0 or 30.0%) from day-old to 50 d of age. All diets were formulated to be isocaloric and isonitrogenous and 3 phase-feeding diets were used, starter (0–14 d), grower (14–35 d), and finisher (35–50 d). Birds were assigned to 24 flour pens with total of 15 birds per pen with 4 replicate pens per treatment. Feed intake and body wt were recorded at 14, 35, and 50 d of age. At 53 d of age, 2 birds per pen were selected for whole carcass processing and parts yield. Birds were cut into 8 pieces to determine parts yield (breast, wing, drumstick, and thigh yields). Weight gain and feed intake were significantly different ($P < 0.05$) during the starter period between dietary treatments with the highest wt gain and feed intake for chicks fed 30% DDGS. However, no differences were observed ($P > 0.05$) during grower, finisher or the whole period between dietary treatments for weight gain and feed intake. Feed conversion ratio was not affected ($P > 0.05$) by level of DDGS during all periods. Dressing percentage was similar ($P > 0.05$) between levels of DDGS. Breast yield, wing yield and drumstick yield as percentage of live or carcass weight were not significantly ($P > 0.05$) different between levels of DDGS. Thigh yield as percent of live or carcass weight was different ($P < 0.05$) between levels of DDGS with the highest yield for broilers fed 25% DDGS. In summary, feeding DDGS at higher levels did not negatively affect chick wt, feed intake, feed conversion ratio, wt gain, mortality or dressing percentage compared with a basal diet. Percentage thigh yield was affected by levels of DDGS, while breast yield, wing yield, and drumstick yield were not influenced by DDGS. Feeding DDGS at 30% had an economical benefit with an average of $60/ton compare with basal diet (0% DDGS) when DDGS priced at $146/ton.

Key Words: DDGS, broiler, dressing percentage

T189 Effect of pellet quality on utilization of distillers dried grains with solubles (DDGS) in broiler diets. C. A. Coto*[1], C. Lu[1], Y. Min[1], A. J. Karimi[2], F. Yan[1], and P. W. Waldroup[1], [1]*University of Arkansas*, *Fayetteville,* [2]*University of Kurdistan*, *Kurdistan, Iran*.

DDGS can be used in broiler diets but at high levels a loss in performance is observed with much attributed to reduction in pellet quality. A study was conducted to evaluate different types of pellet binders in diets with addition of 25% DDGS, a level which provides a marginal but detectable reduction in performance. Dietary treatments consisted of a 2 × 4 factorial arrangement with 2 levels of DDGS and 4 levels of binder for a total of 8 treatments. Two basal diets were formulated to contain either 0% or 25% DDGS. The binder applications were as follows: No binder (fed as mash), No binder (fed as pellets), Pel-Stik (fed as pellets) and PellTech (fed as pellets). One-day old birds of a commercial strain were placed in floor pens with 35 birds per pen and 6 replicates per treatment. Pellet quality was determined by quantifying the amount of fines. Birds were weighed and feed consumption determined at d 14, 28 and 41 d. At d 41, 5 birds per pen were processed to determine dressing percentage and parts yield. The inclusion of 25% DDGS in the diet significantly increased the amount of fines in the diet. No significant effect of the binder applied in the diet was found for the amount of fines. The amount of fines in the finisher diet was significantly increased in the following order: No binder (mash) > PellTech > Pel-Stik > No binder (pellets). Birds fed pellets had BW and FCR than those fed mash diets. Birds fed 25% DDGS showed higher BW at d 28 with no difference during the remaining feeding stages. No difference among pellet binders was observed for BW at 41 d. An improved FCR at 28 and 41 d was observed when DDGS was included in the diet. The addition of Pelltech increased FCR at 41 d. A significantly higher mortality rate was observed when birds received diets containing 25% DDGS. The addition of 25% DDGS in the diet significantly reduced the dressing percentage, no other effect from the addition of DDGS was observed for yield. Birds receiving pellet diets regardless of the binder showed a significantly higher yield for breast, leg quarters and wings than birds receiving diets in the mash form.

Key Words: DDGS, broilers, pellets

T190 Effect of distillers dried grains with solubles and an enzyme supplement on performance and egg quality of brown egg layers. A. J. Pescatore*, P. Rossi, A. H. Cantor, J. L. Pierce, T. Ao,

L. M. Macalintal, M. J. Ford, W. D. King, and H. D. Gillespie, *Alltech-University of Kentucky Nutrition Research Alliance*, *Lexington*.

Effects of diets containing 15 or 23% distillers dried grains with solubles (DDGS) with and without a naturally occurring enzyme complex (Allzyme SSF, Alltech Inc., Nicholasville, KY)was evaluated in brown egg laying hens. Egg production and egg quality was evaluated during 36 wk of production. At 17 wk of age, 420 Hy-Line Brown hens were randomly assigned to 5 treatments with 7 replicate groups of 12 hens each. Treatments consisted of feeding: 1) positive control (corn-soybean meal) formulated to be adequate in all nutrients 2) 15% DDGS, 3) 15% DDGS + enzymes, 4) 23% DDGS, and 5) 23% DDGS + enzymes. Diets containing DDGS had reduced levels of ME (2800 vs. 2877 Kcal/kg), Ca (4.1 vs. 4.2%) and available P (0.17% for 15% DDGS or 0.2% for 23% DDGS vs. 0.29%), compared with the control diet. Six eggs were collected from each replicate every 4 wk to determine egg quality. Feed intake was significantly ($P < 0.05$) decreased by DDGS during wks 5–8 and 17–20. Dietary treatment did not affect feed conversion. Allzyme SSF increased HDP during wks 21–24. Egg weight at wk 20 and yolk weight at wk 20 were decreased by DDGS. Percent yolk was not significantly affected by the addition of DDGS. The diet with 15% DDGS + enzyme increased albumen wt at Week 20. The diet with 23% DDGS + enzyme increased percent shell at wk 36 and shell breaking strength at wks 4, 32 and 36. Haugh unit values were significantly increased by DDGS at wks 16 and 28. Shell weight, percent shell, specific gravity and shell breaking strength were initially lower for DDGS diets at 4 wks of production. By 36 wks the addition of Allzyme SSF to the DDGS diets improved shell weight, percent shell, specific gravity and shell breaking strength. Hens fed 15 or 23% DDGS, +/− enzymes, had lower yolk lightness (L*). Hens fed 23% DDGS had higher yolk redness (a*) and yolk yellowness (b*) values vs. hens fed 15% DDGS or control diet. This study suggests that DDGS could be included to the diet up to 23% without negative effects on feed efficiency and can be used to improve yolk color. Using Allzyme SSF in DDGS diets increase shell quality and albumen weight.

Key Words: DDGS, shell strength, yolk color

T191 Feeding value of DDGS for pigs: Correlating in vitro dry matter digestibility and crude protein digestibility to its nutrient content and color. M. Rudar*, C. F. M. de Lange, I. B. Mandell, C. L. Zhu, and P. McEwen, *University of Guelph*, *Guelph, Ontario, Canada*.

Distillers dried grains with solubles (DDGS), a co-product of ethanol production, may be cost effective for supplying energy and protein in pig diets. However, concerns about the variation in digestible nutrient content of DDGS prevent more widespread use. Techniques to rapidly evaluate the feeding value of DDGS are necessary to properly formulate diets. The study was conducted to determine how the feeding value of DDGS can be estimated via product color, nutrient analysis, and in vitro digestibility assays. Seventy-two DDGS samples were collected from 6 corn-based ethanol plants (12 samples per plant collected over 3 mo) that supply DDGS to Ontario. Each sample was analyzed for dry matter (DM), crude protein (CP), fat, starch, NDF, ADF, acid detergent insoluble nitrogen (ADIN), ash, P, Na, K, Mg, S, and color (before and after grinding to < 1mm particle size) using the CIE, L* a* b* scale. Samples contained (mean ± SD, %): 26.6 ± 1.62 CP, 10.0 ± 0.75 fat, 2.9 ± 1.60 starch, 31.6 ± 2.47 NDF, 2.5 ± 1.13 ADIN, 0.8 ± 0.05 P, and 1.1 ± 0.08 K. Fecal DM and ileal CP digestibility values were determined using in vitro incubations with a series of porcine gastric, enteric, and hindgut enzymes. Step-wise regression analysis was carried out to correlate nutrient content and product color to in vitro DM and CP digestibility values, and to predict DM and CP digestibility. DM digestibility was predicted as $y = -0.43(L^*ground) + 88.03$ ($R^2 = 0.54$, $P < 0.0001$) while inclusion of P, K, starch, and CP improved R^2 to 0.78. CP digestibility was predicted as $y = -0.55(b^*) + 106.22$ ($R^2 = 0.49$, $P < 0.0001$) while inclusion of ADIN, CP, starch, and L* improved R^2 to 0.69. From the analyzed samples, b* was a better predictor of CP digestibility than L*. These models provide a rapid way to estimate the feeding value of DDGS from simple nutrient and color analyses, but relationships with in vivo measurements still need to be determined.

Key Words: DDGS feeding value, pigs, in vitro digestibility

T192 Substitution of sorghum and soybean meal by distillers dried grains with solubles in diets for fattening rabbits. H. Bernal-Barragán*[1,4], Y. Vázquez-Pedroso[2], M. Valdivie-Navarro[2], C. A. Hernández-Martínez[1], M. A. Cerrillo-Soto[3,4], A. S. Juárez-Reyes[3,4], and E. Gutiérrez-Ornelas[1,4], [1]*Universidad Autónoma de Nuevo León*, *Monterrey, Nuevo León, México*, [2]*Instituto de Ciencia Animal*, *La Habana, Cuba*, [3]*Universidad Juárez del Estado de Durango*, *Durango, Durango, México*, [4]*Red Internacional de Nutrición y Alimentación en Rumiantes*, *Monterrey, Nuevo León, México*.

A trial was conducted to evaluate the partial substitution of sorghum grain and soybean meal by distillers dried grains with solubles (DDGS) in diets for fattening rabbits. Fifty-six 35-d old rabbits (Negro Azteca × Chinchilla) of both genders were allocated in cages, according to a complete randomized design, with 4 treatments (0, 10, 20 and 30% of DDGS in diet) and 7 replicates by treatment. Diets were isonitrogenous (17.4% CP) and isoenergetic (2.80 Mcal DE/kg) and were formulated to meet NRC rabbit requirements. Basal ingredients were alfalfa hay, ground sorghum grain, soybean meal and a commercial vitamin and mineral mix. Feed and water were offered ad libitum. At an age of 96 d viability was 100% and morbidity 0%. There were no differences ($P > 0.05$) among treatments at final weight (1914, 1961, 1853 and 1810 g), average daily gain (21, 22, 20 and 19 g/day), feed intake (93, 93, 92, and 98 g/day) and feed/gain ratios (4.51, 4.32, 4.64, and 5.24) for the 4 treatments, respectively. Carcass yield varied from 46.6 to 49.7% and was not different among treatments ($P > 0.05$). Meat content of carcass was lower ($P < 0.07$) and bone proportion was higher ($P < 0.07$) in rabbits fed 20% DDGS in the diet. Results indicate the possibility to include up to 30% DDGS in diets for fattening rabbits without affecting performance indicators. Effect of DDGS in carcass composition warrants further investigation.

Key Words: rabbits, DDGS, carcass traits

T193 Evaluation of in vitro procedures to measure digestibility of fiber in distillers dried grains with solubles. P. E. Urriola* and H. H. Stein, *University of Illinois*, *Urbana*.

Four experiments were conducted to develop and evaluate an assay for measuring in vitro digestibility of dietary fiber in distillers dried grains with solubles (DDGS). Exp. 1 was conducted to validate the 3-step in vitro digestibility assay (pepsin, pancreatin, viscozyme) in our laboratory. In vitro apparent ileal digestibility (AID) and in vitro apparent total tract (ATTD) digestibility of OM in 4 diets and corn (83.7 and 93.1%) were not different from values analyzed at a reference laboratory (82.4 and 92.4%) indicating that we were able to repeat the assay. Exp. 2 was conducted with the objective of increasing the amount of sample that was used for the in vitro digestibility assay from 0.5 g to 2.0 or 4.0 g. Results of this experiment showed that ATTD of DM was not different among the 3 sample sizes (85.1, 83.7, 83.3% for 0.5, 2.0, and 4.0 g, respectively). Exp. 3 was conducted to measure AID and ATTD of NDF

in DDGS. In vitro AID of NDF was different ($P < 0.01$) among sources of DDGS (21.9 to 40.4%). Values for AID of NDF were greater than expected considering that at this point there were no fiber degrading enzymes added to the samples. The ATTD of NDF (32.5 to 52.2%) was different ($P < 0.01$) among sources of DDGS. These observations suggested that the average concentration of NDF in DDGS (40.2%) in the current experiment may be overestimated. The objective of Exp. 4 was to measure in vitro hindgut fermentation of NDF using purified enzymes or fecal inoculums in 10 sources of DDGS that had in vivo data available. Values for hindgut disappearance of DM and NDF obtained after fecal inoculation (23.0 and 54.3%) were greater ($P < 0.05$) than values obtained using purified enzymes (6.3 and 5.6%), values obtained using fecal inoculums were also closer to values observed in vivo (23.3%). In conclusion, modifications to the 3 step in vitro digestibility assay allowed measuring the in vitro AID and ATTD of DM and NDF in DDGS. Results obtained with the fecal inoculum are closer to in vivo values than values obtained using purified enzymes. Concentration of NDF in DDGS may be overestimated if CP contaminates the NDF residue.

Key Words: in vitro digestibility, DDGS, inoculum

T194 Effects of distillers dried grains with solubles and lactose on fecal *Lactobacillus* biota of nursery pigs. H. Tran*, R. Moreno, J. W. Bundy, E. Hinkle, J. Walter, T. E. Burkey, and P. S. Miller, *University of Nebraska*, *Lincoln*.

An experiment was conducted to evaluate the effects of distillers dried grains with solubles (DDGS), lactose, and their interaction on fecal *Lactobacillus* biota of nursery pigs. Ninety-six pigs (age, 23 d; initial BW, 6.43 kg) were randomly allotted into each of 16 pens by gender, ancestry, and weight (6 pigs/pen; 4 pens/treatment). In phase 1 (wk 1 and 2), pigs were fed 1 of the 4 treatments: 1) control (no DDGS or lactose), 2) 15% DDGS, 3) 20% lactose, or 4) 15% DDGS + 20% lactose. In phase 2 (wk 3 and 4), all pigs were fed a common diet containing 15% DDGS and 10% lactose. Fecal samples were randomly collected from 2 pigs/pen on d 0, 7, 14, and 21. A subsample was taken from 1 pig/pen (4 pigs/treatment) for DNA extraction. *Lactobacillus* specific primers were used for PCR and subsequent denaturing gradient gel electrophoresis (DGGE). Staining intensities of DGGE bands were determined as a proportion of peak surface area of the entire molecular fingerprint of the sample. No interactions of DDGS and lactose on *Lactobacillus* biota were observed; however, tendencies for a main effect of both DDGS and lactose were observed with respect to putative *L. sobrius/amylovorus* on d 7. Pigs fed diet containing DDGS had greater (41.95 vs. 25.36%; $P = 0.06$) staining intensities of *L. sobrius/amylovorus* than pigs not receive DDGS. Similarly, decreased (26.36 vs. 40.95%; $P = 0.09$) staining intensities of *L. sobrius/amylovorus* were observed in pigs fed lactose compared with non-lactose fed pigs. On d 14, a main effect of lactose was observed with respect to putative *L. reuteri* where lactose-fed pigs had greater (54.67 vs. 20.07%; $P = 0.02$) staining intensities of this species compared with pigs not receiving lactose during phase 1. On d 21, DDGS-fed pigs had greater (72.26 vs. 42.02%; $P = 0.05$) staining intensities of *L. reuteri* compared with pigs not receiving DDGS in phase 1. These research findings suggest that feeding lactose and DDGS may affect fecal *Lactobacillus* ssp. in nursery pigs.

Key Words: distiller dried grains with solubles, *Lactobacillus*, lactose

T195 Bone breaking strength of laying chickens fed increasing levels of omega-3 PUFA DHA (22:6) using algae as vehicle of diet enrichment. N. P. Johnston*, C. B. Evans, and R. T. Davidson, *Brigham Young University*, *Provo, UT*.

In recent years a host of health benefits have been associated with the intake of omega-3 fatty acids in general and DHA (22:6 n-3) in particular for both and humans and animals. During a 12-wk feeding trial 60 SCWL pullets were fed omega-3 PUFA-rich diets with increasing levels of docosahexaenoic acid (DHA) 22:6 (n-3) to determine the dietary effects on bone breaking strength (BRS) measured by Young's Modulus (YM). Two of the diets were DHA-free including a corn oil-enriched control and a flaxseed-enriched diet and in the remaining 4 diets a portion of the diet was replaced with increasing levels of algae ranging from 10% to 50%. As a result- dietary DHA ranged from 0 to 0.94% of the diet. The birds were evenly divided by treatment and housed in individual cages in environmentally controlled rooms where they received feed/water ad libitum and a light-dark cycle of 14L:10D. It was hypothesized that with increasing levels of DHA there would be a corresponding increase in bone strength. At the conclusion of the feeding trial the femur, tibia and humerus bones were broken on an Instron 3345 to determine bone strength (YM). Diet improved ($P < 0.05$) the strength of the tibia, femur and humerus (3.08, 2.04, 3.13 N/mm2) at the 50% level and the femur at all added algae levels. In conclusion the 10, 20, and 50% algae-fed birds ($P < 0.05$) had stronger femurs and the 50% ($P < 0.05$) stronger humerus and tibias than the controls; hence, the replacement of flaxseed with DHA-rich algae had a beneficial effect on the bone strength of laying chickens.

Key Words: bone breaking strength, omega-3, algae

Nonruminant Nutrition: Energy

T196 Energy requirement of broiler breeder hens: Egg weight, egg composition and progeny. C. Salas*, R. D. Ekmay, J. England, S. Cerrate, and C. N. Coon, *University of Arkansas*, *Fayetteville*.

Under or overfeeding dietary energy to broiler breeders (BB) can lead to a reduction in hatching egg production. The objective of this study was to evaluate the effects of energy intake (EI) on egg composition, hatchability, fertility and progeny performance. Cobb 500 BB pullets were reared in 3 groups as follows: a control group (SBW), a group 20% heavier (HBW) and a group 20% lighter (LBW). At 21 wks, pullets of each group were moved to cages and fed 1 of 6 diets (each diet had 2860 kcal ME and 20.8-14.3% CP). The EI for each diet was adjusted to provide 330, 360, 390, 420, 450 and 480 kcal ME/hen/d and 24 g of ideal protein/d at peak production. Birds fed 390 kcal ME/d produced 177.1 hatching eggs, 14 and 16.4 more eggs than the BB fed 330 and 480 kcal ME/d, respectively ($P < 0.0001$). The same BBs produce .4g to 1.5g heavier eggs than the other groups ($P < 0.0001$). BBs were inseminated every 5 wks to monitor egg fertility, hatchability and chick weight. At hatch, chicks from LBW hens were always lighter; this translated into BW*EI interactions. The LBW and SBW hens fed 330 and 360 kcal ME/d produced lighter chicks. Chicks from breeders fed 390 to 480 kcal ME/d weighed ≥42g in all hatches. Egg fertility and hatchability were ≥90% and 85%, respectively; for all groups.
Egg composition was determined every 5 wks for each BB group during the production period. In wks 30 and 35 BB fed 480 kcal ME/d produced eggs with the highest % yolk ($P < 0.01$). BB fed 480 kcal ME/d produced eggs with a higher yolk:albumen ratio (0.46 to 0.65)($P < 0.05$), but this had no effect on progeny performance. All progeny from the 50 wk hatch was reared in floor pens until 42d and 5 birds/pen were further processed. There were no differences between the progeny groups in BW gain, feed:gain ratio or processing yields. This study shows that BBs in cages perform well with an EI of 390 kcal ME/d throughout the production period.

Key Words: broiler breeders, energy intake, eggs

T197 Determination of metabolizable energy content of meat and bone meal for broilers using regression method. O. A. Bolarinwa*[1], O. A. Olukosi[1], R. A. Hamzat[2], and O. Adeola[1], [1]*Purdue University*, *West Lafayette, IN,* [2]*South Suburban College*, *Chicago, IL*.

An experiment was conducted to determine the ME content of 2 meat and bone meal (MBM) samples by the regression method. Gross energy of MBM1 and MBM2 were 4.383 and 4.857 kcal/g DM, respectively. The CP, ash, and crude fat contents for MBM1 or MBM2 were 585 or 614, 272 or 218, and 109 or 120 g/kg DM. A standard corn-soybean meal diet with GE and ME of 4.601 and 3.310 kcal/g DM, respectively, and 6 test diets were used for the study. In the standard diet, corn, soybean meal, corn starch and soy oil were used as the sources of energy. In the test diets, each of the 2 MBM samples were added at the rate of 30, 60 or 90 g/kg diet to partly replace corn, soybean meal, corn starch and soy oil such that the ratio of all energy-yielding feedstuffs to one another was the same in all the assay diets. Each of the 7 dietary treatments had 8 replicates with 6 birds per replicate. Birds received a starter diet from d 1 to d 15 post-hatch. Birds with an average BW of 397 g at d 15 post-hatch were assigned to 7 diets in a randomized complete block design. Experimental diets were fed for 7 d and excreta were collected twice daily on d 20 and 21. Average weight gain and feed efficiency were between 391 to 424 g and 700 to 757 g/kg, respectively. The ME content of each MBM sample was determined from the slope of the regression of MBM contribution to apparent ME intake in kilocalories against amount of MBM intake in grams. Metabolizable energy values for meat and bone meal samples derived from the regression analyses were 3.364 and 3.691 kcal/g DM, for MBM1 and MBM2, respectively. It is likely that the difference in energy value is due to greater GE and fat and lower ash in MBM2 compared with MBM1.

Key Words: broiler, meat and bone meal, metabolizable energy

T198 Determination of the chemical composition and true metabolizable energy of high oil poultry by-product meal. M. G. Olyayee*, H. Janmohammadi, A. Taghizadeh, A. Rafat, and S. Ostan, *University of Tabriz*, *Tabriz, Iran.*

Poultry by-product meal (PBPM) is one of the by-products resulting from poultry meat processing and is produced from slaughter wastes of broilers, spent laying hens and breeders. In Iran, the term PBPM refers only to meals which are produced from viscera, feathers, heads and some feet and blood, and are produced by simple low cost technology. The chemical composition of PBPM can vary greatly depending on the raw material source, storage time of raw material before rendering and processing methods. This product is used mostly in poultry diets but there is not enough data of its chemical composition and True Metabolizable Energy (TMEn) content. The present study was conducted to determine the chemical composition and TMEn content of high oil PBPM from Iran. Three composed samples were obtained from local poultry slaughterhouses. The chemical composition of PBPM such as DM, CP, ether extract (EE) and ash content was determined according to AOAC (1990) methods. Gross energy was measured by Parr adiabatic calorimetric bomb and then TMEn was determined by Sibbald precision fed assay. Twenty 4 12-wk-old Ross 308 broiler roosters with similar body weight (2280 ± 80g) were selected. Each sample was replicated 6 times as well as 6 replications for endogenous energy collection. Descriptive statistical responses of all data were obtained by using proc means of SAS (2003). The results showed that this product in comparison with standard tables of nutrient composition has high EE (23.8 ± 1.6%), low ash (6.53 ± 0.8%) and approximately the same CP (57 ± 2.6%) contents. Dry matter was 91.5 ± 0.57. The TMEn values of 3 studied samples were 2798 ± 80, 3518 ± 114.92 and 3220 ± 108.5 kcal/kg. The results showed that TMEn value of high oil PBPM from Iran poultry rendering plants is relatively variable, therefore should be considered by users in poultry diet formulation.

Key Words: TMEn, high oil poultry by-product meal

T199 Metabolizable energy and nutrient digestibility coefficient determination of ingredients with nutritional adjustment. A. G. Bertechini*, V. A. Costa, S. F. Castro, J. C. C. Carvalho, and C. Meneghetti, *Universidade Federal de Lavras*, *Lavras, MG, Brazil*.

Because of the imbalance of the nutrient supplies to the chickens when using the conventional methodology for metabolizable energy and nutrient digestibility coefficients determination, the results cannot be appropriate, for that reason different methods must be developed. In the present study the effect of nutritional adjustment of basal diets after inclusion of the ingredient test (using enzyme) were evaluated. A total of 640 male Cobb 500 broiler chicks from 14 to 21 (n = 400) and 35 to 42 (n = 240) d of age were placed in metabolic cages and assorted into 10 dietary treatment groups with 5 and 3 birds each to first and second phases, respectively. A 5 × 2 factorial treatment scheme, with 5 dietary

adjustments and 2 protease levels (0 and 200 ppm) in a completely randomized design with 8 replicates each was used. The dietary adjustments were: 1) Corn-soybean meal based diet (C-SBM), 2) C-SBM + vitamin + mineral premix, 3) C-SBM 2 + energy, 4) C-SBM 2+ amino acids and 5) C-SBM 2 + energy + amino acids .The variables analyzed were the apparent metabolizable energy (AME) and N corrected (AMEn), the apparent digestibility of crude protein (CPD), dry matter (DMD) and ether extract (EED). The studied ingredient was meat and bone meal (20% of replacement of C-SBM), using total excreta collection (for 3 consecutive days). Results indicated that from 14 to 21 d of age, higher values of AME and AMEn ($P < 0.05$) were observed on treatment 2, followed by treatments 3 and 4. The CPD, DMD and EED were improved ($P < 0.05$) for all treatments where the dietary adjustment was made. Improvements ($P < 0.05$) on AME, AMEn, CPD, DMD and EED with enzyme supplementation was verified. From 35 to 42 d of age highest values ($P < 0,05$) of AME and digestibility coefficients were observed on treatment 5. It is concluded that conventional methodology (without nutritional adjustments) underestimates the nutritional values assigned to meat and bone meal in broiler diets.
Research supported by FAPEMIG, MG.

Key Words: nutrient adjustment, nutrient imbalance, digestibility methodology

T200 True and apparent metabolizable energy values of various wheat screening samples. M. Mazhari and A. Golian*, *Ferdowsi University of Mashhad*, *Mashhad, Khorasan Razavi, Iran*.

Three trials were conducted to determine the available energy of different wheat screening samples collected from different locations of Khorasan in Iran. In experiment 1, chemical composition and the nitrogen corrected true metabolisable energy (TMEn) were evaluated. A precision-fed rooster assay was used, in which, each wheat screening sample was tube fed to adult roosters, and the excreta were collected for 48 h. In exp. 2 and 3, 5 and 2 wheat screening samples-based diet with or without xylanase and phytase were fed to 16 d old battery reared chicks and total consumption and excreta were measured during 3 next days. The variable nature of wheat screening varieties led to significant differences in mean TMEn values ($P < 0.01$). The TMEn values of samples determined with adult roosters varied by ± 5.03% of the mean value (3097.65 ± 49.32 kcal/kg) and ranged from 2734.90 to 3245.12 kcal/kg. There was a significant correlation ($P < 0.05$) between chemical composition (CP, EE, ash and CF) and TMEn. The best equation for TMEn yielded an R2 = 0.86, with crude fiber being the most efficient compound. The average AMEn values of 5 and 2 samples determined with young broiler chickens were 2968.41 ± 25.70 kcal/kg and 2976.38 ± 8.34 kcal/kg in exp2 and exp3 respectively. Addition of xylanase and phytase to wheat screenings resulted in significant ($P < 0.01$) improvement in AMEn (4.21 and 2.92% respectively).

Key Words: wheat screening, true and apparent metabolisable energy, xylanase and phytase

T201 Effect of various levels of energy and protein on Humoral immune response in broiler chicks. M. Pilevar, A. Golian*, and M. Aami Azghadi, *Ferdowsi University of Mashhad*, *Khorasan Razavi, Iran*.

A complete randomized design experiment with a 4 × 4 factorial arrangement consisted of 4 levels of energy (2900, 3000, 3100 and 3200 kcal/kg) and 4 levels of protein (17, 20, 23 and 26%) was conducted to assess the effect of dietary energy and protein on humoral immune response of chickens. All birds in each replicate were injected intramuscular with SRBC (15% suspension in PBS, 1 mL/chick) at d 15 and 25. Blood samples were collected at d 5 and 10 of injections. The serum from each sample was analyzed for total anti-SRBC antibody as described previously (Cheema et al., 2003). The data were transformed and then analyzed using the GLM procedures of SAS software (v. 9.1). Total anti-SRBC titers were increased in birds fed low energy diet in both postprimary (PPI) and postsecondary injections (PSI), but dietary protein contents did not influence antibody titers of birds. Increasing the level of energy and protein in broiler diets improved growth rate which may cause a negative effect on humoral immune response. Broiler bursa of Fabricius size decreased gradually with increasing dietary energy level, which could affect on immune response. It seems that, there is a negative phenotypic association between immunocompetence and rapid growth in chickens.

Table 1. Effect of various levels of ME and CP on total anti-SRBC titers in postprimary (PPI) and postsecondary (PSI) injections

		Days PPI		Days PSI	
	Level	5	10	5	10
ME	2900	5.304a	2.424	6.450	4.894a
	3000	4.958b	3.060	6.990	4.559ab
	3100	5.048ab	3.555	7.410	4.389b
	3200	5.132ab	3.630	6.780	4.096
CP	17	5.341	2.968	7.000	4.372
	20	5.233	2.887	6.833	4.508
	23	4.929	2.876	7.037	4.639
	26	5	3.166	6.775	4.383
		Probability			
ME		0.0152	0.95	0.113	<0.001
CP		0.202	0.145	0.831	0.843
ME×CP		0.766	0.397	0.112	0.179

Key Words: humoral immune, energy and protein, broiler chicks

T202 Effect of xylanase supplementation in a pig diet on ileal and postileal energy and fiber fraction digestibility. L. Babinszky*[1], J. Tossenberger[1], D. Ottó[1], and I. Kühn[2], [1]*Kaposvár University*, *Kaposvár, Hungary*, [2]*AB Vista*, *Darmstadt, Germany*.

The trials studied the impact of supplementing high grain/high crude fiber (CF) diets with xylanase (Xyl) on ileal [intake-ileal excretion/intake × 100] and postileal [ileal excretion-fecal excretion/ileal excretion × 100] digestion of GE, NDF, ADF in growing pigs. Each of 4 treatments (Trt) used 5 hybrid barrows (initial live weight 37.3 ± 2.9 kg) in 2 replicates (10 pigs/Trt). Prior to trial pigs were fitted with PVTC-cannulas. Ileal and post-ileal digestibilities (DGY) were determined in same animal using Cr_2O_3 as marker. The wheat, barley, rye, wheat bran, DDGS, soybean hulls based basal diet contained 12.2 MJ MEs, 170.3g CP, 51.1g CF, 223g NDF, 68g ADF, 9.5g LYS, 6.4g M+C / kg. Diets equivalent to 2.6 times maintenance energy requirement (458 KJ MEs/$kg^{0.75}$/d) were fed. TrtI diet had no added Xyl (negative control: NC). Trt2 and 3 diets were supplemented with 8000 BXU/kg and 16000 BXU/kg ECONASE XT (thermostable Xyl from *Trichoderma reesei*). Trt4 was a wheat-barley based positive control diet (PC) with recommended energy level (13.2 MJ MEs). Data were analyzed by ANOVA (SAS, 2004).Trt2 improved ileal DGY over NC from 61.2% to 67.5% (GE), 30.6% to 38.8% (CF), 47.3% to 57.2% (NDF), and 24.0% to 35.3% (ADF); postileal DGY improved from 79.2% to 84.4% (GE), 81.9% to 87.0% (CF), 81.0% to 90.0% (NDF) and 78.0% to 85.5% (ADF) ($P \leq 0.05$). Neither ileal, nor postileal DGY-s increased further in Trt3 ($P \geq 0.05$). DGY-s in Xyl trts

were similar or higher than those in energy balanced Trt4 (PC). Added Xyl also shifted location of energy absorption. While ileal/postileal split of total energy absorption was 74.7% / 25.3% in NC group, Trt2 changed this to 81.2% / 18.8%, supporting that added Xyl improves nutrient DGY in the small intestine. The results show the importance of improved nutrient absorption caused by Xyl supplementation (8000-16000 BXU/kg) to high fiber/NDF grain based diets, if the aim is to provide optimum energy supply for animals.

Key Words: pig, ileal-postileal, digestibility

T203 Influences of four kinds of exogenous enzymes on performance, jejunal digesta viscosity and litter moisture of broilers fed wheat-based diet. H. Shirzadi*, H. Moravej, and M. Shivazad, *University of Tehran*, *Karaj, Tehran, Iran*.

The intention of this work was to determine the effects of 4 enzyme preparations containing xylanase and β-glucanase activities on performance of broiler chicks fed wheat-based diet compare with those that fed corn-based diet without enzyme. Enzyme A provided per kilogram of diet (endo-1,4-β-glucanase activity: min 800 units; endo-1,(4)-β-glucanase activity: min 1800 units; endo-1,4-β-xylanase activity: min 2600 units), enzyme B (endo-1,3(4)-β-glucanase: 100 AGL; endo-1,4-β-xylanase: 1100 visco units), enzyme C (endo-1,4-β-glucanase: 1500 BGU; endo-1,4-β-xylanase: 3600 FXU), enzyme D (1420 units; xylanases: 660 units). Two hundred thirty-four male day-old broiler chicks (Ross 308) were randomly allocated to 6 treatment groups, with 3 replicates and 13 birds per replicate in floor pen. All data was analyzed through the General Linear Model procedure of SAS for a randomized complete block design. The 6 dietary treatments consisted of a 60% corn-based ration without enzyme and 5 other rations containing 60% wheat supplemented with and without enzyme (A, B, C, and D). All parameters were measured at 42d, except viscosity (at 28d). Body weight was not significantly ($P > 0.05$) affected by enzyme addition. Furthermore, feed intake and feed conversion ratio were also not affected by enzyme supplementation ($P > 0.05$), and there were no significant differences between all treatment. In addition, litter moisture was not affected by enzyme, and these results were similar to results of corn-based diet ($P > 0.05$). In addition, the results demonstrated that the viscosity of jejunal contents was not significantly ($P > 0.05$) reduced by enzyme addition, however, this parameter had decreasing trend. The results of current study led to the conclusion that xylanase and β-glucanase activities of these enzymes did not seem to positively affect the xylans and β-glucans content of wheat used in this trial.

Key Words: enzyme, performance, viscosity

T204 Cloning, expression and characterization of a thermostable beta-propeller phytase from *Bacillus licheniformis*. S. J. Fu*[1,3], J. Y. Sun[1], X. Y. Weng[2], L. C. Qian[1], and Z. Q. Shen[4], [1]*Microbiology Division, Institute of Feed Science, College of Animal Science, Zhejiang University*, *Hangzhou Zhejiang, People's Republic of China*, [2]*College of Life Science, Zhejiang University*, *Hangzhou Zhejiang, People's Republic of China*, [3]*Key Laboratory of Preventive Veterinary Medicine and Animal Biotechnology, Binzhou Animal Husbandry and Veterinary Research Institute*, *Binzhou Shandong, People's Republic of China*, [4]*Shandong Lvdu Biological Technology Co., Ltd*, *Binzhou Shandong, People's Republic of China*.

A novel sabler phytase gene (phyC) was cloned from *Bacillus licheniformis*. It was 1146 bp in size and encoded a polypeptide of 381 amino acids. The mature peptide of phyC was successfully expressed in *Pichia pastoris* under the control of AOX1 promoter. The recombinant PhyCm (rePhyCm) was secreted into culture medium. After 96 h of 0.5% methanol induction, the activity of the rePhyCm in the culture supernatant reached the peak, 8.64 U/mg, which was 5.1 times as high as that of the native PhyC (1.7 U/mg). Studies on enzymatic properties showed that the optimum temperature and pH of the rePhyCm were 70°C and 7.5, respectively. The rePhyCm was very stable in a wide pH range of 5.0–9.0 and showed relatively good thermal stability. After incubation at the pH 5.0–9.0, 37°C for 1 h, all the residual activities of the rePhyCm were over 80%. After being exposed to 80°C for 2min in the presence of 1mM CaCl2, the rePhyCm retained 80% of the initial enzyme activity. The rePhyCm exhibited a molecular mass of approximately 42 kDa on SDS-PAGE, indicating that the rePhyC was expressed and efficiently secreted into the growth medium.

Key Words: *Bacillus licheniformis*, phytase, *Pichia pastoris*

T205 Body weight and feed conversion responses in broilers after feeding a lysophospholipid bio-surfactant and β-mannanase based feed enzyme. G. Mathis[1], B. Lumpkins[1], H. Stomp[2], A. Lamptey[2], and A. G. Yersin*[2], [1]*Southern Poultry Research*, *Athens, GA,* [2]*Kemin AgriFoods*, *Des Moines, IA*.

Energy utilization by poultry is dependent on many factors including age of the animal, the amount of lipase and bile salt present in the gut and overall digestibility of the ration components. The use of emulsifiers (lecithin) has been shown to improve nutrient utilization. Studies were conducted to evaluate the effects of a lysophospholipid bio-surfactant and β mannanase based feed enzyme in the diets to improve growth performance in broilers during a 42 d period. Two separate experiments were conducted using a basal corn and soybean meal ration. In study 1, there were 6 treatments based on different fat levels and the presence of the surfactant (454 g/ton inclusion), enzyme (114g/ton inclusion) or both as adjusted on a caloric basis. In study 2, the enzyme was added to all treatments, but the level of fat and surfactant were adjusted based on either a caloric basis or on the feeding phase of the ration (starter, grower or withdrawal phase). Body weight gain, feed conversion and mortality were measured at each dietary feed change in both studies. In study 1, the control (no bio-surfactant, no enzyme) group had a similar ($P < 0.05$) feed conversion and gain response at both 21 and 42 d of age as compared with treatments with either enzyme alone, bio-surfactant alone or the combination. However, the cost per pound of live weight was reduced in the bio-surfactant alone treatment compared with all others. In study 2, the enzyme and bio-surfactant combination group (fed in all phases) had a significantly better ($P < 0.05$) feed conversion and gain response at both 19 (4.9 points, 0.01 kg) and 42 d (3.8 points, 0.073 kg) as compared with all other treatments. The data indicates that both phase of feeding (starter, grower, and withdrawal) as well as the presence of enzyme with a surfactant contribute to overall performance improvements.

Key Words: broilers, bio-surfactant, enzyme

T206 Impact of a new phytase on apparent phosphorus and calcium availability, bone mineralization and performance of broilers. R. Angel*[1], W. Saylor[2], and N. Ward[3], [1]*University of Maryland*, *College Park,* [2]*University of Delaware*, *Newark,* [3]*DSM Nutritional Products*, *Parsippany, NY*.

To determine the impact of adding graded levels of a new phytase (IPA, DSM) to corn-soy starter diets and to compare it with an existing commercial phytase, 9 diets with Celite as marker were fed to 8 replicates of 5 broilers each (Ross 708) from 6 to 20d: Positive Control (PC, 0.45% non-phytate phosphorus (nPP); 0.9% Ca); Moderate and Low nPP (MP and NC, 0.30 and 0.15% nPP, respectively; 0.7% Ca); NC with 250, 500, 1000, 2000, and 4000 FYT IPA /kg; and NC with 1850 Ronozyme P CT (R) (DSM). At 20 d, performance was determined, tibias sampled and

ileal contents removed for apparent Ca and P availability determination. Body weight (20 d) and feed efficiency (FE) were similar ($P > 0.05$) for birds fed the PC, MP, and the NC plus 1000, 2000 and 4000 IPA diets. Broilers fed the NC+R diet had greater BW than those fed the NC diet and similar to those fed the NC+ 200 and 500 IPA. Tibia ash was lowest ($P < 0.01$) in broilers fed the NC diet (38.1%) followed by those fed the NC+R (41.7%) and highest ($P < 0.01$) for broilers fed the PC (50.85%) and NC+4000 IPA (50.45%). There was a quadratic effect ($P < 0.001$; R-squared 0.87) of IPA inclusion on tibia ash. Apparent Ca and nPP retentions were lowest ($P < 0.001$) for broilers fed the PC diet, followed by those fed the NC diet and the NC+R and highest for broilers fed the NC+4000 IPA (51.9 and 42.2; 57.8 and 49.4; 60.7 and 51.7; and 67.9 and 60.1% for Ca and nPP, respectively). IPA inclusion had a quadratic effect ($P < 0.01$) on Ca and nPP apparent availability. In vitro analysis of the pH optima curve of IPA showed it has a higher ($P < 0.001$) P release per unit at all pHs including the 2 to 3.5 pH range compared with phytases from Peniophora l.- and an *E. coli*.

Key Words: broilers, phytase, phosphorus availability

T207 Effects of co-administration of phytase and energy enzymes on broiler performance, tibia strength, bone ash, and processing parameters. J. R. Coppedge*[1], J. Klein[1], A. Jordan[1], K. Jessen[1], S. Pohl[1], B. Brown[2], F. Ruch[2], and J. T. Lee[1], [1]*Texas A&M University*, *College Station,* [2]*Enzyvia LLC*, *Sheridan, IN*.

An experiment was conducted to determine if dietary NSPase inclusion enhances phytase activity during a 40-d growout. The experimental design included 4 non-supplemented diets including an industry control (3090 kcal/kg ME and 0.40 available phosphorus (aP) in the starter diet), a low energy (LE) diet (−132 kcal/kg ME), a low phosphorus (LP) (- 0.10% aP), and a low energy and low phosphorus (LEP) diet (−132 kcal/kg of ME and −0.10% aP). Enzyme supplementation treatments included phytase inclusion of 200 or 250 FTU/kg into the LP diet. In addition, the LEP diet was supplemented with an NSPase enzyme and 200 or 250 FTU/kg phytase. Each of the 8 treatment groups contained 8 replicates of 48 chicks/ replicate. Broilers were fed a starter diet through 14 d of age, a grower diet from 15 - 26 d of age, and a finisher diet through termination of the study on d 40. Following each dietary phase, 3 broilers from each replicate were killed and tibias removed for bone strength and ash determination. On d 40, 10 male broilers from each replicate were processed for determination of carcass and breast yield. Average body weight was reduced ($P < 0.05$) and mortality rates increased ($P < 0.05$) in the LP and LEP diets. Phytase inclusion in the LP diets increased ($P < 0.05$) body weight, reduced mortality, improved feed conversion ratio, and increased bone strength and ash. Phytase inclusion of 250 FTU/kg outperformed the inclusion at 200 FTU/kg in most evaluated parameters regardless of NSPase inclusion. These data confirm that phytase inclusion improves growth performance and bone strength in diets containing inadequate levels of aP, but NSPase inclusion did not enhance phytase activity.

Key Words: broiler, phytase

T208 Effect of CTCZyme β-mannanase on broiler nutrient digestibility in corn-soybean meal diets. F. Mussini*[1], C. A. Coto[1], S. Goodgame[1], C. Lu[1], A. J. Karimi[2], J. Lee[3], and P. W. Waldroup[1], [1]*University of Arkansas*, *Fayetteville,* [2]*University of Kurdistan*, *Kurdistan, Iran*, [3]*CTC Bio Inc.*, *Seoul, Korea*.

The possibility of improving digestibility of nonstarch polysaccharides present in broiler diets by the use of different carbohydrases appears as an opportunity to enhance feed utilization by the birds. In this study, the effect of a β-Mannanase (CTCZyme) on nutrient digestibility in corn-soybean meal diets was investigated. One-day-old chicks received a nutritionally complete corn-soybean meal diet for 19 d. At that time birds were randomly allocated to 4 treatments, each of which had 6 replicates of 5 birds housed in battery brooders with wire floors. Aliquots of the basal diet were supplemented with 4 levels of CTCZyme (CTC Bio Inc., Seoul Korea): 0%, 0.025%, 0.05% (recommended level) and 0.1%. Chromic oxide was used as an indigestible marker. Feed was analyzed for gross energy, Chromium, and amino acid content. After 8 d of acclimation to the test diets, birds were sacrificed and ileal contents collected. Analysis of the ileal contents indicated that digestibility of Lys, Met, Thr, Trp, Arg, Leu, Ile, Cys, and Val were significantly ($P \leq 0.0001$) improved in a linear manner for each increment of CTCZyme inclusion. Lys digestion was increased 4.6% and Met by 3.1% by the highest level of enzyme. Ileal metabolizable energy also increased with each increment of CTCZyme level. These results show that the enzyme improves feed digestibility by making amino acids more available for the bird and increases energy utilization from the feed. These results suggest that lower levels of protein and energy could be used with the same results but further studies are required to estimate potential levels.

Key Words: broilers, mannanase, digestibility

T209 Effect of phytase supplementation on the digestibility of crude protein and amino acids of cowpea (*Vignia unguiculata*) in broilers. E. A. Iyayi*, *University of Ibadan*, *Ibadan, Oyo, Nigeria*.

Cowpea (*Vignia unguiculata*) a tropical legume is being promoted for use in poultry feeding. To determine the digestibility of crude protein (CP) and amino acids (AAs) in the bean, 6 experimental diets were formulated containing 0, 150 or 300 g/ kg of heated cowpea in place of maize starch and 0 or 500 units of phytase enzyme (Natuphos), according to a 3 × 2 factorial arrangement. A total of 288 d old broiler chicks (Ross strain) were distributed into 36 cages on weight basis. Each diet was assigned to 6 cages containing 8 birds each.TiO2 was added as an indigestible marker in the diets. Increase in cowpea level had no significant effect on the amount of dietary CP and AAs digested except for arginine, glutamic acid and phenylalanine which were significantly ($P < 0.05$) reduced. Supplementation with phytase caused a significant ($P < 0.05$) increase in the digestibility of dietary CP and AAs at the terminal ileum. Interaction between cowpea and phytase had no significant effect on CP and AA digestibility in the diets. Digestibility of CP and AAs in cowpea was increased with phytase supplementation. The results showed an increase in the digestibility coefficients. Nevertheless, regression analysis indicated that phytase in this study affected both the CP and AA losses on the basal level and the digestion of CP and AAs from cowpea.

Key Words: phytase, CP and AA digestibility, broilers

T210 Effect of phytase supplementation on the digestibility of phosphorus of cowpea (Vignia unguiculata) in broilers. E. A. Iyayi*, *University of Ibadan*, *Ibadan, Oyo, Nigeria*.

Cowpea (Vignia unguiculata) a tropical legume rich in phytate phosphorus is being promoted for use in poultry feeding. To determine the digestibility of P in the bean and the performance of the birds, 6 experimental diets were formulated containing 0, 150 or 300 g kg-1 of heated cowpea in place of maize starch and 0 or 500 units of phytase enzyme (Natuphos), according to a 3 × 2 factorial arrangement. A total of 288 d old broiler chicks (Ross strain) were distributed into 36 cages on weight basis. Each diet was assigned to 6 cages containing 8 birds each.TiO2 was added as an indigestible marker in the diets. Phytase supplementa-

tion had a significant ($P < 0.05$) improvement on the digestibility of P in the diets and cowpea at the terminal ileum. The digestibility of P in the cowpea increased from 0.55 to 0.67 with phytase supplementation. The level of cowpea and its interaction with phytase had no significant effect on P digestibility and reduction in the loss of P at the basal level. Phytase supplementation caused a significant ($P < 0.05$) increase in feed intake and body weight in the birds but cowpea level or its interaction with phytase had no significant effect on the performance parameters. Results of the study showed that heated cowpea can be included at the rate of 300 g/kg in diets of broilers and that supplementation of such diets with phytase resulted increased P digestibility and better performance in broilers.

Key Words: phytase, phosphorus digestibility, broilers

T211 Effect of Ronozyme ProAct supplementation on growth and meat yield responses of broilers during a forty-two-day production period. W. A. Dozier III*[1], N. E. Ward[2], and S. L. Vieira[3], [1]*Auburn University*, *Auburn, AL*, [2]*DSM Nutritional Products, Inc.*, *Parsippany, NJ*, [3]*Universidade Federal do Rio Grande do Sul*, *Porto Alegre, RS, Brazil*.

Large price differentials between corn and soybean meal have resulted in strategies to reduce diet cost for broilers. A novel protease (Ronozyme ProAct) has been reported to improve amino acid digestibility of feed ingredients. This study examined growth and meat yield responses of broilers provided diets with reduced amino acid density supplemented with or without Ronozyme ProAct. Sixteen hundred Ross × Ross 708 male broilers were randomly distributed into 64 floor pens (25 birds per pen; 0.09 m^2/bird) at 1 d of age and fed 5 dietary treatments until 42 d of age. Dietary treatments consisted of a 1) Positive Control (PC), 2) Negative Control (NC) 4% reduction in amino acid density, 3) Dietary treatment 2 + 200 ppm of Ronozyme ProAct, 4) NC 6% reduction in amino acid density, and 5) Dietary treatment 4 + 200 ppm of Ronozyme ProAct. Dietary amino acid specifications of the PC were considered to be moderate density. Dietary treatments 2 to 5 had amino acid density reduced by 4 or 6% compared with the PC. Primary ingredients consisted of corn, soybean meal, distillers dried grains with solubles (5% inclusion), and meat and bone meal (5% inclusion). Each treatment was represented by 12 replicate pens. BW gain, feed intake, feed conversion, mortality, and processing yields were assessed. Ronozyme ProAct supplementation increased ($P \leq 0.001$) BW gain from 1 to 14 d of age compared with NC with both 4% and 6% amino acid reductions and Ronozyme ProAct inclusion improved ($P \leq 0.02$) 14 d feed conversion with decreasing amino acid density by 4%. Broilers fed the PC diet had advantages ($P \leq 0.05$) in growth performance, carcass weight, and total breast meat weight compared with NC diets. In summary, Ronozyme ProAct supplementation improved growth performance during the starter period.

Key Words: amino acid, broiler, protease

T212 Influences of several enzyme containing β-glucanase and xylanase on meat yield of broilers fed barley-based diet. H. Shirzadi*, H. Moravej, M. Shivazad, and F. Fatehi, *Department of Animal Science, Faculty of Agriculture and Natural Resources, University of Tehran*, *Karaj, Tehran, Iran*.

The goal of this investigation was to compare the effects of 4 enzyme preparations containing β-glucanase and xylanase activities on performance and meat yield of broiler chicks fed barley-based diet with and without enzyme. Enzyme A provided per kilogram of diet (endo-1,4-β-glucanase activity: min 800 units; endo-1,(4)-β-glucanase activity: min 1800 units; endo-1,4-β-xylanase activity: min 2600 units), enzyme B (endo-1,3(4)-β-glucanase: 100 AGL; endo-1,4-β-xylanase: 1100 visco units), enzyme C (endo-1,4-β-glucanase: 1500 BGU; endo-1,4-β-xylanase: 3600 FXU), enzyme D (1420 units; xylanases: 660 units). One hundred ninety-five male day-old broiler chicks (Ross 308) were randomly allocated to 5 treatment groups, with 3 replicates and 13 birds per replicate in floor pen. All data was analyzed through the General Linear Model procedure SAS for a randomized complete block design. The 5 dietary treatments consisted of the barley (60%) supplemented with and without enzyme (A, B, C, and D added on top to diets). All parameters were measured at 42d. Body weight was increased by addition all enzymes ($P < 0.05$), and significant differences were not observed among all enzymes. However, feed intake was not significantly affected by enzyme supplementation. Feed conversion ratio, carcass weight and relative weight of the abdominal fat were significantly improved by addition all enzymes compared with the barley-based diet without enzyme ($P < 0.05$), and no significant differences were found among all enzymes. Carcass yield, relative weight of the breast, legs, liver, and gizzard as percentage of live weight were not affected by enzyme supplementation ($P > 0.05$). The results of current study led to the conclusion that there were similar improvements on performance and meat yield of birds fed diets with enzyme supplementation. Therefore, choice preference of supplementation should be based on its economic value.

Key Words: xylanase, β-glucanase, meat yield

T213 Effect of high levels of phytase for broilers. C. Meneghetti, A. G. Bertechini*, J. A. G. Brito, and S. F. Castro, *Universidade Federal de Lavras*, *Lavras, MG, Brazil*.

Three trials were carried out to evaluate the effects of supplementation of Citrobacter braaki, an *E. coli* derived phytase preparation (Genophos), on the performance, AMEn, retention and excretion of minerals and bone ash of broiler chickens. Broiler performance was evaluated using 3-phase feeding program (1–21 d, 22–35 d and 36–42 d of age). In trial 1, a total of 1456 d-old, male Cobb 500 broiler chicks were placed in 56 litter floored pens in a complete randomized design with 8 replicates/treatment. The treatment diets were: (1) Control (C-SBM based diet and no added phytase); (2) 1,500; (3) 3,000; (4) 4,500; (5) 6,000; (6) 8,000 and (7) 10,000 FTU/kg of supplemented phytase. All treatments with phytase had reduction in ME of 85 kcal/kg, Ca of 0.2% and available P 0.12%. In trial 2, 280 10-d-old male Cobb 500 broiler chicks were allotted in 56 metabolism cages to obtain the apparent digestibility of DM, CP, AMEn, Ca and P retention using the same diet from 1 to 21 d of the trial 1, and the excreta collection from 15 to 17 d of age. For trial 3, 168 28-d-old male Cobb 500 broiler chicks were placed in the same diet from 22 to 35 d of trial 1 and excreta collection between 33 and 35 d of age. Results showed that bird performance was similar of controls when 4,500 FTU/kg or higher of phytase inclusion occurred from 1 to 21 d. From 1 to 35 and 1–42 d, the treatments were comparable to control. A quadratic effect ($P < 0.05$) was observed (10–17 d) for AMEn and Ca retention at maximum values obtained with 7,727 and 5,500 FTU/kg of diet, respectively. A linear ($P < 0.05$) improvement in P retention was observed with increased phytase supplementation. At 32–35 d, a quadratic effect ($P < 0.05$) was observed on Ca retention with maximum values at 5,000 FTU/kg of diet. P retention increased (linear effect) with phytase supplementation ($P < 0.05$). Ash, Ca and P in the tibia (42 d) were not affected by treatments. Phytase supplementation starting at 4,500 FTU/kg improved broiler performance challenged in ME, Ca and P.

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Key Words: available P, Ca retention, nutrient digestibility

T214 Effect of enzymes in the diet of hens on egg quality. F. G. P. Costa*[1], M. L. Ceccantini[2], C. S. Santos[1], C. C. Goulart[1], C. F. S. Oliveira[1], G. B. V. Lobato[1], J. M. Freire[1], V. P. Rodrigues[1], R. C. Lima[1], I. S. Nobre[1], and R. C. L. Neto[1], [1]*Federal University of Paraiba*, *Areia, PB, Brazil*, [2]*Adisseo Brazil Animal Nutrition*, *Sao Paulo, SP, Brazil*.

This study aims to demonstrate the technical feasibility and economic use of the set of a 6-phytase, 17 Carbohidrolases and 2 proteases (from the supply Rovabio Max AP) in diets for laying hens. The experiment was divided in 5 periods of 28 d each, which were used 360 hens, distributed in a completely randomized design with 5 treatments and 8 replicates of 9 birds per experimental unit. The treatments consisted of 2 diets without enzyme and 3 with the addition of the enzyme. Diets without enzymes were negative and positive controls. The positive control diet (PC) was formulated to meet the requirements of hens. The negative control diet (NC) was formulated with nutrient reduction (100 kcal / kg and 0.36, 0.014, 0.012, 0.12, and 0.153% in the levels of CP, lysine, methionine + cystine, calcium and phosphorus available, respectively). Diets supplemented with 50 g / ton of Rovabio Max AP were formulated to address different levels of linoleic acid, one with the linoleic acid diet equal to CN, the other with an intermediate value and the last with linoleic acid equal to diet PC. These diets have been reformulated considering the nutritional enzyme formulation. Thus, the three diets supplemented with enzymes have been reformulated to meet the nutritional levels of the control diet, except for linoleic acid.). All diets based on corn and soybeans. The data were subjected to analysis of variance with means tested with Tukey and orthogonal contrasts. The weight and percentage of egg specific gravity and pigmentation of the eggs were influenced (P <0.05) by nutrition and supplementation with enzymes. Enzyme supplementation Rovabio Max AP proves efficient in the availability of nutrients to improve the quality of eggs.

Key Words: additive, linoleic acid, production

T215 Use of enzyme complex on the performance of layer hens. F. G. P. Costa*[1], M. L. Ceccantini[2], C. S. Santos[1], C. C. Goulart[1], C. F. S. Oliveira[1], G. B. V. Lobato[1], and J. M. Freire[1], [1]*Federal University of Paraiba*, *Areia, PB, Brazil*, [2]*Adisseo Brazil Animal Nutrition*, *Sao Paulo, SP, Brazil*.

This study aims to demonstrate the technical feasibility and economic use of the set of a 6-phytase, 17 Carbohidrolases and 2 proteases (from the supply Rovabio Max AP) in diets for laying hens. The experiment was divided in 5 periods of 28 d each, which were used 360 hens, distributed in a completely randomized design with 5 treatments and 8 replicates of 9 birds per experimental unit. The treatments consisted of 2 diets without enzyme and 3 with the addition of the enzyme. Diets without enzymes were negative and positive controls. The positive control diet (PC) was formulated to meet the requirements of hens. The negative control diet (NC) was formulated with nutrient reduction (100 kcal / kg and 0.36, 0.014, 0.012, 0.12, and 0.153% in the levels of CP, lysine, methionine + cystine, calcium and phosphorus available, respectively). Diets supplemented with 50 g / ton of Rovabio Max AP were formulated to address different levels of linoleic acid, one with the linoleic acid diet equal to CN, the other with an intermediate value and the last with linoleic acid equal to diet PC. These diets have been reformulated considering the nutritional enzyme formulation. Thus, the three diets supplemented with enzymes have been reformulated to meet the nutritional levels of the control diet, except for linoleic acid. The production and feed conversion per dozen eggs were affected (P <0.05) by nutrition and supplementation with enzymes. The enzyme Rovabio Max AP was effective in providing nutrients from food for birds. Despite reductions in nutrient levels are higher than recommended by the manufacturer, the use of carbohidrolase, phytase e protease ensures the same productivity in the control group, confirming the effectiveness of the enzyme complex.

Key Words: additive, linoleic acid, production

T216 Dietary supplementation with two types of enzyme preparations improves nutrient digestibility in growing pigs. X. Ao*[1], S. M. Hong[1], H. Y. Park[2], K. H. Son[3], B. H. Ku[3], D. H. Shin[3], and I. H. Kim[1], [1]*Department of Animal Resource and Science, Dankook University*, *Cheonan, Choongnam, Korea*, [2]*Korea Research Institute of Bioscience and Biotechnology*, *Daejeon, Korea*, [3]*Insect Biotech Co. Ltd.*, *Daejeon, Korea*.

The objective of this experiment was to determine the effects of 2 types of enzyme preparations (single or complex) on fecal digestibility and ileal apparent digestibility (AID) in the hindgut of growing pigs. Three ileal–cannulated growing barrows (28.56 ± 0.58kg) were housed in individual metabolism crates and randomly assigned to 1 of 3 treatments within a 3 × 3 Latin square design. The treatments were as follows: 1) CON (basal diet), 2) P1 (basal diet + 0.1% protease), and 3) P2 (basal diet + 0.1% complex enzyme including protease, xylanase and lipase). The 3 feeding periods consisted of 4 d of acclimation to the diet followed by 5 d of fresh feces samples collection and 6 and 7 d of ileal-digesta collection. Ileal effluents were continuously collected for the same 12–h interval each day. Pigs fed the P1 diet had a higher DM and energy digestibility ($P < 0.05$) than pigs fed the CON and P2 diets, while the N digestibility was greater ($P < 0.05$) in the CON and P1 groups than in the P2 group. The AID of DM and energy was increased ($P < 0.05$) in the P1 and P2 groups when compared with the CON group, with the P1 treatment showing the highest levels. The AID of N digestibility was also greater ($P < 0.05$) for pigs fed the P1 diet than for those fed other diets. Pigs fed the P1 diet had a higher AID of total essential AA and non-essential AA ($P < 0.05$) than those fed the CON and P2 diets. A similar tendency was also observed in individual AA ileal digestibility. In conclusion, these results showed that the single protease addition improved nutrient digestibility.

Key Words: enzyme, nutrient digestibility, growing pigs

T217 Effects of dietary Tylan inclusion level on the growth performance and carcass characteristics of growing–finishing pigs. C. L. Puls*[1], M. Mercedes[1], M. Ellis[1], A. M. Gaines[2], B. A. Peterson[2], B. F. Wolter[2], and M. Kocher[2], [1]*University of Illinois*, *Urbana*, [2]*The Maschhoffs*, *Carlyle, IL*.

This study was carried out to evaluate the effect of including Tylan in the diet of growing-finishing pigs on growth performance and carcass characteristics. The study was carried out from 39.9 ± 1.45 kg to 127.2 ± 1.13 kg BW and compared 2 Tylan inclusion levels (0 vs. 10 g/ton). Diets were formulated to meet or exceed the nutrient requirements proposed by NRC (1998). The study involved 144 barrows housed in pens of 9 with 8 pens per inclusion level. Pigs had ad libitum access to feed and water throughout the study period. At the end of the study period, pigs were sent to a commercial facility for harvest and carcass evaluation. There was no effect ($P > 0.05$) of Tylan inclusion level on overall ADG, ADFI, or G:F ratio. Mortality levels were lower for pigs fed Tylan compared with the control (0.00 vs. 2.82%, respectively); however, this difference was not significant ($P = 0.15$). There was a trend ($P = 0.06$) for carcass yield to be greater for pigs fed Tylan compared with the control (74.9 vs. 74.3%, respectively; SEM 0.42) and this resulted in an improvement ($P < 0.01$) in carcass G:F ratio for pigs fed Tylan (0.26 vs. 0.25 kg:kg, respectively; SEM 0.004). There was no

effect ($P > 0.05$) of Tylan inclusion level on back fat thickness, *Longissimus* muscle depth, or predicted carcass lean content. In conclusion, this study suggests that feeding Tylan (at 10 g/ton) to growing-finishing pigs does not affect live weight growth performance but could reduce mortality, and improve carcass yield and carcass feed efficiency, findings that warrant validation.

Key Words: pigs, growth, Tylan

T218 Effect of a protease enzyme on performance of weanling piglets fed corn-soybean diets with different protein levels. D. Wang[1], X. Piao[1], F. C. Guo[2], H. Cao[2], J. Zhao[2], and R. J. Harrell*[2], [1]*China Agricultural University*, *Beijing, China*, [2]*Novus International Inc.*, *St Charles, MO*.

Application of exogenous enzymes can improve the digestibility of feedstuffs, lower dietary costs, and improve animal performance. The objective of the present study was to examine the benefits of supplementing nursery pig diets with a protease enzyme (NZ) at 2 levels of dietary protein. A total of 190 pigs (8.31 ± 0.63 kg of BW) were allotted by weight and sex to one of 4 treatments in a 2 × 2 factorial arrangement with the factors being high (HP, 20.3% CP) vs. low dietary protein (LP, 18.3% CP) and 0 vs. 500 mg/kg protease (Cibenza DP100, Novus International Inc., St. Charles, MO) for a period of 21 d with 6 replicates (n = 7 or 8 pigs/pen). All the diets were formulated according to an ideal amino acid pattern. CP level did not alter ADFI ($P > 0.83$), ADG ($P > 0.73$), or GF ($P > 0.57$). No differences were observed for the NZ on ADG ($P > 0.20$) or ADFI ($P > 0.22$). The GF was improved by 17% with the addition of NZ (0.623 vs. 0.728 ± 0.016; $P < 0.01$), regardless of dietary CP level. The digestibility of DM, OM, or energy was not affected by dietary CP level ($P > 0.45$). The addition of NZ increased CP digestibility by 3.5% (84.3 vs. 87.2 ± 0.5%, $P < 0.01$), increased DM digestibility by 2.2% (86.1 vs. 88.0 ± 0.4%, $P < 0.01$), and energy by 2.3% (86.5 vs. 88.5 ± 0.4%, $P < 0.01$), regardless of dietary CP level. Blood urea nitrogen levels were higher in pigs fed HP compared with LP (4.0 vs. 2.58 ± 0.21 mmol; $P < 0.01$). The addition of NZ interacted with CP level on BUN levels by increasing BUN in HP, but not in LP dietary CP ($P < 0.02$). These results indicate that the addition of a protease enzyme can improve digestibility of feedstuffs and improve feed efficiency in nursery pigs.

Key Words: swine, nursery, protease

T219 Effects of supplementing different enzymes on performance, nutrient digestibility and blood metabolites in growing pigs. J. K. Jo[1], P. L. Shinde[1], J. S. Kim[1], Y. W. Kim[1], K. H. Kim[1], J. D. Lohakare[1], C. S. Ra[1], J. H. Lee[2], and B. J. Chae*[1], [1]*Kangwon National University*, *Kangwon National University, Chuncheon, Rep. of Korea*, [2]*CTC Bio. Inc.*, *CTC Bio. Inc., Seoul, Rep. of Korea*.

A 28-d growth study was conducted to investigate the effects of mannanase (M), amylase + mannanase (AM), mannanase + protease (MP) and amylase + mannanase + protease (AMP) supplementation on the performance, apparent total tract digestibility (ATTD) of nutrients and blood metabolites in growing pigs. A total of 240 growing pigs (initial BW 55.58 ± 0.85 kg) were randomly allotted to 5 treatments on the basis of BW. Each treatment was comprised of 4 replicates with 12 pigs in each. A corn-soybean meal based diet (control) was supplemented with 0.05% M, AM, MP or AMP as dietary treatments. Pigs fed enzyme supplemented diets had greater ($P < 0.05$) ADG and ATTD of DM than pigs fed control diet. Moreover, pigs fed AMP diet had higher ($P < 0.05$; 949 vs. 918, 933 and 929 g) ADG than pigs fed M, MP and AM diets. Pigs offered AMP and MP diets had better F/G ($P < 0.05$; 2.91 and 2.95 vs. 3.05 g/g) than pigs fed control diet. In addition, pigs fed MP diet gained more ($P < 0.05$; 933 vs. 918 g) when compared with pigs offered M diet. The ATTD of DM was higher ($P < 0.05$; 81.29 vs. 80.50%) in pigs fed AMP diet when compared with pigs fed M diet; while the ATTD of CP was higher ($P < 0.05$; 76.44 vs. 75.24 and 75.21%) in pigs fed AMP diet when compared with pigs fed AM and control diets. Additionally, the blood urea nitrogen concentration was greater ($P < 0.05$; 17.75 vs. 14.15 and 13.50 g/dl) in pigs fed MP diet when compared with pigs fed AM and control diet. These results indicate supplementation of different enzymes in combination (mannanase + protease and amylase + mannanase + protease) to be more efficient in improving the performance and nutrient digestibility in growing pigs.

Key Words: enzymes, performance and nutrient digestibility, growing pigs

T220 Evaluation of the effects of dietary enzyme on growth performance, nutrient digestibility, blood characteristics and ileal digestibility in growing pigs. L. Yan*, H. D. Jang, T. X. Zhou, X. Ao, J. H. Jung, and I. H. Kim, *Department of Animal Resource and Science, Dankook University*, *Cheonan, Choongnam, Korea*.

Two experiments with growing pigs were conducted to investigate the effects of 2 distinct multi–enzyme preparations on nutrient digestibility, growth performance and blood profiles. In Exp.1, a total of 96 pigs (29.7 ± 0.69 kg) were used in a 42-d performance and digestibility trial using 4 dietary treatments: CON (control diet), E (control+0.10% Endopower), N1 (control+0.10% NSPase) and N2 (control+0.20% NSPase). Endopower is a commercial multi-enzyme preparation that contains α-galactosidase, galactomannase, xylanse and β-glucanase. NSPase primarily contained α-1,6-β-galactosidse, β-1,4-mannanase, and β-1,4-mannosidase. There were 6 replication pens per treatment with 4 pigs per pen. Pigs fed the N1 diet had a higher ADG ($P < 0.05$) and G:F ($P < 0.05$) than those fed the control diet. There were no significant differences in the ADG and G:F among the multi-enzyme treatments ($P > 0.05$). When compared with the control, the apparent digestibility of DM was increased ($P < 0.05$) by E treatment. The N digestibility was improved ($P < 0.05$) in response to multi-enzyme treatments during the experimental period. In addition, BUN was higher ($P < 0.05$) in the E treatment group than in the CON and N1 treatment groups at the end of the experiment, while the level of glucose was improved ($P < 0.05$) by E and N2 treatments. In Exp.2, 4 ileal-cannulated growing barrows (20.17 ± 1.31 kg) were housed in individual metabolism crates and randomly assigned to 1 of 4 treatments (same as Exp.1) within a 4 × 4 Latin square design. Enzyme supplementation improved the majority of apparent ileal AA digestibility ($P < 0.05$). These findings demonstrated that supplementation of the diet of these enzymes could improve the feeding values of growing pigs fed a diet based on corn and soybean meal.

Key Words: enzyme, digestibility, growing pigs

T221 Protease increased in vitro digestibility of various feed ingredients. F. Yan*, P. Disbennett, M. Schulz, M. Vazquez-Anon, N. Odetallah, S. Carter, and D. Dowell, *Novus International Inc.*, *St. Charles, MO*.

A protease (CIBENZA DP100, Novus International Inc.) was evaluated in an in vitro system to evaluate its ability to degrade proteins in a variety of feed ingredients and it was also compared with a commercial protease, denoted as Protease B. Soybean meal, canola meal, cottonseed meal, DDGS, corn, wheat, lupin, poultry meal, meat and bone meal, fish meal, feather meal, and blood meal were tested in the study. Each

test ingredient was solubilized for 4 h at pH 2.4 and protein concentration of 8 mg/ml, buffered to pH 7.5, and then incubated with either DP100 or Protease B for 18 h at 37°C, at an enzyme concentration that it would encounter in the digesta in vivo when it is used at the recommendation dose based on the assumption of water intake being twice of feed intake. For negative control, deionized water was added. After 18 h of incubation, OPA (o-phthaldialdehyde) analysis with UV-vis spectroscopy was performed to measure β ± -amino groups. All tests were performed in quadruplicate. Both DP100 and Protease B demonstrated proteolytic activity for all ingredients tested ($P < 0.0001$) compared with the negative control, which indicated broad substrate specificity of these proteases. Their ability to hydrolyze proteins from different feed ingredients varied where they were most effective in hydrolyzing blood meal proteins and less efficient for corn and feather meal proteins. Cibenza DP100 outperformed Protease B for all ingredients ($P < 0.05$) except for corn. The percent increase in absorbance of DP100 over Protease B was 23.0% for soybean meal, 27.3% for canola meal, 42.0% for cottonseed meal, 59.4% for DDGS, 39.5% for wheat, 51.6% for lupin, 13.4% for poultry meal, 20.9% for meat and bone meal, 12.8% for fish meal, 7.3% for feather meal, and 32.1% for blood meal. These results demonstrated efficacy of CIBENZA DP100 in digesting proteins from various feed ingredients and it can be beneficial in improving protein digestion of animals fed diets containing these ingredients.

Key Words: protease enzyme, in vitro, digestibility

T222 Effects of graded levels of phytase on the apparent and standardized total tract digestibility of phosphorus in corn and corn co-products. F. N Almeida* and H. H. Stein, *University of Illinois*, *Urbana*.

An experiment was conducted to measure the effects of graded levels of microbial phytase on the standardized total tract digestibility (STTD) of P in corn, distillers dried grains with solubles (DDGS), high protein distillers dried grains (HP-DDG), and corn germ. A second objective was to develop regression equations to predict the response of adding phytase to each of these ingredients. Four corn based diets, 4 DDGS based diets, 4 HP-DDG based diets, and 4 corn germ based diets were formulated. The 4 diets with each ingredient contained 0, 500, 1,000, or 1,500 phytase units (FTU) per kg (Optiphos 2000, Enzyvia, Sheridan, IN). A P-free diet was also formulated to measure the basal endogenous losses of P. A total of 102 pigs (initial BW: 18.2 ± 2.1 kg) were individually housed in metabolism cages equipped with a feeder and a nipple drinker and a screen floor that allowed for total collection of feces. Pigs were allotted to the 17 diets in a randomized complete block design with 6 replicates per diet. Supplementation of microbial phytase increased (linear, $P < 0.01$; quadratic, $P < 0.05$) the STTD of P in corn from 40.9 to 67.5, 64.5, and 74.9%, tended to increase (linear, $P = 0.07$) the STTD of P in DDGS from 76.9 to 82.9, 82.5, and 83.0%, increased (linear, $P < 0.01$; quadratic, $P < 0.05$) the STTD of P in HP-DDG from 77.1 to 88.0, 84.1, and 86.9%, and increased (linear and quadratic, $P < 0.01$) the STTD of P in corn germ from 40.7 to 59.0, 64.4, and 63.2% in diets supplemented with 0, 500, 1,000, or 1,500 FTU/kg of phytase, respectively. Regression equations were developed to allow the calculation of the STTD of P with any level of phytase (Optiphos 2000, Enzyvia, Sheridan, IN) for each of the test ingredients. Therefore, results of this experiment allow the prediction of the amount of digestible P in these ingredients containing any level of phytase between 0 and 1,500 FTU.

Key Words: digestibility, phosphorus, phytase

T223 Effects of multi-enzyme on nutrients digestibility and metabolizable energy values of pure corn and wheat diets. G. G. Zhang*, Z. B. Yang, Q. Q. Zhang, W. R. Yang, and S. Z. Jiang, *Shandong Agricultural University*, *Taian, China*.

Objectives of this study were to determine effects of enzyme supplementation in pure corn- and wheat-based diets on energy efficiency and nutrients utilization in poultry. By force-fed true metabolizable energy bioassay (TME Bioassay) method, a metabolic trial was conducted, 90 healthy adult roosters with similar weight were randomly assigned to 10 dietary groups with 3 replicates of 3 roosters for each, 2 of the groups (controls) were not force-fed during experiment for collecting endogenous excreta, other groups were force-fed corn with different levels multi-enzyme (0, 50, 100, and 150 mg/kg of diet), or force-fed wheat with different levels multi-enzyme (0, 50, 100, and 150 mg/kg of diet), respectively. The results showed the use of multi-enzyme preparation in corn enhanced the apparent/true digestibility (AD/TD) of neutral detergent fiber (NDF) ($P < 0.05$), dry matter (DM) ($P < 0.05$), and starch ($P < 0.05$), the apparent metabolizable energy (AME) value and true metabolizable energy (TME) value were increased by 6.76%, and 5.86% respectively. Inclusion of multi-enzyme in wheat improved the AD/TD of NDF($P < 0.05$), DM($P < 0.05$) and starch ($P < 0.05$), AME and TME were enhanced by 9.75%and 8.88% respectively. Nutrients digestibility and metabolizable energy values showed linear or quadric increasing trend, with the amount of multi-enzyme added in corn and wheat. It appears from this study that the nutrients utilization of pure corn or wheat diet could be enhanced by using appropriate multi-enzyme supplement. However, an proper addition is necessary in corn to maximize the nutrients utilization and energy conversion, and higher rates of supplementation did not lead to further increase in nutrients digestibility and ME values.

Key Words: multi-enzyme, digestibility, metabolizable energy

T224 Effect of Rovabio Max on energy and nitrogen utilization in diets high in distillers dried grains with solubles. A. J. Karimi*[2], Y. Min[1], J. H. Park[1], C. A. Coto[1], C. Lu[1], F. Yan[1], and P. W. Waldroup[1], [1]*University of Arkansas*, *Fayetteville,* [2]*University of Kurdistan*, *Kurdistan, Iran*.

The inclusion of DDGS in poultry diets is limited due the reduced content of starch and high levels of Non Starch Polysaccharides (NSP). An improvement on the nutrient availability through the use of exogenous enzymes represents an alternative to increase its utilization. Rovabio Max is a preparation containing xylanases, β-glucanases, pectinases, mannanases, phytase and α-galactosidase. A study was conducted to evaluate the use of Rovabio Max on utilization of diets containing high levels of DDGS. The experimental design consisted of a 2 × 4 factorial arrangement. Two isocaloric (ME = 3020 kcal/kg) basal diets were formulated, one with no DDGS and the second with 30% DDGS of known composition. Chromic oxide was used as an indigestible marker. Aliquots of the 2 basal diets were supplemented with no enzyme or 3 levels of Rovabio: The recommended level (1X), twice (2X) and 4 times (4X) the recommended level. One hundred and 90 2 male chicks of a commercial strain (Cobb 500) were fed a common nutritionally complete diet to 18 d at which time they were placed on the study. Each experimental diet was fed to 4 pen replicates of 6 male chicks in wire floor battery cages. After a 5-d adaptation period, excreta samples were collected and freeze-dried to determine GE, AME and N retention. Birds were weighed and feed consumption determined. The ANOVA considered DDGS level, enzyme, and interaction. No significant ($P > 0.05$) effect of Rovabio, DDGS and their interactions was found on body weight, feed intake, feed conversion and mortality. No effect of the enzyme was found for

GE, N in excreta, N retention, AME and AMEn. No interaction between DDGS and Rovabio was found for nitrogen and energy utilization. The inclusion of 30% DDGS in the diet significantly ($P < 0.05$) increased the GE and N in excreta with no effect on AME and AMEn values. The increased concentration of nutrients in excreta deserves consideration due to environmental implications.

Key Words: DDGS, enzymes, digestibility

T225 Effect feed processing method and enzyme supplementation of wheat- based diets on performance, gastrointestinal and carcass characteristics in broiler chicks. Z. Qobadi and A. Karimi*, *University of Kurdistan, Sanandaj, Kurdistan, Iran*.

This study was carried out to compare the effects of feed processing (pelleted vs. mash) and enzyme supplementation (with and without 0.3g Grindazym GP 15000 /kg of wheat in complete diet) in a wheat-based diet on performance, gastrointestinal and carcass characteristics of broiler chicks to 36 d of age. Ross 308 straight-run broiler chicks (n = 336) were randomly allocated to 4 dietary treatments, each replicated 4 times (21 chicks per pen) in a completely randomized design in a 2 × 2 factorial arrangements. Measurements included body weight (BW), daily gain (DG), feed intake (FI) and feed conversion ratio (FCR) at 20 and 36 d of ages. The relative weights of gastrointestinal organs to body weight were determined at 20 and 36 d of ages. The pH of ileum digesta content was also determined at 20 d of age. The results showed that the broiler chicks fed pelleted diets had significantly improved BW at 36 d of age, DG during 20 to 36 and 0 to 36 d of ages and FI during 0 to 20, 20 to 36 and 0 to 36 d growth period. Feed conversion ratio was significantly increased in pelleted fed treatment during 0–20 and 0 - 36 d growth period. Enzyme supplementation had significantly improved BW at 20 and 36 d of age, DG during 0–20, 20–36 and 0–36 d of ages, FI during 0 to 20 and 0 to 36 d of ages and FCR during 0–36 d of ages. The interaction between feed processing and enzyme supplementation was only significant on FCR during 20–36d. Neither feed processing nor enzyme supplementation had significant effects on ileum digesta pH measurements, carcass and gastrointestinal characteristics, except gizzard relative weight at 36 d of age. In conclusion, the results of this experiment confirmed the beneficial effects of both pelleting and feed enzyme supplementation on broiler chicks' performance.

Key Words: wheat, processing, enzyme

T226 Calcium chloride reduces the negative impact of feeding high potassium and co-product containing diets to finishing pigs. J. Guimaraes*, C. L. Zhu, D. Wey, and C. F. M. de Lange, *University of Guelph*, *Guelph, Ontario, Canada*.

Co-products from the biofuel and human food industries may serve as alternative pig feed ingredients. Previously, we observed a reduction in animal performance when pigs were liquid-fed high potassium (K) diets containing corn steep water (CSW) and whey permeate (WP). This study was conducted to investigate the addition of calcium chloride ($CaCl_2$) to pig diets to reduce the negative impact of feeding high K levels. A total of 192 purebred Yorkshire pigs (average initial BW 45.5 kg; 4 gilts and 4 barrows per pen) were liquid-fed 1 of 6 diets over a 9 week period: (1) CSBM (Corn and soybean meal based diet with added 0.9% potassium carbonate; 0.98% K); (2) CSBM/$CaCl_2$-mEq (CSBM with added 0.84% $CaCl_2$); (3) CSBM/$CaCl_2$ (CSBM diet with added 1.05% $CaCl_2$); (4) Co-prod (22% WP, 6% CSW, 1.28% K); (5) Co-prod/$CaCl_2$-mEq (Co-prod diet with added 0.87% $CaCl_2$); (6) Co-prod/$CaCl_2$ (Co-prod diet with added 0.68% $CaCl_2$). Diets 2 and 5 were formulated to an electrolyte balance of 166 mEq/kg; diets 3 and 6 were designed to maintain a target balance between K and Cl. Data were exposed to analyses of variance using GLM of SAS with treatment as the only source of variation; treatment means were compared using orthogonal contrasts. Diet did not influence feed intake ($P > 0.05$). For CSBM, adding $CaCl_2$ at both levels improved feed to gain (2.36 vs 2.57; $P < 0.01$); such response was not seen for Co-prod ($P > 0.10$). Hot carcass weight and carcass lean yield did not differ among treatments ($P > 0.05$). For Co-prod, adding $CaCl_2$ reduced plasma carbon dioxide levels ($P < 0.01$). Based on quantitative histology observations, the addition of $CaCl_2$ to Co-prod eliminated damage to walls of glomeruli capillaries. Optimal $CaCl_2$ additions to high K diets are still to be confirmed. These results suggest that some of the negative effects of feeding high K co-product containing diets to pigs can be reduced, reducing the reliance on traditional feed ingredients for pigs.

Key Words: pigs, calcium chloride, co-products

T227 Production and characterization of a thermostable beta-propeller phytase from *Bacillus licheniformis*. S. J. Fu*1,3, J. Y. Sun[1], X. Y. Weng[2], L. C. Qian[1], and Z. Q. Shen[4], [1]*Microbiology Division, Institute of Feed Science, College of Animal Science, Zhejiang University*, *Hangzhou Zhejiang, China*, [2]*College of Life Science, Zhejiang University*, *Hangzhou Zhejiang, China*, [3]*Binzhou Animal Husbandry and Veterinary Research Institute*, *Binzhou Shandong, China*, [4]*Shandong Lvdu Biological Technology Co., Ltd*, *Binzhou Shandong, China*.

A novel β-propeller phytase producing thermophilic strain of *Bacillus licheniformis* was isolated from soil. The optimal fermentation parameters for producing phytase by *B. licheniformis* under shake flask culture were determined by single factor test and the results were as follows: 1.0% dextrose used as carbon source, 0.1% $(NH_4)_2SO_4$ as nitrogen source, initially pH7.5, incubation temperature 55°C. After incubation for 36h under these conditions, the activity of neutral phytase reached 0.267 U/mL with specific activity 0.701U/mg. The optimum temperature and pH of the phytase from *B. licheniformis* (PhyC) were 55°C and 7.0, respectively. After treated at 80°C, pH 7.0 for 10 min, the residual activity of PhyC was 57.36%. Over 80% of PhyC activity was retained after treatment by preincubation over a pH range of 6.5–9.0 for 1 h at 25°C. As for substrate specificity, it was very specific for sodium phytate and showed no activity on other phosphate esters. Its activity was greatly inhibited by EDTA and metal ions such as Cd^{2+}, Mn^{2+}, Cu^{2+} and Ba^{2+}.

Key Words: *Bacillus licheniformis*, phytase, characterization

T228 A Lysozyme supplement for piglets: Weaned pigs responses to *Escherichia coli* K88$^+$ (ETEC) oral challenge. E. Kiarie*[1], S. Bhandari[1], D. O. Krause[1], G. Zhang[2], and C. M. Nyachoti[1], [1]*University of Manitoba*, *Winnipeg, MB, Canada*, [2]*Neova Technologies Inc.*, *Abbotsford, BC, Canada*.

Lysozyme is a low-molecular-weight protein with antimicrobial properties. An experiment was conducted to investigate response of piglets receiving Entegard (EG, a water-soluble lysozyme antimicrobial blend) upon oral challenge with ETEC. A total of 36 individually housed weanlings were randomly allotted to 1 of the 4 treatments to give 9 pens per treatment. Treatments were control (C, no additive), antibiotic (AB, in-feed) and EG (EG1 and EG2, in-water). All pigs received a basal diet similar in composition and nutrients (NRC, 1998), except AB pigs which had an added Aureo SP 250. Entegard was delivered in the drinking water: EG1, 0.1% and EG2, 0.2%. Pigs were acclimatized to treatments for a 7-d period to monitor growth performance. On d 8, each pig was bled to obtain serum and gavaged with 6 mL (2×10^9 cfu/ml) of

ETEC. Pigs were monitored for another 7 d to assess severity of diarrhea using a fecal consistency scoring system and growth performance, subsequently all pigs were killed to obtain intestinal tissues and digesta samples. Treatments did not influence ($P > 0.10$) growth performance throughout the study. More ETEC counts were observed on the ileal ($P = 0.001$) and colon ($P = 0.025$) mucosal scrapings of the C pigs than AB and EG1 pigs which in turn showed numerically lower incidences on diarrhea than C. Pigs receiving AB and EG1 had higher small intestine weight and ileal villous height than those receiving C, however, ileal villi height to crypt depth ratio for EG1 (1.56) and EG2 (1.38) was similar to that of AB (1.68) pigs which was in turn higher than that of C (1.34) pigs. Pigs in the EG1 group showed higher ($P < 0.001$) serum tumor necrosis α (TNF-α) and interleukin 6 (IL-6) before ETEC challenge, however, 7-d post-challenge pigs receiving EG2 showed ($P < 0.05$) the least circulating TNF-α and IL-6. Overall, better intestinal growth and development as well as lower ETEC counts on the intestinal mucosal and serum pro-inflammatory cytokines suggest that Entegard can maintain gut health and function in piglets commensurate to antibiotics.

Key Words: lysozyme, piglet performance, gut health and function

T229 Effect of microbial phytase on growth performance, plasma phosphorus concentration and tibia mineralization of broilers according to dietary calcium and phosphorus concentrations. M. P. Letourneau Montminy*[1], N. Meme[2], M. Magnin[3], and A. Narcy[2], [1]*Agriculture and Agri-Food Canada*, *Sherbrooke, Qc, Canada*, [2]*INRA UR83*, *Nouzilly, France*, [3]*BNA Nutrition Animale*, *Chateau-Gontier, France*.

One hundred ninety-two 4-d-old Ross broilers were used to investigate the effect of microbial phytase according to various dietary non-phytate P (NPP) and Ca concentrations on growth performance, plasma P concentration and bone mineralization. Broilers were fed maize-soybean meal diets from 4 to 21 d of age in a 4 × 2 x 2 factorial arrangement with varying concentrations of Ca (0.5, 0.75, 1.0 and 1.25%), NPP (0.2, 0.3 and 0.4%) and microbial phytase (Natuphos; 0 and 500 FTU/kg). The effect of dietary NPP on ADG, ADFI, feed conversion ratio, plasma P concentration, tibia weight, ash weight and ash concentration was dependent on dietary concentration of Ca (NPP × Ca, $P < 0.001$) and microbial phytase (NPP × Phyt, $P < 0.001$). Thus, the negative impact of decreasing dietary NPP concentration on these variables was more important in high than in low Ca diets. Also, the positive impact of phytase on growth performance, plasma P concentration and tibia mineralization was increased when NPP was decreased. Additionally, the impact of phytase on growth performance, plasma P, tibia weight, ash weight ($P < 0.001$) and tibia ash concentration ($P < 0.05$) is affected by Ca concentration. These results show that broilers are sensitive to P deficiency which decreases growth performance, plasma P concentration and bone mineralization. However, the impact of P deficiency in animal responses is higher when birds are fed high Ca diets. Furthermore, the response of broilers to phytase was affected by dietary Ca and NPP concentrations, increasing phytase effects when Ca was increased or NPP was decreased. Thus, the more severe the P deficiency (high Ca or low NPP), the more the response of birds to phytase for the studied criteria was important. Optimal dietary concentration of NPP should be established according to dietary Ca and phytase addition. It is also worth noting that these results emphasize the needs to normalize dietary conditions in which P equivalency of phytase are determined.

Key Words: calcium, phytase, broilers

T230 Effect of phytase application on the calcium and phosphorus retention and balance of layers in the last third of the laying cycle. J. Tossenberger[1], L. Babinszky*[1], and I. Kühn[2], [1]*Kaposvár University*, *Kaposvár, Hungary*, [2]*AB Vista*, *Darmstadt, Germany*.

Calcium (Ca) and phosphorus (P) retention (RET) and the amount and percentage of Ca and P release via eggs were studied in the last third of the laying cycle (wk 39 of egg production). A corn–soybean meal based diet was fed to 96 Hy-Line Brown hybrid layers (3 layers/cage) distributed over 4 treatments (Trts). Feeds had identical Ca levels (39.3 g/kg); P levels and phytase activities differed. P content of TrtI was 2.0 g/kg non-phytate P (NPP) (positive control: PC). P content of Trt2 was 1.0 g/kg NPP (negative control: NC). Trts3 and 4 had same P content as Trt 2 but also had an added 6-phytase, (FINASE EC, from *Trichoderma reesei*), at 125 PPU/kg (Trt3) and 250 PPU/kg (Trt4). Data were analyzed by ANOVA (SAS, 2004). Ca and P RET was lowest in NC group (Ca: 1686 mg/d, P: 78 mg/d). Adding 125 PPU/kg phytase increased Ca and P RET to the PC group levels ($P \geq 0.05$), i.e. 1888 mg/d and 129 mg/d ($P \leq 0.05$). Ca and P RET increased only numerically in Trt4 ($P \geq 0.05$). While NC birds secreted 84.6% of retained Ca (1420 mg/d) and 84.9% of retained P (66 mg/d) with the egg, these values were 98% (1869 mg/d) and only 67.3% (87 mg/day) for Trt3 birds. In consequence Ca balance dropped from +6.9% (NC) to +0.3% (attributable to increased production of birds), while P balance grew from +3.9% to +12.5% (attributable to relatively low egg P level which offsets increased production) (data not shown). The higher phytase dosage (Trt4) did not lead to further Ca and P output in the egg, their amount and ratio being close to those found in Trt3. The Ca balance of PC birds was at an equilibrium, and their P balance showed a surplus of +6.3%. To conclude, adding the tested 6-phytase to low P (1.0 g NPP/kg) layer diets at a level of 125 PPU/kg already improves the Ca and P RET of layers also in the last third of the laying cycle, beside improving their P balance. This should be considered when choosing the P content of the diets and can be used as a tool to reduce P excretion by layers.

Key Words: layer, phosphorus/calcium, retention/balance

T231 Effect of enzyme preparation on nutrient digestibility, digestive enzyme activities and pancreatic enzyme mRNA expression of hens during late laying period. C. Wen*[1], L. Wang[1], T. Wang[1], Y. Zhou[1], G. Hou[2], and Z. Zhou[2], [1]*Nanjing Agricultural University*, *Nanjing, Jiangsu, China*, [2]*Guangdong VTR Bio-Tech Co., Ltd*, *Zhuhai, Guangdong, China*.

This experiment was conducted to study the effect of enzyme preparation on nutrient digestibility, digestive enzyme activities and pancreatic enzyme mRNA expression of hens during late laying period. Thirty-six 58-wk-old ISA Brown hens were randomly allocated to 2 groups with 6 replicates (3 birds per replicate), and fed corn-soybean meal based diets with or without an enzyme preparation (including phytase, xylanase, cellulase, α-amylase and acid protease) for 4 weeks. The apparent digestibility coefficients of protein, fat and Ca were increased ($P < 0.05$) by enzyme supplementation. The birds fed diets containing enzyme preparation also had a higher ($P < 0.05$) protease activity in jejunal digesta compared with the control group. The pancreatic enzyme activities and their mRNA expression were reduced by enzyme supplementation, but the differences were not significant. The data show that the enzyme preparation is effective in improving nutrient digestibility, but may depress the synthesis of digestive enzymes in pancreas.

Key Words: hen, nutrient digestibility, digestive enzyme activity

T232 Effects of multi-enzyme and *Bacillus subtilis* on sow reproductivity. T. X. Zhou*, J. S. Yoo, H. J. Kim, Q. W. Meng, J. H. Jung, and I. H. Kim, *Department of Animal Resource and Science, Dankook University*, *Cheonan, Choongnam, Korea*.

The objective of the experiment was to evaluate the effect of multi-enzyme (Endopower: α-galactosidase, β-glucanse, galactoamannanase and xylanase) and *Bacillus subtilis* on sow productivity. A total of 100 sows (Landrace × Yorkshire) were randomly allotted into 4 dietary treatments and each treatment had 25 sows. The experiment was conducted from July to August 2009. Sows were fed experiment diets from 4 d before farrowing to 21 d of weanling. No crossfostering was done. Dietary treatments were as followed: 1) CON (basal diet), 2) E (basal diet + 1 g/kg Endopower), 3) B (basal diet + 0.4 g/kg *Bacillus subtilis*), and 4) EB (basal diet + 1 g/kg Endopower + 0.4 g/kg *Bacillus subtilis*). Differences among treatments were separated by Duncan's multiple range test. Sows fed multi-enzyme and *Bacillus subtilis* had a higher ($P < 0.05$) ADFI than that of sows in CON treatment (4.99 kg/d vs. 4.71 kg/d). The back fat difference of sows fed multi-enzyme and *Bacillus subtilis* was lower ($P < 0.05$) than that of sows in CON treatment (−5.64 mm vs. −3.68 mm). Sows fed multi-enzyme had a higher ($P < 0.05$) litter size than sows fed *Bacillus subtilis* at birth (11.3 vs. 9.6). Sows in E treatment had a greater ($P < 0.05$) number of litters at weanling than sows in B treatment (9.4 vs. 8.1). No difference was observed on litter performance among treatments. Estrus was not affected by dietary treatments. In conclusion, multi-enzyme and *Bacillus subtilis* increased the ADFI of sows and reduced the backfat loss. Besides, multi-enzyme reduced the mortality of piglets.

Key Words: multi-enzyme, Bioplus 2B, sow

T233 EconomasE decreases sterol carrier protein-2 (SCP2) gene expression levels in breast muscle from 6-week-old chickens. K. M. Brennan*, T. Ao, J. L. Pierce, R. F. Power, and K. A. Dawson, *Center for Animal Nutrigenomics and Applied Animal Nutrition, Alltech Inc.*, *Nicholasville, KY*.

EconomasE (Alltech Inc.) is a proprietary blend of dietary ingredients designed to enhance antioxidant status. Previous studies have shown that supplemental EconomasE increases serum total antioxidant capacity and decreases breast meat drip loss compared with birds fed a control diet (Ao et al., 2009). Based on these data, breast muscle gene expression profiles were compared from birds fed supplemental vitamin E (VE) and EconomasE. Dietary treatments included 1) corn-soy control diet containing 0.3 ppm Se as selenite, but no VE; 2) Diet 1 plus 50 IU VE / kg; 3) Diet 1 plus 100 IU/kg VE; 4) Diet 1 plus 200 g EconomasE /tonne. Birds were house in pens of 22 birds, with 8 replicate pens per treatment. Seven chicks from each of 4 dietary treatments were randomly selected and killed after 42d on treatment. Total RNA was isolated from frozen breast muscle and gene expression was measured using the Affymetrix microarray system. Gene expression data showed that a potential target, sterol carrier protein 2 (SCP2), decreased with both 50 IU and 100 IU of VE (−1.92-fold and −1.59 fold, respectively) and with EconomasE supplementation (−1.67-fold, $P \leq 0.05$). SCP2 plays an important role in the cellular metabolism of lipids, but SCP2 overexpression leads to increased cellular lipid peroxide damage. The decrease in SCP2 mRNA levels was confirmed using real-time PCR. Relative levels of SCP2 mRNA were significantly decreased with both VE treatments (−1.36-fold and −1.34-fold, respectively) and EconomasE supplementation (−1.42-fold, $P \leq 0.05$). These data show that EconomasE mimics VE in breast muscle, potentially through reducing SCP2 levels and peroxidation of cellular membranes.

Key Words: gene expression, vitamin E, broiler

T234 Effects of different dietary sources of n-3 PUFA on reproductive performance of laying hens. M. Pilevar[1], J. Arshami[1], A. Heravi Moussavi[1], A. Golian*[1], M. R. Basami[1], and A. R. Rezaee[2], [1]*Ferdowsi University of Mashhad*, *Khorasan Razavi, Iran*, [2]*Mashhad University of Medical Sciences*, *Khorasan Razavi, Iran*.

This study was conducted to evaluate the effects of n-3 polyunsaturated fatty acids (PUFAs) on reproductive performance in hy-Line W-36 pullet chicks at the onset of laying period. Two hundred eighty-eight 1-day-old pullet chicks with initial BW of 40.73 g were used in a CRD design to a 2 × 2 factorial arrangement. The main effects were 2 sources of n-3 (flaxseed or fish oil) and 2 levels of n-3 (1.5% and 0.5%) in the diet. The concentration of n-6 PUFA was kept constantly (3% of diet) by soybean oil in all experimental phases. During the 5 experimental phases (starter, grower, developer, pre-developer and pre-peak), feed and water were provided ad libitum. Each dietary treatment (fish1.5, fish0.5, flax1.5 and flax0.5) was assigned to 6 replicate cages with 12 newly hatched pullet chicks per cage. The chicks were raised in cages under optimum environmental conditions until 22 wk as recommended by the Hy-line commercial management guide (2007). On wk 15 of experiment, pullets were transferred to the laying house and individually placed in standard laying cages to determine the day of sexual maturity (first oviposition). All birds were photostimulated at 18 wk of ages. The weight of first egg at sexual maturity and 22 wk egg production were numerically decreased in birds fed diet fish1.5 ($P > 0.05$). However, egg production was affected by the sources ($P = 0.005$) and levels of n-3 ($P = 0.003$) of the diet at 21 wk. At the end of wk 18, no significant differences were observed in the BW and FI between sources and levels of n-3 PUFA ($P > 0.05$). In this study, time of sexual maturity was negatively affected by the sources ($P = 0.029$) and interaction between main effects ($P = 0.03$). Laying hens fed fish oil came into oviposition later, after photostimulation according to this: fish1.5; 20d, fish0.05; 14d, flax1.5; 11d and flax0.5; 14d. Our results show that high levels of fish oil delay the time of first oviposition compared with flaxseed.

Key Words: n-3 PUFA, first oviposition, laying hen

T235 Docosahexaenoic acid does not increase insulin sensitivity in gilts. J. H. Eisemann*, S. Whisnant, and J. Odle, *North Carolina State University*, *Raleigh*.

Dietary fish oil increased insulin sensitivity in several species including miniature pigs. Fish oil is rich in eicosapentaenoic acid (EPA, 20:5, n-3) and docosahexaenoic acid (DHA, 22:6, n-3). The objective was to measure insulin sensitivity in gilts consuming diets containing added DHA. Gilts were fed diets formulated to contain 0% DHA (Control, Cont; n = 5) or 0.54% added DHA provided by DHAgold (Martek Biosciences Corp., Columbia, MD; n = 7). Inclusion of DHAgold also provided 0.23% added docosapentaenoic acid (DPA, 22:5, n-6). Diets were fed for 6 wks before measurement of insulin sensitivity. Body weight at the time of sampling was 110.0 kg (SEM 7.3 kg) for gilts fed Cont and 111.4 kg (SEM = 6.0 kg) for gilts fed DHA. An i.v. glucose tolerance test (IVGTT; 1.25 g glucose/kg BW $^{0.75}$) and an i.v. insulin tolerance test (IVITT; 0.30 IU insulin/kg BW $^{0.75}$) were conducted on successive days. Blood samples were taken from indwelling jugular catheters at 30, 15, and 5 min before and 2.5, 5, 10, 15, 20, 30, 40, 50, 60, 75, and 90 min after infusion to measure concentrations of Gluc and Ins (IVGTT) or Gluc only (IVITT). Basal concentrations of Gluc and Ins did not differ between diets and were 5.06 and 4.82 mM Gluc; and 12.6 and 9.2 uIU/mL Ins for Cont gilts and DHA gilts, respectively. The area under the response curve (AUC) for Gluc response to the Gluc infusion (mM Gluc x 30 min) tended to be greater ($P < 0.07$) in gilts fed DHA (113.9) compared with Cont gilts (94.0). There was a tendency ($P = 0.10$) for greater Gluc half-life (min) in gilts fed DHA (9.96) than gilts fed Cont (8.52). The AUC for Ins response to the Gluc infusion and the AUC for Gluc response to the Ins infusion did not differ for the 2 groups and were 1002 and 1266 (uIU insulin/mL x 30 min) for Cont and DHA gilts, respectively, and 182 and 170 (mM Gluc x 90 min) for Cont and DHA gilts, respectively. Lack of response suggests that fish oil may not increase Ins sensitivity in these pigs, the response observed due to feeding fish oil is due to EPA rather than DHA, or the presence of DPA diminished the response.

Key Words: DHA, fatty acid, insulin sensitivity

T236 Conjugated linoleic acid (CLA) modifies carcass traits and fatty acid composition in finishing pigs fed with high linoleic acid diets. G. Cordero[1,2], B. Isabel[2], J. G. Vicente[2], J. Morales[1], C. Piñeiro*[1], and C. J. López-Bote[2], [1]*PigCHAMP Pro Europa*, *Segovia, Spain*, [2]*Universidad Complutense de Madrid*, *Spain*.

Conjugated linoleic acid (CLA) in swine nutrition has the potential to improve feed efficiency and decrease carcass fat. Moreover, it may also alter fatty acid synthesis and metabolism, thus leading to more saturated fat. Therefore, CLA supplementation in finishing pigs might ameliorate the deleterious effect that a high concentration of polyunsaturated fatty acids (PUFA), particularly linoleic acid (LA), produces on carcass and meat consistency. The objectives of this experiment were to study the effect of a commercial source of CLA (60% of CLA isomers, 30% c9,t11 and 30% t10,c12) supplied with 2 high levels of LA on performance, carcass traits and fatty acid composition of subcutaneous fat. Therefore, there were 4 treatments arranged factorially with 2 CLA dietary contents (0 vs 1%) and 2 LA dietary levels (1.45 vs. 1.17). For the experiment, 40 pigs Large White × (Large White × Landrace) with 129.4 (±4.83) kg live weight were used. Either supplementation with CLA or LA did not affect average daily gain (ADG), average daily feed intake (ADFI) and feed efficiency. Carcass, ham and foreleg weights were recorded, but were not affected by CLA supplementation. The highest level of LA tended ($P = 0.05$) to increase the foreleg weight. No effect of LA was observed on backfat thickness, but a trend ($P = 0.09$) to reduce backfat thickness was shown when pigs received a diet containing CLA. No difference in intramuscular fat content was observed among treatments. A marked effect of CLA administration was observed in most fatty acids, with an increase in the concentration of saturated fatty acids and a decrease in the concentration of total monounsaturated fatty acids, but not effect on PUFA concentration was observed. The highest level of LA increased the concentration of C18:2 n-6, C18:3 n-3, C20:3 n-9 and total PUFA ($P < 0.01$). We conclude that 1% of CLA supplementation enhance fatty acid saturation, which may help to overcome problems of oil and low consistency meat.

Key Words: conjugated linoleic acid, linoleic acid, finishing pigs

T237 Effects of high oil poultry by-product meal in laying hen performance, egg quality, egg components and blood parameters. G. O. Majid*, J. Hossein, T. Akbar, and R. Abass, *University of Tabriz*, *Tabriz, Iran*.

Poultry by-product meal (PBPM) is usually composed of the wastage from poultry meat processing. To examine the effects of high oil PBPM

from Iran on laying hen performance, egg quality, egg components and blood parameters, 160 HyLine W-36 hens at the age of 42 wk housed in laying cages with 4 hens per cage. The trial was conducted using the completely randomized design with 5 experimental diets as treatments and 4 replications for each treatment. Five experimental diets were prepared with inclusion of 0%, 2%, 4%, 6% and 8% PBPM and all diets were isocaloric and isonitrogenous. Egg weight and egg production was recorded daily. Feed intake was recorded every 2 weeks. The egg mass and feed conversion ratio (FCR) was calculated according to the HyLine W-36 2003–2005 commercial management guide. Three eggs from each treatment replicate were randomly collected for measuring egg shape index, Haugh units, shell thickness and egg yolk, shell and albumen weight. Finally for determining blood parameters such as serum glucose, triglyceride, calcium, phosphorous, low-density lipoprotein (LDL) and high-density lipoprotein (HDL), 2 hens from each treatment replicate were randomly selected and were determined by using commercial kits. The results showed that egg weight, egg production, egg mass and feed intake was significantly decreased and FCR was significantly increased by increasing level of PBPM in diets ($P < 0.05$). Egg shape index, shell thickness, albumen weight and all blood parameters were unaffected by different levels of PBPM in diets ($P < 0.05$). Increasing level of PBPM in diets significantly decreased Yolk weight and shell thickness ($P < 0.05$). Results indicated that up to 2% PBPM can be used in laying diets with no negative effects in laying performance and egg quality.

Key Words: laying hen, egg quality, high oil poultry by-product meal

T238 Viability of *Lactobacillus plantarum* in different protective agents and its effects on growth performance and immunity of weaned pigs. J. Wang, H. F. Ji*, R. L. Ge, S. X. Wang, D. Y. Zhang, and Y. M. Wang, *Institute of Animal Husbandry and Veterinary Medicine, Beijing Academy of Agriculture and Forestry Sciences*, *Beijing, China*.

This experiment was conducted to evaluate the effect of different protective agents on the viability of *Lactobacillus plantarum* after freeze-dried and the effects of *Lactobacillus plantarum* on growth performance and immunity of weaned pigs. The strain of *Lactobacillus plantarum* was originally isolated from the gastrointestinal tract of healthy weanling pigs in our laboratory and strains were identified through standard morphological, biochemical, physiological tests, and by 16s rRNA gene sequence analysis by the China Center of Industrial Culture Collection. *Lactobacillus plantarum* were freeze-dried for 24 h in the presence of 10 different combinations of skim milk powder, lactose, soluable starch, ascorbic acid, sodium glutamate, glycerin, L-cysteine, dextrine, and sucrose. The viable count of *Lactobacillus plantarum* reached 1.6×10^{12} cfu/g after freeze-dried under the protective agents of 16% skim milk powder + 2% lactose + 10% dextrin + 0.5% L-cysteine + 1.5% sodium glutamate, showed the highest viability. Sixty-four piglets weaned at 28 d of age (8.13 ± 0.35 kg BW), were divided into 4 groups comprising of control with chlortetracycline at 50 mg/kg, 3 treatments of different *Lactobacillus plantarum* levels (freeze-dried; 0.3%, 0.5%, and 0.7% of diet). The experiment lasted 30 3 d. The results showed that the supplementation of *Lactobacillus plantarum* at 0.3% of diet level had the same effect on average daily gain (ADG) (405 vs. 393 g/d), feed/gain (F/G) (1.95 vs. 1.98), and mortality rate (0% vs. 0%) ($P > 0.05$) compared with chlortetracycline addition. But the 0.5% and 0.7% of diet level showed lower ADG and significant higher F/G and mortality rate compared with control ($P < 0.05$). *Lactobacillus plantarum* supplementation at any level showed significant higher antibody titers against classical swine fever (OD at 630 nm, $P < 0.05$). The present study implies that freeze-dried *Lactobacillus plantarum* at 0.3% of diet may be the most ideal concentration in ensuring growth performance and immunity of weaned pigs compared with chlortetracycline.

Key Words: *Lactobacillus plantarum*, growth performance and immunity, weaned pigs

T239 Effect of dietary delivery controlled antioxidant on the performances of cold stressed broiler. V. Noirot*, *Phodé Laboratories*, *Albi-Terssac, France*.

A product based on the dietary antioxidant curcumin formulated with delivery vehicles designed to control the release in the digestive tract (Phodé Laboratories, France), was tested on 4 groups (0, 50, 500, and 1000 ppm doses in feed) of 6 replicate pens each containing 25 Ross × Ross broiler chickens. Temperature was decreased from 22.5 to 12°C beginning on d 18, to induce an oxidative stress. Birds were individually weighed at 7, 18, 30, and 38 d. Feed conversion was evaluated per pen at each weighing. Serum glutathione peroxidase (GSH-Px) was measured on 2 birds per pen at 37 d of age. Performance data were subjected to the Mixed model procedure of SAS with treatment as fixed, pen as random and time as repeated factors. Chi-squared tests were performed on mortality rates. Mortality rate over the first 30 d tended to be lower ($P = 0.10$) in birds given 50 ppm (0.6%) compared to control birds (1.9%). After 30 d birds receiving 50 ppm were heavier (2,331 kg) than control birds (2,299 kg) ($P < 0.05$). Feed conversion was improved ($P < 0.05$) over the period 0 to 18 d with the levels of 50 and 500 ppm (1.955 and 1.981 respectively) compared to control (2.072) and 1000 ppm (2.009). The GSH-Px levels were increased by 50 ppm (2341 IU/L) compared to the other treatments (1436, 1914, 1371 IU/L for 0, 500, 1000 ppm respectively). The 50 ppm dose reduced mortality associated with cold stress and improved feed conversion and growth before 30 d, but higher doses were not beneficial. The 50 ppm dose may improve birds' antioxidant status.

Key Words: antioxidant, chicken

T240 Effects of feeding oregano essential oil to broilers on ileal digestibility and performance under high altitude conditions. L. Betancourt*[1,3], C. Ariza-Nieto[2], and G. Afanador-Téllez[3], [1]*Universidad de La Salle*, *Bogotá, Colombia*, [2]*CORPOICA*, *Bogotá, Colombia*, [3]*Universidad Nacional de Colombia*, *Bogotá, Colombia*.

It has long been acknowledged that some plant essential oils exhibit diverse functional activities. Oregano essential oil (OEO) has been shown to possess antibacterial activity; however, comparison of ileal digestibility of nutrients due to the supplementation of different varieties of OEO is scarce in the literature. The aim of this study was to test the effect of OEO supplementation on apparent ileal digestibility (AID) of energy, protein and fat of broilers diets. Seven hundred fifty 1-day-old Hybro male broiler chicks were randomly allotted to one of the 6 treatment groups: Control (C), 500 ppm chlortetracycline (AB), 50 ppm of OEO from *O. vulgare* H. ground in Greece (OG) and 3 additional treatments with 200 ppm of OEO from 3 varieties ground in Sabana of Bogota-Colombia (2650 AMSL): *O. vulgare* H. (OH), *O. vulgare* L. (OL) and *O. majorana* (OM). During a 7-d period (14–21 d), the chicken received a diet with 0.5% chromium oxide as an indigestible marker. On the last day, 20 birds per treatment were slaughtered and Ileal digesta samples were collected and stored at −20°C. Dry matter, protein, fat, energy and chromium were analyzed in feed and ileal content and nutrients AID were calculated. AB group showed a higher AID of protein compared with control (83.7% vs. 75.3%, $P < 0.05$), but not significant differences ($P > 0.05$) were observed among the other treatments. Both OM and AB groups showed a higher value of AID for energy and fat compared with control (92.3%, 91.7% vs.84.2%) ($P < 0.05$). Additionally, OM and AB presented the highest body weight at 21d. ($P < 0.05$). These results suggest that the addition of EO from *O. majorana* to broiler diets could enhance their performance.

Key Words: oregano essential oil, protein digestibility, fat digestibility

T241 Utilization of glandless and standard cottonseed meal in broiler diets. C. Salas*, R. D. Ekmay, J. England, S. Cerrate, and C. N. Coon, *University of Arkansas*, *Fayetteville.*

A 42d study was conducted to determine the field performance and processing yield of broilers fed corn-soy diets containing glandless cottonseed meal (GCSM), commercial CSM (CCSM), or only corn/SBM (CSBM). The nutritional value of both CSM samples was determined and utilized to formulate grower (11–21d) and finisher (22–42d) diets. All broilers were fed a starter corn-soy diet from 1 to 10d. The inclusion level of GCSM and CCSM in corn-soy diets was 12.42% based on the gossypol content of the meals to expose the broilers to 200 and 4.1 ppm of free gossypol, respectively. An additional set of all diets was formulated by adding 500 units/kg of phytase and decreasing NPP by

0.10%. The grower and finisher nutrient contents were based on specifications for Cobb 500 and were formulated based on digestible AA. Body weight (BW), feed intake (FI), feed conversion ratio (FCR) and mortality were monitored. At 42d, 5 birds/pen were further processed. The carcass yield was determined and weight of fillet, tenders, wings, leg quarters and rack were expressed as % of chilled weight.
The broilers had significant differences in BW, FI and FCR at 21d ($P < 0.05$). The birds fed the GCSM + phytase diet were the heaviest (946g) followed by the birds fed the CCSM diet (923 g). Broilers fed the CCSM + phytase diet had the poorest BW gain (886 g) and the poorest FCR from 11-21d (1.62) compared to the other treatments ($P = 0.0136$). The FCR, BW and mortality were not significantly different at 42d. The results indicate the protein source did not produce a significant effect on % carcass yield, but had an effect on fillet, tender and leg quarters % yield. The processing data shows significantly higher ($P < 0.01$) % yield for breast meat (≥25%) and tenders (≥5%) for broilers fed the GCSM diets compared to the CSBM diets. Broilers fed CCSM diets produced a higher ($P < 0.01$) % yield of leg quarters (≥31.5%). These results indicate that broilers can be fed standard CSM in broiler grower and finisher diets if free gossypol in total diet does not exceed 200 ppm.

Key Words: broilers, cottonseed meal, performance

T242 TMEn and amino acid digestibility of glandless and commercial cottonseed meal for broilers. C. Salas*, D. R. Ekmay, J. England, S. Cerrate, and C. N. Coon, *University of Arkansas*, *Fayetteville*.

Cottonseed meal (CSM) is an alternative protein source for poultry diets, but CSM use is limited mainly due to the presence of gossypol. Cotton genetic cultivars are presently being developed with a significant lower concentration of gossypol in the seed.
A digestibility study was conducted to determine the TMEn and amino acid (AA) digestibility of a glandless (GCSM) and a commercial (CCSM) cottonseed meal. Thirty male broilers (42d) in individual cages were fasted for a 48 hr period and 30 g of GCSM, CCSM, and dextrose were each precision fed to ten broilers. The dextrose (protein-free) was utilized to estimate endogenous AA losses. Excreta were quantitatively collected after 48 hr and freeze dried for further analysis. The chemical composition, gossypol content, TMEn and digestibility coefficients for AA were obtained for both meals. The crude protein and fat content of the GCSM was higher than the CCSM (48% and 45%, 5.3 and 1.75%, respectively, as is basis). The CCSM had a higher content of total and free gossypol (1.52% and 0.161%, respectively, %DM) when compared to the GCSM (0.02 and .003%, respectively, %DM). The GCSM contained a thousand additional kcal (27% more) of TMEn than the CCSM (3975 vs 2963 kcal/kg, %DM), because the true DM digestibility was 97% compared to 78% for CCSM. The AA content was determined for both meals and was higher for the GCSM when compared to the CCSM, but both had higher contents than the reports in the literature. When compared with the literature, methionine content was 2-fold higher for both GCSM and CCSM; cystine was 74-84% and 84-93% higher for CCSM and GCSM, respectively. The true digestibility coefficients for essential AA ranged from 73.9% for isoleucine to 91.8% for arginine, for CCSM, whereas the digestibility coefficients for GCSM were all higher than 90% for the essential AA.

Key Words: broilers, cottonseed meal, amino acid digestibility

T243 Effects of coated sodium butyrate on the performance and gut morphology of broiler chickens. Y. Zou[1], Z. B. Yang*[1], W. R. Yang[1], S. Z. Jiang[1], G. G. Zhang[1], and R. Yu[2], [1]*Shandong Agricultural University*, *Tai-an, Shandong, China*, [2]*Kangdequan Feed Co., Ltd*, *Hangzhou, Zhejiang, China*.

An experiment was performed to assess the effects of dietary coated sodium butyrate (CSB) on growth performance and morphological aspects of small intestine in broiler chickens at different ages. Three hundred sixty 1-d-old Arbor Acres broilers were randomly distributed into 3 treatments with 3 pens of 40 each and were fed starter rations from d1 to 21 and finisher rations from d22 to 42. Dietary treatment included 1) BD (basal diet), 2) BD+ antibiotics (40 mg/kg bacitracin zinc and 8 mg/kg colistin sulfate), 3) BD+200 mg /kg CSB. Broilers were fed for ab libitum intake and had free access to water. Body weight and feed intake of chicks of each pen were measured weekly for determination of average daily gain (ADG), average daily feed intake (ADFI), and feed conversion rate (FCR). Twelve birds of each treatment were slaughtered at d14 and d35 of the experiment and the intestinal samples were removed to determine gut morphology. All broilers had similar ADFI over the entire experimental period. However, supplementation with 200 mg/kg coated sodium butyrate increased final weight and ADG ($P < 0.05$), but reduced FCR as compared with that of basal and antibiotics diets. Supplementation of CSB increased ($P < 0.05$) villus height of duodunum and jejunum and reduced ($P < 0.05$) the crypt depth at 14-d of age, but did not affect the morphology of ileum. The antibiotics supplementation significantly increased ($P < 0.05$) villus height of jejunum and ileum, but had no effect on villus height of duodunum and on crypt depth of the 3 segments at 14-d of age. Although broilers received butyric acid or antibiotics (zinc bacitracin 40 mg/kg + colistin sulfate 8 mg/kg) as feed additive at 35-d of age had greater villus height and lower crypt depth than the control chicks, the tendency were not significant among the 3 experimental groups ($P > 0.05$). In the current study conducted, the addition of coated sodium butyrate at 200 mg/kg level showed a positive effect on performance and intestinal morphology, and coated sodium butyrate can be a possible substance to replace antibiotics as growth promoters for farm animals.

Key Words: coated sodium butyrate, broiler, performance and gut morphology

T244 Study on the utilization of oregano essentials oils (oeo) by tilapia *Oreochromis niloticus* var. *chitralada* in a commercial production cycle. D. Rodriguez*[1,2], C. Ariza-Nieto[2], A. Munoz[1], and G. Afanador[1,2], [1]*Universidad Nacional de Colombia*, *Bogota, Colombia*, [2]*CORPOICA*, *Bogota, Colombia*.

Carvacrol and thymol are the 2 main active components of oregano essential oil (OEO). The aim of this study was to investigate the effect of different ratios of carvacrol to thymol on growth performance of Nile Tilapia. Five hundred 20 8 10 g tilapia were randomly assigned to one of the 4 treatments groups: C) control group; HT) high thymol (Colombian native oregano); TC) thymol:carvacrol 1:1 ratio (Colombian native oregano+Greek Oregano); and HC) high carvacrol (Greek oregano). Fish were placed in 24 tanks during starter-finish phase and their performance was determined every other week until 550g of body weight. Data were analyzed under a completely randomized design using the GLM procedure of SAS. Specific growth rate (SGR) and daily growth coefficient (DGC) of fish fed HT were higher than those of fish fed both C and TC (1.5929, 1.5187 and 1.5015; 3.186, 3.000 and 2.986, %/day, respectively) ($P < 0.05$). Days to market (550g) of fish fed HT was lower than that of HC (165.7 vs 186.5) ($P < 0.05$), but not significant differences ($P > 0.05$) were noted among other treatments.

It can be concluded that natural Colombian native oregano, can act as a growth promoter when added to nile tilapia feed.

Key Words: Nile tilapia, oregano, carvacrol:thymol

T245 Dietary supplementation effects of oregano essential oils and two sources of fat on the performance of brown laying hens under high altitude conditions. D. Botero[1], F. Silva[1], L. Betancourt*[1,3], C. Ariza-Nieto[2], and G. Afanador-Téllez[3], [1]*Universidad de La Salle*, *Bogotá, Colombia*, [2]*CORPOICA*, *Bogotá, Colombia*, [3]*Universidad Nacional de Colombia*, *Bogotá, Colombia*.

Fish oils have been used to the incorporation of n-3 fatty acids into eggs, but this practice can exert a negative influence on their sensory properties. On the other hand, Oregano Essential Oil (OEO) has been shown to possess anti-oxidant activity. Thus, the aim of this study was to evaluate the effect of OEO carvacrol:thymol ratio and 2 sources of fat on production performance of laying hens and eggs sensory properties. One hundred sixty brown laying hens were randomly assigned to one of 8 treatment combination in a 4 × 2 factorial arrangement. Factors included were, source of fat, fish oil (FO) or palm oil (PO) and carvacrol:thymol ratio supplemented with 200 ppm of OEO; high carvacrol (HC), high thymol (HT), carvacrol:thymol 1:1 ratio (CT) and control (C) without OEO supplementation. Hens were housed in 80 conventional cages (2 per cage) and the study was conducted over a period of 16 weeks. Eggs were collected, numbered and weighed every day. Sensory evaluation was carried out with 40 tasters. When PO was used as a source of fat, the HC improved production egg, mass egg and feed conversion ratio; in contrast, HT and CT decreased egg production and egg mass ($P < 0.05$). The supplementation of OEO HC, HT and CT improved production performance ($P < 0.05$) when the source of fat was FO. HT significantly improved egg taste perception when FO was included in the diet; but HC improved it when PO was included ($P < 0.05$). It can be concluded that OEO can enhance laying hen performance and high thymol ratio has positive effects on flavor when FO is added to diet for functional eggs design.

Key Words: fish oil, n-3 FA, egg taste

T246 Effect of supplementing the diet of sows with a source of yeast-derived proteins during lactation on performances of sows and piglets. P.-A. Plante*[1,2], J.-P. Laforest[2], and C. Farmer[1], [1]*Agriculture and Agri-Food Canada, Dairy and Swine R&D Centre*, *Sherbrooke, QC, Canada*, [2]*Animal Science Dept., Laval University*, *Québec, QC, Canada*.

The impact of supplementing the diet of sows with a source of yeast-derived proteins (NuPro) during lactation on the performances of sows and their piglets was studied. Sixty-five crossbred sows were fed one of 3 levels of yeast proteins (YP) from 0 to 21 d of lactation. Treatments were: control without YP (CTL, n = 22); 30 g of YP per day (Y30, n = 22) and; 60 g of YP per day (Y60, n = 21). Jugular blood samples were obtained from sows on d 2, 7 and 20 of lactation to measure urea concentrations. Milk samples were obtained on d 7 and 20 of lactation for compositional analyses (fat, lactose, dry matter) and quantification of 5`monophosphate nucleotides. Litter size was standardized to 10 ± 1 at 48 h postpartum. Sow BW loss and backfat loss during lactation (from d 2 to 21) were recorded as well as weights of piglets on d 0, 2, 7, 14, 21, 24, 28, 35, 42, 49, and 56. Feed intakes of sows during lactation and of piglets for 5 wk post-weaning were noted. Statistical analyses were performed with PROC MIXED using an ANOVA with one factor (3 levels) according to a completely randomized design. None of the animal performance data differed between treatments ($P > 0.1$). Standard milk composition was also similar across treatments ($P > 0.1$). There were more nucleotides in milk on d 7 than on d 20 of lactation (means ± SD for AMP, CMP, GMP, IMP and UMP were 12.7 ± 2.8, 9.4 ± 2.1, 14.6 ± 2.8, 2.5 ± 0.7 and 281.3 ± 45.1 µmol/100 mL on d 7 and 6.0 ± 1.1, 3.6 ± 0.9, 7.5 ± 1.0, 1.5 ± 0.6 and 138.7 ± 15.4 µmol/100 mL on d 20; $P < 0.001$) but these concentrations were not affected by treatments ($P > 0.1$). On d 2 of lactation, circulating concentrations of urea tended to be greater for Y60 than CTL sows ($P = 0.1$). In conclusion, supplementing the diet of lactating sows with yeast proteins had no beneficial effect on sow and piglet performances.

Thanks to Alltech for financial support.

Key Words: sow, lactation, yeast proteins

T247 Microencapsulation of *Lactobacillus plantarum* and its effects on growth performance of weaned pigs. J. Wang, H. F. Ji*, L. J. Lv, S. X. Wang, D. Y. Zhang, and Y. M. Wang, *Institute of Animal Husbandry and Veterinary Medicine, Beijing Academy of Agriculture and Forestry Sciences*, *Beijing, China*.

This experiment was carried out to study the most suitable method and wall material for microencapsulation of the probiotic bacterium *Lactobacillus plantarum* to maintain cell viability during gastric challenge, and the effect of *L. plantarum* microcapsule on growth performance of weaned pigs. Strains of *L. plantarum* were individually encapsulated using different method of extrusion or emulsion. The optimum wall material formula of making microcapsule was studied through the orthogonal experiment. The survival of planktonic cells and encapsulated cells of *L. plantarum* treated with simulated gastric juice were detected. The results showed that extruded microcapsules were larger and more uniformly shaped. The viable count was reached 7.76×10^{10} cfu/g under the wall material formula as 3% alginate, 4% skim milk, 6% milk sugar, and 2% calcium chloride. When planktonic cells and encapsulated cells of *L. plantarum* were subjected to simulated gastric juice challenge at pH 2.1 for 3 h. The survival of *L. plantarum* cells treated with simulated gastric juice was significantly better ($P < 0.05$) when microencapsulated. Thirty-two piglets weaned at 28 d of age (8.11 ± 0.32 kg BW), were divided into 2 groups comprising of control diet with *L. plantarum* (0.5% of diet) and diet with *L. plantarum* microcapsule (0.5% of diet). The experiment lasted 30 d. The results showed that the supplementation of *L. plantarum* microcapsule had higher average daily gain (ADG) (390 vs. 326 g/d; $P < 0.05$) and lower diarrhea rate (3.25 vs. 6.67) and mortality rate (0 vs. 6.25) compared with control. In general, microencapsulation using selected wall material formula by extrusion was found to provide bacteria significantly greater protection ($P < 0.05$) against simulated gastric juice, and had positive effect on growth performance of weaned pigs.

Key Words: *Lactobacillus plantarum*, microencapsulation, weaned pig

T248 Effect of xylo-oligosaccharides on growth performance, enzyme activity and volatile fatty acid production of post-weanling pigs. H. S. Huang[1], S. Zhou[1], Z. B. Yang*[2], W. R. Yang[2], and L. Xiao[3], [1]*Qinghai University*, *Xining, China*, [2]*Shandong Agricultural University*, *Taian, Shandong, China*, [3]*Shandong Longlive Bio-technology Co., Ltd*, *Dezhou, Shandong, China*.

The experiment was conducted to assess the effects of Xylo-oligosaccharides (XOS) on growth performance, volatile fatty acid (VFA) production and intestinal enzyme activity of piglets. A total of 300, 28-d-old post-weanling pigs were randomly assigned to one of 6 dietary

treatments with 5 replicates of 10 piglets each. Treatments included control diet without Xylo-oligosaccharides and test diets supplemented with 40, 60, 80, 100 and 120 mg XOS /kg DM, respectively. Average daily gain (ADG), average daily feed, intake feed (ADFI) and gain ratio (F:G) were measured weekly of each replicate. Diarrhea piglets were recorded 3 times a day to determine diarrhea rate (DR). Five piglets of each treatment were slaughtered at d28 of the experiment and the intestinal contents were removed to determine intestinal VFA (gas chromatography) and digestive enzyme activities (colorimetric method). All pigs had similar ADG and ADFI but XOS diet decreased ($P < 0.05$) DR. However, Supplementation with 40, 60 and 80 mg XOS /kg DM had lower ($P < 0.05$) F:G as compared with that of control. Increasing supplementation of XOS linearly ($P < 0.05$) and quadratically ($P < 0.05$) increased concentrations of acetic acid, propionic acid and butyric acid in the jejunum, ileum and cecum. Lipase activity was quadratically ($P < 0.01$) increased in the duodenum, jejunum and ileum, trypsin activity was linearly ($P < 0.05$) increased in duodenum and jejunum, as well as amylase activity was linearly ($P < 0.05$) increased in the ileum with the increasing supplementation of XOS. In conclusion, supplementation of XOS decreased DR and 40, 60, 80 mg XOS/kg DM reduced F:G. Concentrations of VFA were linearly ($P < 0.05$) and quadratically improved in jejunum, ileum and cecum. Lipase activity and tryptic activity were linearly ($P < 0.05$) and quadratically ($P < 0.05$) increased in duodenum and jejunum and lipase activity and amylase activity were linearly ($P < 0.05$) and quadratically ($P < 0.05$) changed in the ileum with the increasing supplementation of XOS.

Key Words: xylo-oligosaccharides, pigs, volatile fatty acid and enzyme activity

T249 Effect of short-term benzoic acid and chlortetracycline treatment of feed on splanchnic metabolism of valine in growing pigs. N. B. Kristensen*[1], R. G. Engberg[1], B. B. Jensen[1], J. V. Nørgaard[1], H. D. Poulsen[1], H. D. Zacho[2], and N. M. Sloth[3], [1]*Aarhus University*, *Tjele, Denmark*, [2]*Viborg Hospital*, *Viborg, Denmark*, [3]*Danish Agriculture and Food Council*, *Aarhus, Denmark*.

The present study aimed to investigate the effects of short-term feed treatment with benzoic acid (BA) and chlortetracycline (CTC) on portal-drained visceral (PDV) metabolism of arterial [U-13C]Val as well as portal absorption and hepatic uptake of Val in growing pigs fed a low-protein diet. Eight female pigs (70 ± 2 kg BW) fitted with permanent indwelling catheters in the abdominal aorta, v. cava, hepatic portal vein, hepatic vein, and the mesenteric vein were used in the study. Pigs were fed a diet based on wheat (72%), soybean meal (12%), and barley (10%), supplemented with crystalline Lys, Met, Thr, Trp, and Val (0.08%), and containing 14.7% crude protein (as fed). Intake was restricted to 3.6% of BW/d. Pigs were randomly assigned to either control (CON; basal diet) or treatment (TRT; basal diet + 10 g BA and 0.7 g CTC/kg feed). Feed was offered in 3 equal sized meals at 8-h intervals and treatments were applied for 24 h. Blood samples were collected hourly during the last 8 h of the treatment period. Primed continuous infusion of [U-13C] L-Val (0.085 ± 0.005 mmol/h) into the v. cava was initiated 1 h before first sampling. Plasma samples were analyzed for AA by GC/MS and C-13 abundance in Val was determined using GC/C/IRMS. Data were analyzed using the MIXED procedure in SAS by a model including the fixed effects of treatment and block and with pig by block designated as a random effect. The arterial concentration of Val tended ($P = 0.07$) to increase with TRT (0.47 ± 0.02 mmol/L) compared with CON (0.41 ± 0.02 mmol/L). The PDV extraction of arterial Val (4.6 ± 0.4%) did not differ ($P = 0.21$) among treatments. The net portal flux of Val tended ($P = 0.10$) to be less for TRT, but the portal absorption of Val corrected for PDV uptake of arterial Val did not differ ($P = 0.82$) among treatments. The net hepatic and net splanchnic fluxes of Val were not affected by treatment ($P = 0.61$ to $P = 0.94$). Data indicate that upper gut microbial deamination is without quantitative importance to availability of Val in growing pigs fed a low-protein diet added crystalline Val.

Key Words: amino acid, metabolism, pig

T250 Characterization of the gastrointestinal microbiota in neonatal piglets from sows supplemented a *Bacillus*-based direct fed microbial. A. Baker*, E. Davis, and T. Rehberger, *Danisco*, *Waukesha, WI*.

Direct fed microbials (DFMs) supplemented in sow diets may confer health benefits to the host and the piglets by reducing pathogens in the sow and environment. In this study we evaluated the effect of a *Bacillus*-based DFM on the gastrointestinal microbiota of neonatal piglets. A total of 208 sows were divided into 2 treatments: a control diet and the control diet supplemented with a *Bacillus*-based DFM (3.75×10^5 cfu/g feed). Twenty-one piglets sampled from each sow treatment group were killed on d 3 of lactation as well as 15 piglets per treatment on d 10 of lactation. Terminal restriction fragment length polymorphism (T-RFLP) was used to characterize the microbiota in the ileum and colon of the piglets using 3 enzymes (MspI, BstUI, and *Hae*III) to generate terminal restriction fragments (TRFs). The presence and quantity of TRFs were compared between control and DFM pigs and presumptively identified using the Microbial Community Analysis III (MiCA 3) database. There was a greater incidence and quantity of TRFs B423 and H330 (Binary $P = 0.01$, 0.08; Quantitative $P = 0.01$, 0.05 respectively), putatively identified as *Lactobacillus gasseri/johnsonii*, in the ileum of pigs nursing sows supplemented with DFM at d 3. TRF peaks B423 and H330 were also greater (Binary $P = 0.01$, 0.08; Quantitative $P = 0.01$, 0.01 respectively) in the colon of pigs nursing sows supplemented with DFM at d 3. Peaks M495 and B394, putatively identified as *E. coli*, were greater (Binary $P = 0.01$, 0.04; Quantitative $P = 0.01$, 0.01 respectively) in the colon of the control pigs at d 3. At d 10, both presence and quantity of *Lactobacillus* species were greater ($P < 0.05$) in the colon of the DFM treatment. Additionally, there was a tendency for TRFs B227 and H257 (Binary $P = 0.07$, 0.07 respectively), putatively identified as *Clostridium perfringens*, to be present in the ileum of the control pigs at d 10 compared with treated pigs. The results of this study demonstrate the ability of a DFM to influence the gastrointestinal microbiota of a neonatal piglet through supplementation of the DFM to the sow.

Key Words: T-RFLP, swine, direct-fed microbial

T251 Cloning of a porcine trypsinogen gene and over-production of the protein as a feed additive. F. Wang[1], H. Zhao[1], X. J. Xia[1], and X. G. Lei*[1,2], [1]*Int. Ctr. of Future Agriculture for Human Health, Sichuan Agri. Univ.*, *Chengdu, China*, [2]*Cornell University*, *Ithaca, NY*.

Trypsin is a serine protease that plays a key role in the activation cascade of pancreatic digestive enzymes, and may be used to improve feed protein digestion by young animals. To produce a recombinant pancreatic trypsinogen, we used RT-PCR to amplify the full-length cDNA of porcine trypsinogen gene (submitted to GeneBank: FJ969506.1) from the porcine pancreas mRNA and inserted the DNA fragment into the pPICZαA expression vector (Invitrogen, Shanghai, China). The plasmid construct was transformed into *Pichia pastoris* X33 cells, and the transformants were screened by SYBR-green quantitative real-time RT-PCR analysis (ABI 7900HT, Applied Biosystems, Foster City, CA) for high levels of expression. After the transformants were induced by 0.5% methanol for 98 h, the extracellular recombinant trypsinogen contain-

ing a histidine tag in the C terminus was purified using Ni-Sepharose affinity chromatography (GE Healthcare, Piscataway, NJ). The purified protein exhibited a molecular mass of approximately 30 kDa as determined by SDS-PAGE analysis. The successful expression of the recombinant trypsinogen in *P. pastoris* enabled us to further study the enzyme function in animal feed.

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Key Words: porcine, trypsinogen, feed enzyme, *Pichia pastoris*, gene expression

T252 Effects of various cereals on nursery pigs: Specific bacteria identified from the gastrointestinal tract. Y. Liu*, M. Rossoni, J. Barnes, and J. E. Pettigrew, *University of Illinois*, *Urbana*.

A study was conducted to evaluate the influence of different cereal grains on the bacterial populations in the gastrointestinal tract of young weaned pigs. A total of 24 pigs (7.71 kg BW) were weaned at 21 d of age and randomly allotted to one of 4 treatments. Each diet contained corn, barley, rolled oats, or rice as the only cereal. Pigs were allowed ad libitum access to feed and water throughout the 14-d experimental period. At the end of the experiment, all pigs were killed to collect mucosal and digesta samples from ileum and distal colon. Denaturing gradient gel electrophoresis (DGGE) was used to assess the microbial population structures. In a few cases, specific bands were present in most pigs fed one treatment, but absent from most pigs fed other treatments. Major bands were excised and sequenced to identify the bacterial species that appear or disappear under different cereal treatments. The results showed that most pigs fed barley lacked significant populations of several species of *Sphingomonas* that were often present in the distal colon digesta and mucosa of pigs fed the other cereals. Most pigs fed rice differed from those fed other cereals in having a significant distal colon mucosal population of a *Corynebacterium* species but lacking a species of *Veillonella*. In conclusion, feeding of different cereals as sources of energy altered microbial diversity in the GI tract, especially with regard to *Sphingomonas* species.

Key Words: cereal, microbial diversity, nursery pigs

T253 Effects of dietary benzoic acid supplementation on net portal absorption and hepatic uptake of amino acids in growing pigs. N. B. Kristensen*[1], H. D. Zacho[2], J. V. Nørgaard[1], and H. D. Poulsen[1], [1]*Aarhus University*, *Tjele, Denmark*, [2]*Viborg Hospital*, *Viborg, Denmark*.

The present study aimed to investigate the effects of adding 1% benzoic acid (BA) to a standard finishing diet for growing pigs on net portal, net hepatic, and net splanchnic fluxes of amino acids (AA). It was hypothesized that BA supplementation would increase the portal absorption of AA, increase hepatic glycine uptake, and decrease splanchnic glycine release. Eight female Duroc × (Danish Landrace × Yorkshire) weighing 63 ± 1 kg at time of sampling and fitted with permanent indwelling catheters in the abdominal aorta, hepatic portal vein, hepatic vein and the mesenteric vein were used in the study. Pigs were fed a diet based on barley and soybean meal with intake restricted to 3.6% of BW/d. Pigs were allocated to 4 sampling blocks and randomly assigned to either control (CON; basal diet) or BA treatment (B; 10 g benzoic acid as top-dress; VevoVitall, DSM Special Products, Rotterdam, The Netherlands) within block. Feed was offered in 3 equal sized meals and blood samples collected hourly for 8 h with first sampling 0.5 h before feeding. Plasma samples were pooled by catheter and pig and analyzed for individual AA by a GC/MS based isotope dilution method following silylation. Data were analyzed using the MIXED procedure in SAS with a model including the fixed effects of treatment and block and with pig by block designated as a random effect. Amino acid fluxes were analyzed as the net flux in grams of AA per kg feed. The net portal flux of Ala and Thr increased ($P < 0.05$) and the net portal flux of His and Lys ($P < 0.10$) tended to increase with B compared with CON. The net hepatic uptake of Gly was not affected by treatment ($P = 0.91$), but the net hepatic uptake of Ser increased ($P = 0.02$) with B compared with CON. The net splanchnic release of Ser tended ($P = 0.08$) to decrease with B compared with CON. No effects of treatment were detected for net splanchnic flux of any AA other than Ser. Impact of benzoic acid supplementation on AA absorption and metabolism warrants further considerations on AA nutrition of pigs supplemented with benzoic acid.

Key Words: pigs, benzoic acid, amino acid metabolism

T254 Effects of dietary Stafac inclusion level on the growth performance and carcass characteristics of growing–finishing pigs. C. L. Puls*[1], M. Mercedes[1], M. Ellis[1], A. M. Gaines[2], B. A. Peterson[2], B. F. Wolter[2], and M. Kocher[2], [1]*University of Illinois*, *Urbana*, [2]*The Maschhoffs*, *Carlyle, IL*.

The effect of dietary Stafac inclusion level on the growth performance and carcass characteristics of growing-finishing pigs was evaluated from 40.0 ± 1.45 kg to 127.8 ± 1.13 kg BW. A randomized complete block design was used with 1 treatment (Stafac inclusion level) and 2 levels (0 and 10 g/ton). Diets were formulated to meet or exceed NRC (1998) recommendations for nutrient requirements. A total of 144 barrows housed in pens of 9 were used with 8 replicates/treatment level. Pigs were weighed at the start and end of the study, and every 2 weeks during the interim period; all feed additions were recorded. At the end of the study, pigs were harvested at a commercial plant and carcass measures were taken. There was no effect ($P > 0.05$) of Stafac inclusion level on live weight growth performance. Mortality levels were 2.8 percentage units lower for pigs fed Stafac compared with controls; however, this difference was not significant ($P > 0.05$). Including Stafac in the diet increased ($P < 0.05$) carcass yield by 0.7 percentage units and, consequently, improved ($P < 0.01$) carcass G:F ratio by 4%. In conclusion, including Stafac in the diet of growing-finishing pigs (at 10 g/ton) did not improve live weight growth performance in this study; however, the potential reduction in mortality levels and increases in carcass yield and carcass feed efficiency are of economic significance and need to be verified.

Key Words: pigs, growth, Stafac

T255 Expression of interleukins, neuropeptides, and growth hormone receptor (GHR) and leptin receptor (LPR) genes in adipose tissue from growing broiler chickens. G. J. Hausman*[1], C. R. Barb[1], B. D. Fairchild[2], A. Hinton[1], and J. A. Cason[1], [1]*USDA-ARS*, *Athens, GA,* [2]*University of Georgia*, *Athens*.

In this study, total RNA was collected from abdominal adipose tissue samples obtained from 10 broiler chickens at 3, 4, 5, and 6 weeks of age and prepared for real time RT-PCR analysis with custom-designed primers and probes. Studies of the gene expression of cytokines and associated genes in chicken adipose tissue were initiated since the discovery of leptin has shown in many animal species that adipose tissue derived factors can dramatically influence growth and physiology. The influence of age on the expression of adipose tissue IL-15, IL-18, neuropeptide Y and GHR and LPR genes and several other cytokines was examined. Between 3 and 6 weeks of age LPR expression decreased ($P < 0.05$) with age while expression of IL-15 and GHR increased significantly ($P < 0.05$). Furthermore, IL-18 and visfatin expression increased ($P < 0.001$) between 4 and 6 weeks of age. Expression of these cytokines was detected for the first time in chicken adipose tissue. Consequently, this is the first demonstration of age related changes in cytokine gene expression in chicken adipose tissue. Gene expression of several cytokines was not detected in chicken adipose tissue including IL-6 and brain derived neurotrophic factor. Future studies are needed to elucidate the role of adipose tissue cytokines in growth and, possibly, disease resistance. Furthermore, these studies provide indirect evidence that the adipose tissue response to leptin and growth hormone change with age.

Key Words: chicken, cytokine, adipose tissue

T256 Apoptosis in different fat depots of cows treated with conjugated linoleic acids (CLA). S. Haeussler*[1], D. Germeroth[1], D. von Soosten[2], S. Dänicke[2], and H. Sauerwein[1], [1]*University of Bonn*, *Bonn, Germany*, [2]*Federal Research Institute of Animal Health*, *Braunschweig, Germany*.

Changes in adipose tissue mass may be associated with a change in adipocyte number and/or a change in adipocyte volume. For development and maintenance of homeostasis, apoptosis plays an important role within organisms. In mice, dietary CLA causes apoptosis of adipocytes (Miner et al. 2001, Obesity Res, 9:129). To investigate whether apoptosis occurs in bovine fat and if apoptosis is influenced by CLA, 25 Holstein heifers were divided in a control (CTR) and a CLA group; from d 1 postpartum (pp) until sample collection, animals from the CLA group were fed with 100 g CLA (containing 10% each of the cis-9,trans-11- and the trans-10,cis-12-CLA isomers) per day. On d 1, 42 and 105 pp, 5 animals of CTR were slaughtered; from CLA, 5 cows each were slaughtered on d 42 and 105. Retroperitoneal (RP) and subcutaneous (SC) fat from the tail head were obtained from all cows. For the detection of DNA fragmentation, deparaffinized sections (10 µm) were stained using the TUNEL method. For positive and negative controls, bovine lymph nodes were treated either with or without DNase after demasking to initiate DNA strand breaks. The apoptotic cell rate (%) was defined as mean number of TUNEL-positive cells/mean number of total cells × 100 and analyzed using the general linear model and Student's *t*-test (SPSS). We determined TUNEL-positive nuclei within bovine adipocytes. The average value for SC and RP fat in CTR animals was 12.7 ± 1.4% and 5.3 ± 1.0%, respectively. The apoptotic rate in SC depot was twice as high compared to the rate of retroperitoneal fat ($P \leq 0.001$), but did not differ with time of lactation. On d 105 pp, the apoptosis rate was increased by more than 1.5-fold in both fat depots of the CLA cows ($P \leq 0.01$) in comparison to the CTR group. Apoptosis may influence the number of adipocytes in bovine adipose tissue. SC fat as main energy store seems to be more affected by mass changes and dietary CLA, thus presumably showing a higher apoptotic rate than the RP depot.

Key Words: adipose tissue, apoptosis, cow

T257 Differences in the mRNA abundance of the adiponectin system and GPR109A in adipose tissue and liver of the F2 cows of Charolais x German Holstein crosses. M. Mielenz*[1], B. Kuhla[2], H. Sauerwein[1], and H. Hammon[2], [1]*University of Bonn*, *Bonn, NRW, Germany*, [2]*FBN Dummerstorf*, *Dummerstorf, MV, Germany*.

Adiponectin, an adipocyte-derived hormone, is described as an insulin sensitizing agent in monogastric mammals. Less information is available about influences on the regulation of the adiponectin system in ruminant species. As well, the relevance of the β-hydroxybutyrate (BHB) sensing receptor *GPR109A* with anti-lypolytic properties is not characterized yet. We herein tested for differences in diverging phenotypes of the F2 offspring from segregated Charolais x German Holstein crosses exhibiting high differences in body fat accretion (FAT (n = 9) vs. LEAN (n = 9)). The animals were slaughtered at 100 d into 2nd lactation. The mRNA abundance of adiponectin (*Adi*) and its receptors *AdiR1* and *AdiR2* as well as of *GPR109A* was analyzed via real-time PCR in 3 different adipose depots and in liver, except for *Adi*. In liver, *AMPK* and phospho-*AMPK* protein were analyzed as well. Data were analyzed using independent samples *t*-test or Mann-Whitney U-test ($P \leq 0.05$). Milk production was much lower ($P \leq 0.05$) in FAT than LEAN cows. There was a trend ($P \leq 0.1$) for a higher *Adi* mRNA content in mesenteric fat of FAT vs. LEAN cows. *AdiR1* mRNA was more abundant in perirenal and mesenteric fat of FAT cows. For *AdiR2* mRNA there was a trend ($P \leq 0.1$) for higher values in subcutaneous fat of FAT cows but lower values were observed in liver. The content of *GPR109A* mRNA was lower in perirenial fat and as a trend in liver of FAT cows compared with LEAN animals. The ratio between phospho-*AMPK* and *AMPK* did not show any difference. In conclusion, the mRNA expression profile of the *Adi* system in adipose tissue of accretion type cows (FAT cows) seems related to increased lipid accumulation. Lower *AdiR2* abundance in liver of FAT cows might be related to specific features of glucose metabolism in this family but its relevance needs further characterization, as there was no activation of *AMPK* observed. Signal transduction by BHB through *GPR109A* in perirenal fat and liver might be of more relevance for secretion type LEAN cows.

Key Words: adiponectin system, GPR109A, cattle

T258 Changes in plasma concentrations of leptin in ewes during pregnancy. J. A. Daniel*[1], A. B. Milam[1], M. E. Gafnea[1], B. K. Whitlock[2], and D. H. Keisler[3], [1]*Berry College*, *Mount Berry, GA*, [2]*University of Tennessee*, *Knoxville,* [3]*University of Missouri*, *Columbia*.

Previous research has demonstrated circulating concentrations of leptin increase in ewes during mid pregnancy then decline in late pregnancy and early lactation. This study was designed to more narrowly define the timing of changes in circulating concentrations of leptin with pregnancy in ewes. Katahdin ewes (n = 19) located at latitude 34.275 and longitude −85.183 (Mount Berry, GA) were utilized. Blood samples were collected weekly via jugular veinpuncture beginning immediately before ram exposure on September 23 and continuing until 4 weeks post-lambing.

Ewes were exposed to a ram fitted with a marking harness for a 63 d breeding season. Breeding marks were recorded daily. Lambing date and number of lambs born was recorded. Week of gestation was calculated by breeding mark. The blood sample collected before breeding was considered wk 0. Plasma concentration of leptin was determined by radioimmunoassay. Data were tested for effects of date of sample, pregnancy status, and date of sample by pregnancy status interaction using procedures for repeated measures (JMP version 7; SAS Institute Inc., Cary, NC). Data were also tested for effects of week of gestation and number of lambs. Pregnancy had an effect on plasma concentrations of leptin ($P = 0.0407$; 6.06 ± 0.19 vs 4.67 ± 0.64 ng/ml in pregnant vs non-pregnant ewes, respectively). There was also an effect of date of sample ($P < 0.0001$) on plasma concentrations of leptin. Week of gestation had an effect of plasma concentrations on leptin ($P < 0.0001$) with ewes having lower plasma concentrations of leptin during wk 12, 13, 16, and 18–21 of gestation as well as 4 weeks after lambing when compared with before breeding. Plasma concentrations of leptin were higher wk 1–12, 14, 15, and 17 of gestation than after lambing, but did not differ from values before lambing. These data confirm a decline in circulating concentrations of leptin in the last third of gestation and continuing into early lactation in ewes.

Key Words: sheep, pregnant, leptin

T259 Nutritional regulation of body condition score at the initiation of the transition period in dairy cows on grazing conditions: hepatic expression of fatty acid metabolism genes. M. Carriquiry*[1], M. L. Adrien[2], V. V. Artegoitia[2], D. Mattiauda[1], and A. Meikle[2], [1]*School of Agronomy, UDELAR*, *Uruguay*, [2]*School of Veterinary Medicine, UDELAR*, *Uruguay*.

Multiparous Holstein cows (n = 10), blocked by body weight and expected calving date, were used to investigate the effect of different body condition score (BCS) at 30 d before calving (−30 d), induced by a differential nutritional management from −100 to −30 d, on hepatic expression of peroxisome proliferator-activated receptors-α (PPARA), carnitine palmitoyl transferase-1 (CPT1A), acyl-CoA dehydrogenase-very long-chain (ACADVL), and acyl-CoA oxidase (ACO) during the transition period. From −100 to −30 d, cows were offered different planes of nutritionwith 7, 14 or 20 kg/day/cow of dry matter (DM) of a long-term pasture to achieve desired BCS −30 d. BCS (scale 1–5) was determined every 15 d, and cows had to gain 0.5 points (HI) or to maintain (LO) BCS at least in 2 subsequent observations to be included in the study. From −30 to 45 d cows were managed together. Liver biopsies were collected at −15, 15, and 45 d and mRNA abundance was determined by real time PCR using hypoxanthine phosphoribosyltransferase (HPRT) as control gene. Means from repeated measure analyses differed when $P < 0.05$. Cows had similar BCS at −100 d (2.9 ± 0.08) and differed after the nutritional treatment (3.4 vs. 2.8 ± 0.08), but groups presented similar BCS at 15 (2.9 vs. 2.7 ± 0.08) and 45 (2.8 vs. 2.7 ± 0.08) d. NEFA concentrations increased around parturition and were greater in LO than HI cows. Expressions of PPAR (2.7 vs. 1.2 ± 0.45), ACADVL (3.0 vs. 0.9 ± 0.5), and ACO (149 vs. 64 ± 28) mRNA were greater for LO than HI cows along the period evaluated. There was an effect of day on CPT1A and ACO mRNA as their abundance was increased (>2-fold) at 15 d, effect that was more evident in LO cows. There was a trend ($P < 0.09$) for an interaction of treatment by day for ACADVL mRNA as its expression was increased at 45 d only in LO cows. Results indicated nutritional plane before the transition period affected regulation of hepatic fatty acid oxidation genes, being these genes upregulated, in agreement with greater NEFA levels, in cows that maintained BCS from −100 to −30 d.

Key Words: mRNA, liver, dry period nutrition

T260 Gluconeogenic enzymes are differentially regulated by fatty acid cocktails in Madin-Darby Bovine Kidney cells. H. M. White*, S. L. Koser, and S. S. Donkin, *Purdue University*, *West Lafayette, IN*.

Increases in serum NEFA levels and changes in serum fatty acid profiles at calving are characteristic of the transition cow. The objective of this study was to examine the effect of 24 h exposure of Madin-Darby Bovine Kidney cells to fatty acid cocktails on expression of pyruvate carboxylase (PC), cytosolic and mitochrondrial phosphoenolpyruvate carboxykinase (PEPCK-C and PEPCK-M), and glucose-6-phosphatase. Cocktails contained C14, C16, C18, C18:1, C18:2, and C18:3 fatty acids and were designed to mimic the fatty acid profile and concentration of cows pre- and post-calving (PPCALV; 0.25 m*M*) and at calving (CALV; 0.5 m*M*). An additional cocktail mimicked the profile of cows with induced fatty liver at calving (IFL; 1 m*M*). Expression of PC mRNA tended to increase ($P < 0.1$) in cells exposed to IFL (6.0 vs. 2.8 ± 1.0 arbitrary units, control vs. IFL, respectively). Expression of PEPCK-C mRNA was increased ($P < 0.05$) in cells exposed to PPCALV compared with all other cells (5.0 vs. 1.2 ± 0.8 arbitrary units, PPCALV vs. control, respectively). Exposure to IFL increased ($P < 0.05$) the ratio of PC to PEPCK-C by 8.4 and 2.4 fold compared with PPCALV and CALV exposure. Exposure of cells to IFL tended to increase ($P < 0.1$) PEPCK-M mRNA (3.0 vs. 1.7 ± 0.5 arbitrary units, IFL vs. control, respectively) and increased ($P < 0.05$) glucose-6-phosphatase mRNA (3.2 vs. 1.5 ± 0.8 arbitrary units, IFL vs. control, respectively). To elucidate effects of fatty acid profile from concentration, cells were exposed to each profile at lower and higher concentrations. Increased concentrations of PPCALV did not increase ($P \geq 0.05$) PEPCK-C mRNA expression as observed at physiological concentrations. Increasing concentration of CALV decreased ($P < 0.05$) expression of PEPCK-C and increased ($P < 0.05$) expression of PEPCK-M mRNA. Fatty acid profile and concentration alters expression of key gluconeogenic enzymes although the magnitude and directionality of the response was not uniform. Regulation of mRNA expression for these enzymes is likely part of the coordinated response in liver during transition to calving.

Key Words: transition cow, Madin-Darby Bovine Kidney cells, fatty acids

T261 The effects of leptin on phosphorylation of mTOR and rpS6 to signal protein synthesis in bovine mammary epithelial cells. E. K. Evans*, J. A. D. R. N. Appuhamy, and M. D. Hanigan, *Department of Dairy Science, Virginia Polytechnic Institute and State University*, *Blacksburg*.

Poor nitrogen utilization efficiency of dairy cows increases the nitrogen excretion into the environment. Efficiency of milk protein synthesis is regulated through cellular signaling pathways which are responsive to hormones, cellular energy status, and cellular amino acid supply. These signals result in phosphorylation of various signaling proteins including mammalian target of rapamycin (mTOR) and ribosomal protein S6 (rpS6) which regulate initiation of protein synthesis and control polypeptide elongation. Thin cows are known to produce less milk than well-conditioned cows. It was hypothesized that this effect could be mediated through leptin actions directly on mammary epithelial cells. The purpose of this experiment was to study the effects of leptin on the phosphorylation status of mTOR and rpS6 in MAC-T cells. Cells were seeded into 6-well plates at a density of 90,000 cells per well, starved in media containing 20% of normal DMEM essential amino acid concentrations and devoid of fetal bovine serum (FBS) for 12 h and subsequently cultured for 2 h in media without or with 160 ng/mL leptin. Each treatment was replicated trice and each replicate consisted of cells in 3 wells. The cells were lysed in the presence of phosphatase and protease inhibitors

and samples were analyzed by Western immunoblotting to determine the phosphorylation status of mTOR(Ser2448) and rpS6 (Ser235/236). The membranes were first probed for the phosphorylated forms of each protein and subsequently probed for the total forms of each. Statistical analysis of immunoblotting results showed no significant difference between the phosphorylation of mTOR in cells treated with or without leptin, but leptin treatment did cause a statistically significant increase in phosphorylation of rpS6 (67%). These results suggest that leptin acts on rpS6 independent of the Ser2448 site on mTOR. Stimulation of rpS6 should stimulate ribosomal biogenesis which would lead to increased protein synthesis, thus the results are supportive of a direct role of leptin on milk protein synthesis.

Key Words: leptin, protein synthesis, signaling proteins

T262 Glucocorticoid regulation of chicken adipose triglyceride lipase in adipose tissue. J. Serr*, S. Shin, Y. Suh, M. Kim, D. Latshaw, and K. Lee, *The Ohio State University, Department of Animal Sciences*, *Columbus*.

The mechanism of adipose tissue lipolysis is one that has not been fully elucidated. Increasing our understanding of this process would allow for increased feed efficiency and reduced fat content, which would lower feeding costs for poultry production. Adipose triglyceride lipase (ATGL) is an adipose-specific enzyme which cleaves at the Sn-1 position of triglycerides, releasing non-esterified fatty acids (NEFA) into the bloodstream. Glucocorticoids have been proven to elevate the level of circulating NEFAs. To determine the regulation of ATGL by glucocorticoid, 30 Ross 308 broilers received a 200 μL intraperitoneal injection of dexamethasone (4 mg/kg). Saline was administered to an additional 12 birds to determine any effect of stress during handling and injection. Another 6 birds received no treatment and were harvested as a control. Dexamethasone-injected birds were harvested at 0.5, 1, 2, 4, and 6 h after treatment; saline-treated birds were collected at 4 and 6 h (6 per time point). Adipose tissue was collected from abdominal and subcutaneous depots. Blood samples were collected via cardiac puncture. Gene and protein expression were analyzed via quantitative real-time PCR (qRT-PCR) and Western blot, respectively. In comparison with the saline-treated group, ATGL mRNA and protein was increased in broilers injected with dexamethasone, demonstrating that any response of ATGL expression to the stress of handling was minimal compared with that of hormone treatment. When dexamethasone response was observed against the untreated group up to 2 h following injection, an increase in ATGL protein was observed as quickly as 0.5 h and increased further at 1 and 2 h, demonstrating an acute response. Additionally, plasma NEFA analysis was done to confirm the release of free fatty acids into the blood. Plasma NEFA increased gradually from 0 to 6 h, and reached statistical significance (Tukey's Test) at 4 h (concurrent with mRNA and protein expression of ATGL). These data show that ATGL expression and activity is positively regulated by glucocorticoid in a time-dependent manner.

Key Words: chicken, lipolysis, glucocorticoid

T263 Bovine acute-phase response following corticotrophin-releasing hormone (CRH) infusion. R. F. Cooke*, A. B. Scarpa, F. M. Nery, F. N. T. Cooke, and D. W. Bohnert, *Oregon State University - EOARC*, *Burns.*

The objective of this study was to evaluate plasma concentrations of cortisol, ACTH, acute-phase proteins, and pro-inflammatory cytokines in beef steers following CRH infusion. Six weaned, halter-trained Angus steers (BW = 163 ± 7.0 kg; age = 203 ± 5.8 d) were fitted with indwelling jugular catheters on d −1 of the study, and assigned to receive intravenously 0.1 μg of bovine CRH/kg of BW on d 0 of the study. Blood samples were collected every hour via jugular catheters from −2 to 8 h, and every 6 h via jugular venipuncture from 12 to 72 h relative to CRH infusion (0 h). Steer rectal temperature was assessed concurrently with each blood collection. Samples collected from −2 to 8 h relative to CRH infusion were analyzed for plasma concentrations of interleukin (IL)-1 and 6, tumor necrosis factor (TNF)-α, interferon (IFN)-γ, cortisol, ACTH, ceruloplasmin and haptoglobin, whereas samples collected from 12 to 72 h were analyzed for plasma concentrations of ceruloplasmin and haptoglobin only. Data were analyzed with the MIXED procedure of SAS. Plasma ACTH and cortisol concentrations peaked ($P \leq 0.02$) 1 h following CRH infusion, and returned to basal levels at 2 and 4 h following infusion ($P > 0.15$), respectively. Body temperature peaked at 2 and 8 h following infusion ($P < 0.01$), and returned to basal levels after 12 h ($P = 0.40$). Contrasted to all other sampling hours, plasma IFN-γ concentrations were greater ($P = 0.03$) at 1 and 5 h, plasma IL-6 concentrations were greater ($P = 0.04$) from 4 to 6 h, plasma IL-1 concentrations tended ($P = 0.12$) to be greater from 6 to 8 h, and plasma TNF-α concentrations were greater ($P = 0.03$) from 5 to 7 h following infusion. Plasma ceruloplasmin and haptoglobin concentrations increased linearly ($P \leq 0.01$), and peaked at 54 and 66 h following CRH infusion, respectively. In conclusion, infusion of CRH at 0.1 μg/kg of BW increased plasma concentrations of ACTH and cortisol, and stimulated the acute-phase response in beef steers.

Key Words: acute-phase response, corticotrophin-releasing hormone, beef cattle

Physiology and Endocrinology: Hormonal Regulation of the Estrous Cycle in Beef Cattle

T264 Effects of 72-h temporary calf removal prior to fixed-time AI on pregnancy rates and subsequent calf performance in suckled beef cows. G. H. L. Marquezini*[1], V. R. G. Mercadante[1], S. L. Bird[2], B. J. Funnell[2], and G. C. Lamb[1], [1]*University of Florida*, *Marianna,* [2]*University of Minnesota, Grand Rapids.*

We determined whether 72 h calf removal (CR) before fixed-time AI (TAI) would increase pregnancy rates or alter subsequent calf performance in suckled, crossbred beef cows. Cows at 2 locations where stratified by days postpartum and parity and randomly assigned to one of 2 treatments: 1) received 100 μg GnRH and a CIDR insert (d −7), followed in 7 d by 25 mg $PGF_{2\alpha}$ and CIDR removal (d 0), followed in 72 h by GnRH and AI (d 3; Control; n = 105). 2) Same as control but calves were removed from their dams for 72 h between d 0 and d 3 (CR; n = 112). Transrectal ultrasonography was used to follow follicle and corpus luteum development on d 0, 3, and 10 and to determine pregnancy status on d 28. Blood samples were collected on d −14, −7, 0, 3, 10, and 28 to determine concentrations of progesterone. Calf weights were determined on d 0, 3, 32, and 140. Pregnancy rates tended ($P = 0.12$) to differ between Control (33.3%) and CR (43.5%). Calf removal did not alter follicle size on d 3, but on d 10 noncycling cows exposed to CR (3.1 ± 0.3 ng/mL) had greater ($P < 0.02$) concentrations of progesterone than Controls (2.0 ± 0.3 ng/mL). On d 10, no difference in concentrations of progesterone were detect for cycling cows. On d 0 calf weights were similar between Control (96.6 ± 2.4 kg) and CR (96.7 ± 2.4 kg) treatments, whereas on d 3 (99.7 ± 2.4 and 94.0 ± 2.3 for Control and CR, respectively), 32 (125.3 ± 2.4 and 119.0 ± 2.3 kg for Control and CR, respectively) and 140 (226.2 ± 2.4 vs. 212.9 ± 2.3 kg for Control and CR, respectively) weights were greater ($P < 0.05$) for Control than CR calves. When calves were classified into age ranges of young (25 to 40 d), medium (41 to 80 d), and old (>80 d) on d 0, young calves lost ($P < 0.001$) more weight as a percentage of body weight during 72 h of calf removal than older calves, whereas medium calves were intermediate. We conclude that calf removal for 72 h tended to increase pregnancy rates, while having negative impacts on subsequent calf performance.

Key Words: calf removal, beef cows, estrous synchronization

T265 Timed AI pregnancy rates in suckled beef cows in response to equine chorionic gonadotropin (eCG). L. D. Wallace[1], S. L. Pulley*[1], K. C. Olson[1], J. R. Jaeger[1], J. W. Bolte[1], S. K. Johnson[1], L. A. Pacheco[1], K. Bischoff[2], T. Loyd[2], G. C. Lamb[2], and J. S. Stevenson[1], [1]*Kansas State University*, *Manhattan,* [2]*University of Florida, Marianna.*

Previously, eCG administered before induced luteolysis stimulated follicle growth and increased progesterone secretion by the corpus luteum (CL) formed after ovulation in cattle. Our objective was to monitor timed AI pregnancy rate (PR) in beef cattle subjected to eCG. Suckled beef cows (n = 513; pure- and crossbred Angus, Simmental, and Hereford) were enrolled in a 7-d CO-Synch + CIDR protocol (100 μg GnRH at CIDR insertion [d –7]; 25 mg PGF2α (PGF) at CIDR removal [d 0]; and 100 μg GnRH at AI 66 h after PGF [d 3]) at 3 locations. Cows were assigned randomly to be controls or receive eCG (200 IU i.m.) at the time of PGF injection and CIDR insert removal. Pregnancy was diagnosed by transrectal ultrasonography at median d 35 and 67 after AI. Serum progesterone concentration (ng/mL) was determined in blood collected on d –17, –7, 0, 3, and at both pregnancy diagnoses (pregnant cows only) to determine cycling status, luteolysis, and potential differences in CL function after AI. Pretreatment cycling status differed ($P < 0.01$) among locations (locations 1 = 76.5%; 2 = 54.3%; and 3 = 27.4%). For cows having elevated (≥1 ng/mL) progesterone at CIDR insert removal, 97.4% had luteolysis, with 17.3% of cows having low (<1 ng/mL) progesterone at insert removal and at timed AI, and 1.2% having increasing progesterone from insert removal to timed AI. Progesterone did not differ on d 35 of pregnancy (6.0 ± 0.3 and 6.4 ± 0.4) or d 67 (6.6 ± 0.4 and 6.4 ± 0.3) for eCG and controls, respectively. Unadjusted PR on d 35 was 42.9 vs. 49.8% for eCG vs. controls, respectively. Herd, cycling status, technician, and treatment influenced PR. Cycling cows were 1.5 times more ($P = 0.046$; 95% CI = 1.01–2.27) likely to conceive than noncycling cows. Control cows were 1.5 times more ($P = 0.036$; CI = 1.03–2.13) likely to conceive than those treated with eCG. Cows in location 3 were 1.8 to 3.5 times more ($P = 0.004$; CI = 1.1–5.6) likely to conceive than cows at other locations. Pregnancy loss to d 67 did not differ between treatments (3.7 vs. 2.3% for eCG vs. controls), respectively. We conclude that eCG treatment did not increase PR under these experimental conditions.

Key Words: timed AI, eCG, beef cattle

T266 Effect of post-insemination GnRH on the pregnancy rate of beef cattle. W. A. Greene* and C. L. Pickworth, *The Ohio State University*, *Wooster*.

The objective of this study was to determine if administering GnRH 7 d after first artificial insemination (AI) would increase pregnancy rates (PR) in beef cattle. Ninety–3 beef cattle were blocked for breed, parity, postpartum interval (PPI), postpartum cyclicity (as determined by estrus detection and ultrasonography), and breeding method (bred based on observed estrus or timed–bred). Blocks were randomly assigned to either receive GnRH or saline. On d 0, all cattle received 100 μg GnRH i.m. and intra–vaginal 1.38 g progesterone inserts (CIDRs). On d 7, CIDRs were removed and cattle received 25 mg $PGF_{2\alpha}$ i.m. Estrus was observed at 0700 and 1900 and AI occurred 11 – 13 h after estrus was observed. If estrus was not observed, cattle were timed AI (TAI) and received 100 μg GnRH i.m. 70 – 72 h after $PGF_{2\alpha}$. On d 7 post–insemination, cattle received either 2 mL GnRH (100 μg) or 2 mL saline i.m. Blood samples were collected for plasma progesterone (P4) analyses 14 d post–insemination. Following the synchronization period, repeat breedings were done until d 75. Pregnancy status was determined by ultrasonography on d 110. The estrus detection rate [EDR] was 61.3%. Cattle bred following an observed estrus had a higher ($P < 0.05$) PR to synchronization than TAI cattle (61.4 vs. 33.3%). GnRH and Saline groups had similar ($P > 0.05$) PR to synchronization (46.8 vs. 54.4%), overall PR (87.2 vs. 97.8%), and mean P4 concentrations (2.6 ± 1.6 vs. 2.1 ± 1.6 ng/ml). Cycling (n = 49) and anestrous cattle had similar ($P > 0.05$) EDR (57.1 vs. 65.9%), PR to synchronization (44.9 vs. 56.8%), and overall PR (91.8 vs. 93.2%). A higher ($P < 0.05$) PR to synchronization was noted for cows with a long PPI (>50 d; n = 42) than cows with a short (≤50 d; n = 29) PPI (61.9 vs. 31.0%). Cycling animals had higher ($P < 0.05$) P4 concentrations than anestrous animals (2.7 ± 1.9 vs. 2.0 ± 1.1). The pregnancy rate of beef cattle was not affected by the post–insemination administration of GnRH.

Key Words: GnRH, post-insemination, progesterone

T267 Reproductive performance of prepubertal *Bos indicus* heifers after progesterone-based treatments. I. Claro Júnior*[1], O. Sá Filho[1], R. Peres[1], F. Aono[1], M. Day[2], and J. L. Vasconcelos[1], [1]*FMVZ-UNESP*, *Botucatu, SP, Brazil*, [2]*Ohio State University*, *Columbus*.

The objective of this study was to evaluate the effects of treatments with exogenous progesterone (P4) on reproductive performance of prepubertal *Bos indicus* heifers. Prepubertal Nelore heifers (n = 935; 24.0 ± 1.13 mo; 298.0 ± 1.89 Kg; body condition score of 3.2 ± 0.26) were randomly assigned to receive, between experimental Days −12 and 0, no treatments (CIDR0; n = 113), an intravaginal insert containing 1.9 g of P4 (CIDR) that had never been previously used (CIDR1; n = 237), or a CIDR insert that had previously been used 3x, with each use occurring for 9 d (CIDR4; n = 239). An additional treatment group consisted in pubertal heifers receiving a 12.5 mg im injection of dinoprost tromethamine on Day 0 (PGF; n = 346) to be used as controls for evaluation of conception rates. On Day 0, heifers were rectally palpated for uterine score evaluation (UtS; 1 to 3 scale), blood samples were taken for analysis of P4 and follicular diameter (FD) was measured. The breeding season (BS) started on Day 1 and consisted of artificial insemination after detection of estrus between Days 1 and 45, and natural service between Days 46 and 90. There were effects of treatment ($P < 0.05$) on serum concentrations of P4 on Day 0 (CIDR0: 0.37 ± 0.16; CIDR1: 2.31 ± 0.11; CIDR4: 1.20 ± 0.11 ng/mL), FD on Day 0 (CIDR0: 9.45 ± 0.24; CIDR1: 9.72 ± 0.17; CIDR4: 11.42 ± 0.16 mm), UtS on Day 0 (CIDR0: 1.49 ± 0.06; CIDR1: 1.88 ± 0.04; CIDR4: 2.24 ± 0.04), estrus detection rates in 7 d (CIDR0: 19.5%; CIDR1: 42.6%; CIDR4: 38.3%) and 45 d of BS (CIDR0: 52.2%; CIDR1: 72.1%; CIDR4: 75.3%), and on pregnancy rates in 7 d (CIDR0: 5.3%; CIDR1: 14.3%; CIDR4: 18.4%), 45 d (CIDR0: 27.4%; CIDR1: 39.2%; CIDR4: 47.7%) and 90 d of BS (CIDR0: 72.6%; CIDR1: 83.5%; CIDR4: 83.7%). Conception rate in 7 d of BS was greater ($P < 0.05$) in heifers from the CIDR4 (46.8%) and PGF (43.8%) than in CIDR0 (27.3%) and CIDR1 (33.7%) treatments. In conclusion, treatments with P4 hastened puberty and improved pregnancy rates at the beginning of BS, and previously used CIDR inserts are preferable for improvement of reproductive performance in prepubertal *Bos indicus* heifers.

Key Words: *Bos indicus* heifers, puberty, progesterone

T268 Comparison of three doses of prostaglandin $F_{2\alpha}$ in a 5-day CIDR-based synchronization protocol in beef cows. T. Robison*, K. Y. Perry, K. G. Carnahan, T. L. Davis, and A. Ahmadzadeh, *University of Idaho*, *Moscow*.

The most common timed artificial insemination (AI) programs used are based on the CO-Synch approach which includes the use of an intravaginal progesterone releasing insert (CIDR) and administration of $PGF_{2\alpha}$ to synchronize the estrous cycle in beef cattle. The objective of the present study was to compare the effect of various doses of $PGF_{2\alpha}$ on estrus and circulating progesterone (P4) concentrations of beef cattle synchronized using a 5 d CIDR protocol. Charolais cows (24 to 94 d postpartum) received a CIDR (d 0) for 5 d. On d 5 after CIDR removal, cows were randomly assigned to receive one of 3 treatments; 1) a single injection of 25 mg $PGF_{2\alpha}$ (control, n = 17), 2) a single injection of 37.5 mg $PGF_{2\alpha}$ (large, n = 17), or 3) 2 injections of 12.5 mg $PGF_{2\alpha}$ 7 h apart (split, n = 17). All cows were fitted with estrus detection aids and observed for behavioral estrus 3 times daily and artificially inseminated (AI) according to the a.m.- p.m. rule. Animals that were not detected in estrus received 100 µg GnRH and timed AI 96 h post-$PGF_{2\alpha}$ injection. Blood was collected on d 0 (before CIDR insertion) and d 7 (56 h post-$PGF_{2\alpha}$ treatment) to measure serum P4 concentrations. At 56 h post-$PGF_{2\alpha}$ treatment, mean P4 concentrations were less than 1ng/ml for all cows. However, P4 concentrations were lower on d 0 ($P < 0.05$) for cows ≤40 d postpartum (dpp) compared with cows that were >40 dpp in all treatments. The interval from $PGF_{2\alpha}$ treatment to estrus was not different among treatments and averaged: control = 67 ± 5.8 h, large = 58 ± 5.7 h, and split = 54 ± 5.6 h. Based on the current study, there was not sufficient evidence to indicate that observed estrus behavior and serum P4 concentrations after treatment with 25 mg $PGF_{2\alpha}$, 37.5 mg $PGF_{2\alpha}$, or 2 injections of 12.5 mg $PGF_{2\alpha}$ 7 h apart was different among treatments.

Key Words: beef cows, progesterone, prostaglandin $F_{2\alpha}$

T269 Pregnancy per AI (P/AI) of dairy cows following presynchronization and splitting the prostaglandin (PGF) injection in the 5d-Cosynch protocol. E. S. Ribeiro*, R. S. Bisinotto, M. Favoreto, L. T. Martins, R. L. A. Cerri, F. T. Silvestre, L. F. Greco, W. W. Thatcher, and J. E. P. Santos, *University of Florida*, *Gainesville*.

Objectives were to compare P/AI of cows subjected to the 5d-Cosynch protocol either presynchronized or with supplemental progesterone (P4), and with a double dose of PGF either as a single or split injections. In experiment 1, 730 grazing cows were randomly assigned to: Presynchronization (G6G; d −8 0.5 mg of cloprostenol, d −6 GnRH) followed by the 5d-Cosynch protocol with 1 mg of cloprostenol as a single (G6G-SI; d 0 GnRH, d 5 PGF, d 8 GnRH + AI) or split into 2 injections (G6G-TI; d 0 GnRH, d 5 and 6 PGF, d 8 GnRH + AI); or no presynchronization but with an intravaginal P4 insert (CIDR) from the GnRH to PGF with 1 mg of cloprostenol as a single (CIDR-SI; d 0 GnRH + CIDR, d 5 remove CIDR and PGF, d 8 GnRH + AI) or split into 2 injections on d 5 and 6 (CIDR-TI). Ovaries were scanned on d 0 and 5 and plasma analyzed for P4 on d 5 and 8. In experiment 2, 655 cows in a confinement system received an injection of 25 mg of dinoprost at 44 and 60 DIM. On d 72 they were assigned to the 5-d Cosynch with 50 mg of dinoprost as a single (d 0 GnRH, d 5 PGF, d 8 GnRH + AI) or split into 2 injections (d 0 GnRH, d 5 and 6 PGF, d 8 GnRH + AI). Pregnancy was determined 35 and 60 d after AI. In experiment 1, presynchronization with G6G increased ($P < 0.001$) the proportion of cows with a CL on d 0 (80.6 vs. 58.8%), ovulation to the first GnRH (64.2 vs. 50.2%), and presence (95.6 vs. 88.4%) and number of CL at PGF (1.79 vs. 1.30). Luteolysis was greater ($P < 0.001$) for the split injection of PGF (95.9 vs. 72.2%), especially in G6G cows (96.2 vs. 61.7%). An interaction ($P = 0.05$) was observed for P/AI. For CIDR cows, method of PGF administration had no effect on P/AI (CIDR-SI = 30.2 vs. CIDR-TI = 34.3%), whereas for G6G cows, splitting the dose into 2 injections improved P/AI (G6G-SI = 28.7 vs. G6G-TI = 45.4%). In experiment 2, splitting the dose of PGF increased ($P < 0.04$) P/AI on d 35 (44.5 vs. 36.4%) and 60 (40.3% vs. 32.6%) after AI. Presynchronization and splitting the dose of cloprostenol or dinoprost into 2 injections increases P/AI in cows subjected to the 5d-Cosynch protocol.

Key Words: dairy cow, luteolysis, timed AI

T270 Luteal function following a normal versus synchronized estrus in beef heifers. M. F. Smith*[1], D. H. Keisler[1], and F. Stormshak[2], [1]*University of Missouri*, *Columbia*, [2]*Oregon State University*, *Corvallis*.

The objective was to characterize changes in plasma concentrations of oxytocin and progesterone in response to a prostaglandin $F_2\alpha$ (PG) injection on d 6 (d 0 = estrus) following a normal or synchronized estrous cycle. Normally cycling Angus heifers were assigned to the following groups: 1) Normal Cycle (Normal = 5 heifers were given PG on d 6 of the cycle immediately following a normal estrous cycle), 2) Synchronized Cycle (Sync = 5 heifers were given PG on d 6 of the cycle immediately following a synchronized cycle; see below), and 3) Synchronized and Ovariectomized (Sync + Ovx = 4 heifers were synchronized then unilaterally ovxed (luteal ovary) on d 4 of the ensu-

ing cycle and given PG on d 6). The experiment was a randomized complete block design with treatment serving as the block. Estrus was synchronized (Sync and Sync + Ovx groups) as follows: GnRH (100 µg, Cystorelin) injection (im) and insertion of a CIDR followed 7d later with injection (im) of PG (500 µg Estrumate) and CIDR removal. On d 6 of the estrous cycle immediately following a normal or synchronized cycle, each heifer received PG (500 µg Estrumate, iv). Jugular blood samples were collected −10, −5, 0 (immediately before PG injection), 5, 10, 15, 20, and 30 min following injection. Plasma was collected and analyzed for oxytocin and progesterone by RIA. Plasma concentrations of oxytocin increased within 5 min of PG injection in the Normal and Sync heifers but not in the Sync + Ovx heifers indicating an ovarian and likely luteal source of oxytocin in the Normal and Sync heifers. Mean plasma concentrations of oxytocin at 30 min after PG injection were lower ($P < 0.01$) in Sync vs. Normal heifers and plasma concentrations of progesterone were also lower ($P < 0.01$) on d 6 (−15 to 30 min) in Sync vs. Normal heifers. In summary, PG-induced secretion of oxytocin from the developing corpus luteum and plasma levels of progesterone were greater on d 6 of an ensuing cycle following a normal compared with a synchronized cycle.

Key Words: prostaglandin, oxytocin, corpus luteum

T271 Evaluation of 5-day versus 7-day CIDR treatment on reproductive outcomes of beef heifers using a modified timed-AI protocol. A. Ahmadzadeh*[1], D. Gunn[2], J. B. Hall[3], and J. B. Glaze Jr.[4], [1]*Univ. of Idaho*, *Moscow*, [2]*Univ. of Idaho*, *Fort Hall*, [3]*Univ. of Idaho R & E*, *Salmon*, [4]*Univ. of Idaho R & E*, *Twin Falls*.

The objective of this experiment was to determine the effect of reducing the duration of CIDR insert exposure, in a CIDR-based timed AI protocol, on pregnancy per AI (P/AI) and pregnancy rates in beef heifers. The experiment was conducted in 4 consecutive years. British cross-bred heifers (yr 1, n = 82; yr 2, n = 70; yr 3, n = 86; yr 4, n = 54) were stratified by BW and age and were assigned randomly to one of 2 treatments: 1) CIDR7 heifers (n = 147) received a CIDR insert for 7 d; and 2) CIDR5 heifers (n = 145) received a CIDR insert for 5 d. Heifers in CIDR7 and CIDR5 were given $PGF_{2\alpha}$ upon CIDR removal followed by GnRH (75 µg) and timed AI 55- 56 h after CIDR removal. Estrual behavior was monitored following CIDR removal. Heifers were inseminated by a single technician. Starting on d 14 after AI, heifers were exposed to fertile bulls for 45 d. Blood samples were collected on the day of CIDR insertion. Pregnancy status was determined by ultrasonography at d 32 to 35 and d 67 to 85 after AI. Data were analyzed by logistic regression and ANOVA. Percentage of heifers detected in estrus was different ($P < 0.05$) between years (69%, 44%, 51%, and 51% for yr 1, 2, 3, and 4, respectively) but not different between treatments. At CIDR insertion, mean serum progesterone (P4) were greater in CIDR7 heifers than CIDR5; however there was no effect of year or year by treatment interaction on P4 concentrations. There was a treatment by year interaction effect on P/AI ($P < 0.05$). For CIDR7 and CIDR5, in yr 1 P/AI was 39% and 65.8% ($P < 0.05$); in yr 2, P/AI was 64.7% and 41% ($P < 0.05$), yr 3 P/AI was 59% and 73.8% ($P = 0.09$) and yr 4 P/AI was 50% and 66% ($P = 0.25$). Overall P/AI tended ($P = 0.09$) to be greater for CIDR5 compared with CIDR7 (62.5% vs. 52%). Final pregnancy rates were unaffected by the treatment protocols or year (92% and 95.5% for CIDR7 and CIDR5, respectively). The P/AI results from this study suggests that reducing the duration of CIDR treatment from 7 to 5 d in a CIDR-based TAI protocol may improve P/AI.

Key Words: estrous synchronization, CIDR insert, beef heifer

T272 Rumen temperature during the estrous cycle of beef cows. B. H. Boehmer*, T. A. Pye, and R. P. Wettemann, *Oklahoma Agricultural Experiment Station*, *Stillwater*.

The objective of this study was to evaluate rumen temperature (RuT) associated with estrus in May to July. Angus cows (n = 46) were administered temperature boluses (SmartStock, LLC) with a bolus gun and estrus was synchronized with $PGF_{2\alpha}$ at 60 to 90 d postpartum. Temperature boluses were programmed to transmit RuT every hour. The onset of estrus was determined by HeatWatch (CowChips, LLC). Progesterone was quantified in plasma collected daily to verify stage of the estrous cycle. Mean RuT for all cows was 38.19 ± 0.01°C and RuT ≤35.3°C, which are associated with water consumption, were excluded from analyses. Progesterone and RuT during estrus were analyzed using the MIXED procedure (SAS). Ambient temperature ranged from 8 to 39°C during the experiment and was not associated with RuT. On the day of estrus, RuT was greater ($P < 0.05$, 38.6 ± 0.1°C) compared with 3 d before (38.2 ± 0.1°C) or 3 d after (38.3 ± 0.1°C) estrus. Rumen temperature was greater ($P < 0.05$, 38.8 ± 0.1°C) during the first 8 h after the onset of estrus compared with the same daily hours the day before (38.2 ± 0.1°C) or after (38.1 ± 0.1°C) onset of estrus. Rumen temperature was recorded hourly and progesterone in plasma was quantified daily in cows (n = 20) during an estrous cycle. Concentrations of progesterone in plasma decreased before the increase in RuT at estrus. On the day of estrus, RuT was greater ($P < 0.05$, 39.0 ± 0.1°C) compared with the other days of the cycle (38.5 ± 0.1°C). These results support our previous report that RuT can be used for the identification of estrus in beef cows.

Key Words: rumen temperature, estrus, beef cows

T273 Effects of feed supplementation and method of weaning on the physiology and performance of beef calves. C. Campistol*[1], H. G. Kattesh[1], J. C. Waller[1], E. L. Rawls[1], G. M. Pighetti[1], and J. A. Carroll[2], [1]*University of Tennessee*, *Knoxville,* [2]*Livestock Issues Research Unit, USDA-ARS, Lubbock, TX*.

A study was conducted to investigate growth performance and physiological measures of stress in pre- and post-weaned beef calves provided a grain supplement and weaned by fenceline or total separation. Angus steer calves (n = 48; 312.2 ± 27.9 kg), housed on pasture with their dams, were blocked by initial BW and assigned randomly on d 0 to be hand-fed a grain supplement (YS; 4.5 kg/head/d) or no supplement (NS) for 7 d. On d 7, calves (12 NS and 12 YS/group) were weaned by fenceline (Group 1) or total separation to a distant pasture (Group 2). On d 14, Group 1 calves were moved to a pasture lot adjoining Group 2. All calves were weighed and bled on d 0, 7, 10, 14, and 21, and provided access to the grain supplement on d 7–21. Blood was analyzed for plasma cortisol (CORT) and interferon-gamma (IFN-γ) concentration, hematocrit (Hct), red blood cell (RBC) and white blood cell (WBC) total count, and neutrophil:lymphocyte ratio (N:L). By d 7, BW increased ($P < 0.001$) and RBC and IFN-γ decreased ($P < 0.001$) in all calves. However, NS exhibited lower ($P < 0.005$) N:L (0.16 vs. 0.27 ± 0.03) and CORT (74.5 vs. 98.4 ± 7.2 nmol/L) compared with YS calves. By d 10, Group 2 steers experienced a reduction ($P < 0.001$) in BW compared with animals in Group 1, which was more pronounced in the NS calves. Measures for RBC, WBC, IFN-γ and N:L increased ($P < 0.01$) in all calves within 3 d following weaning. Compared with NS, both Hct and CORT for YS calves decreased ($P < 0.01$) over this same period. From d 14–21, Hct decreased ($P < 0.01$) and IFN-γ increased ($P < 0.001$). These results suggest that providing a grain supplement

beginning 7 d before weaning may reduce BW loss and temper the animals stress response due to weaning.

Key Words: beef cattle, pre-weaning supplementation, stress

T274 Effect of serum progesterone levels on conception rate in Creole Rodeo multiparous cows and heifers. J. A. Ramirez-Godinez*[1], L. V. Beltran-Prieto[1], J. Dominguez-Viveros[1], A. Flores-Mariñelareña[1], and A. Quezada-Casasola[2], [1]*Universidad Autonoma de Chihuahua*, *Chihuahua, Mexico*, [2]*Universidad Autonoma de Ciudad Juarez*, *Chihuahua, Mexico*.

The aim of the present study was to compare the conception rate (CR) depending on serum progesterone levels (SPL) in Creole Rodeo cows (CC) and heifers (CH) treated with ECP, eCG or hCG, and estradiol benzoate (EB), eCG, and GnRH, respectively, in addition to a CIDR+EB and $PGF_{2\alpha}$ protocol. Thirty-one multiparous CC and 59 CH were randomly assigned to 1 of 3 treatments: CC of T1 (n = 11) received 1 mg of ECP and T2 (n=10) 500 IU of eCG 24 h after CIDR removal, and T3 (n = 10) 2000 IU of hCG 56 h after CIDR removal; CH of T1 (n = 19) received 1.38 mg of EB and T2 (n = 5) same as CC, T3 (n =2 0) 100 μg of GnRH 56 h after CIDR removal. CH not detected in estrus from T2 were reassigned to T4 (n=15), same as T2, but 56 h after CIDR removal 100 μg of GnRH were administered. CC and CH in T1 and T2 were AI 12h after detected in estrus, and in T3 and T4 were fixed-time AI 56h after CIDR removal. Blood samples were collected in CC at days 0, 7, 8, 9, 17, 26 through 32, and in CH at days −7, 0, 2, 4, 6, 8, 10, 12 after CIDR insertion. CR was analyzed using PROC CATMOD of SAS. The variation coefficient of SPL of day 0 and 7 were analyzed with PROC MEANS of SAS. In CC, the CR was higher ($P<0.05$) in T2 (60%) than in T1 (27.27%) and T3 (30%). In CH, CR was similar ($P > 0.1$) being T4 with 46.67% over T1, T2, and T3 (31.58, 40, and 30%, respectively). The variation coefficient of SPL of day 0 and 7 in CC were 82.25% and 82.75%, respectively; for CH was 83.16% at day 0. The SPL were similar between treatments neither in CC nor in CH ($P > 0.1$), and did not have an effect in CR. These results suggest that the use of eCG after CIDR removal might improve the conception rate in multiparous Creole Rodeo cows; in heifers the use of eCG+CIDR+GnRH to induced ovulation, can improve fertility. In addition, the serum progesterone levels at CIDR insertion and at removal did not have an effect in conception rate in multiparous Creole Rodeo cows and heifers.

Key Words: Creole cattle, CIDR, eCG

Physiology and Endocrinology: Male Reproduction, Gamete Cryopreservation and Embryos

T275 Validity of sperm penetration assay in boar fertility testing. S. A. Oh*, Y. J. Park, S. J. Yoon, W. S. Kwon, Y. H. Kim, E. A. Mohamed, Y. A. You, and M. G. Pang, *Department of Animal Science & Technology and BET Research Institute, Chung-Ang University*, *Ansung, Gyeonggi-Do, Korea*.

The prediction of sperm fertility is of paramount importance for breeding animals. Multiple laboratory approaches have been developed for this purpose, but they have yielded equivocal results. The objective of this study was to develop and standardize to a method for predicting fertility in vivo in boars using the in vitro penetration assay. To increase the sensitivity and reduce false-negative results of the assay, each step in the procedure was standardized and quality control was applied. Maximum penetration of hamster zona-free oocytes and immature porcine oocytes was obtained using heparin-treated sperm cells. Hamster zona-free oocytes showed a significantly higher penetration than immature porcine oocytes. To eliminate interassay variability, 2 frozen bull semen samples were applied. All possible variables related to the female were excluded. The SPA (sperm penetration assay using zona-free oocytes) result showed significant correlation with historic average litter size but had no significant correlation with farrowing rates. To determine the normal range for the SPA, lower limits of the sperm fertility index were established as 1.2 for the small litter sizes (<8 piglets) and 2.5 for the large litter sizes (≥10 piglets). The overall accuracy was 93.33% and 93.33% respectively, for the small and large litter sizes. Our laboratory has standardized the procedure for the SPA, resulting in greatly increased sensitivities for small and large litter sizes. The protocol increases the ability to discriminate between good and poor fertility groups and it was highly effective at ranking 30 boars by litter size into large and small litter groups.

Key Words: sperm, fertility, sperm penetration assay

T276 Comprehensive proteomic analysis to defining sperm fertility in bovine. Y. J. Park*, S. A. Oh, W. S. Kwon, S. J. Yoon, Y. H. Kim, E. A. Mohamed, Y. A. You, and M. G. Pang, *Department of Animal Science & Technology and BET Research Institute, Chung-Ang University*, *Ansung, Gyeonggi-Do, Korea*.

The aim of present study was undertaken to determine whether bovine spermatozoa contained protein markers associated with bull fertility, and whether these markers were of value in predicting bull fertility. We undertook differential proteome profiling of spermatozoa from fertile bulls with extreme non-return rates (NRR): a low fertility group (45.10±4.95) and a high fertility group (82.45±6.26). Two-dimensional gel electrophoresis (2-DE) was carried out with triplicate samples of pooled spermatozoa from 3 low and 3 high fertility bulls. Protein expression levels of sperm from low and high fertility were compared using PD-Quest software. The marked difference in spot intensity was arbitrarily set as a >3-fold difference following analysis data from the software manufactures. From the different protein spots expressed in low and high fertility group, only 14 spots showed highly expression in low fertility, conversely, 4 spots were highly expression in high fertility. Six out of 18 spots detected were identified by LC/MS-MS. Metabolism related protein as ATP synthase subunit, protein tyrosin phosphorylation related protein as cytochrome b-c1 complex subunit 2 and sperm motility and cell death pathway related protein as porin were highly expressed in specimen from low fertility group. The other side metabolism related protein as alpha-2-HS glycoprotein, motility related protein as alpha-tubulin and protein oxidation related protein as phospholipid hydroperoxide glutathione peroxide were highly expressed in high fertility group. This study will enable further elucidation of the molecular mechanisms involved in this particular condition and might shed further light on key sperm proteins involved in fertilization. It is also important prerequisite to the development of diagnostic tests for bull fertility.

Key Words: sperm, fertility, proteome

T277 Effects of two egg yolk-free commercial extenders and centrifugation on freezing ability of semen in Mahabadi goat. M. Ansari*[1], A. Towhidi[1], M. Moradi Shahre Babak[1], and M. Bahreini[2], [1]*University of Tehran, Department of Animal Science*, *Karaj, Tehran, Iran*, [2]*Animal Breeding Center of Iran*, *Karaj, Tehran, Iran*.

The objective of this study was to determine the effects of 2 egg yolk-free extenders (Bioxcell and AndroMed) with or without semen centrifugation in 2 × 2 factorial design on quality of frozen-thawed semen in goat. Five mature Mahabadi bucks were selected for semen collection using an artificial vagina. Semen samples were collected, pooled and divided to 4 groups after quality evaluation. The groups consisted of Andromed (AC) or Bioxcell (BC) with centrifuged semen; and Andromed (A) and Bioxcell (B) with whole semen (without centrifugation). Percentage of motility and progressive motility of sperm were evaluated and recovery rate was calculated using post thaw motility divided by before freezing motility. Data was analyzed using proc GLM of SAS. Effect of extender, centrifugation and their interaction was significant ($P \leq 0.05$). Motility and progressive motility percentage of B (50.0% ± 3.5; 36.0% ± 3.6) was significantly higher than BC (28.0% ± 3.5; 17% ± 3.6) and AC (40.0% ± 3.5 ; 26.0% ± 3.6) ($P \leq 0.05$) and tended to be higher than A (45.0% ± 3.5; 26.0 ± 3.6) ($P = 0.07$). Recovery rate percentage in B (71.4 ± 5.0) was significantly higher than BC (40.0% ± 5.0) and AC (57.1% ± 5.0) ($P \leq 0.05$), with no significant difference between B and A (64.3% ± 5.0). It was concluded that extender Bioxcell with whole semen (without centrifugation) was more efficient for cryopreservation of goat semen.

Key Words: sperm cryopreservation, extender, centrifugation

T278 The effect of ethanol supplemented extender on freezing ability of goat semen. M. Ansari*[1], A. Towhidi[1], M. Moradi Shahre Babak[1], and M. Bahreini[2], [1]*University of Tehran, Department of Animal Science*, *Karaj, Tehran, Iran*, [2]*Animal Breeding Center of Iran*, *Karaj, Tehran, Iran*.

Inclusion of fat soluble material to the semen extender or embryo in vitro culture involves their solution into an appropriate solvent such as ethanol. Ethanol might have detrimental effects on sperm characteristics. Thus, the objective of this study was to investigate the effects of adding ethanol to the Bioxcell extender on goat semen freezing ability. Five mature Mahabadi bucks were selected and semen samples were collected using an artificial vagina during 4 weeks. Semen samples were pooled and divided into 2 groups after evaluation for qualitative characteristics. Treatment groups were including 1) basal extender as a control and 2) basal extender+ ethanol (0.05% v/v). Motility, progressive motility were evaluated by standard methods and recovery rate was calculated using post thaw motility divided by before freezing motility. Data was analyzed using Proc GLM of SAS. Motility percentage and recovery rate were

significantly higher in control than those in the treated group (44% ± 1.58, 58.01% ± 0.02 vs. 37% ± 1.58, 50.76% ± 0.02, respectively) ($P \leq 0.05$) but progressive motility percentage was not affected by treatment (33% ± 2.12 vs. 28% ± 2.12, respectively). The result indicated that ethanol had a toxic effect on sperm characteristics.

Key Words: sperm, ethanol, extender

T279 Natural non-synonymous mutations in the ovine leptin gene affect leptin binding affinity and biological activity. S. Reicher*[1,2], A. Gertler[2], E. Seroussi[1], and E. Gootwine[1], [1]*Institute of Animal Science, ARO, The Volcani Center*, *Bet Dagan, Israel*, [2]*The Robert H. Smith Faculty of Agriculture, Food and Environment, The Hebrew University of Jerusalem*, *Rehovot, Israel*.

The hormone leptin is involved in diverse biological processes, including regulation of feed intake, body-weight homeostasis and energy balance. Polymorphism in the bovine leptin gene has been found to be associated with variations in carcass fat content and average daily gain, as well as in milk yield, milk somatic cell count and several traits governing reproduction. In the current study, we sequenced genomic DNA and cDNA samples of individuals from 5 divergent sheep breeds and revealed synonymous as well as novel non-synonymous mutations at the third exon of the ovine leptin gene *(oLEP)*. In addition, 2 alternatively spliced *(oLEP)* transcripts were found in the abdominal fat tissue. The biochemical and biological significance of these naturally occurring mutations was examined by generating recombinant oLEP muteins which carried the corresponding mutations. Surface plasmon resonance experiments revealed reduced affinity of all oLEP muteins examined, namely: Q28 deletion, N78S, R84Q, P99Q, V123L and R138Q, to chicken leptin-binding domain (chLBD) relative to the wild-type hormone (0.54, 0.38, 0.36, 0.55, 0.69 and 0.60, respectively). In competitive binding assays between biotinylated oLEP and the leptin muteins, N78S and R84Q exhibited the lowest affinity to both chLBD (0.19 and 0.08, respectively) and human LBD (0.18 and 0.41, respectively) as compared with the wild-type hormone. We then tested the muteins' ability to induce proliferation in Baf-3 cells stably transfected with the long form of the human leptin receptor: significant differences in proliferative activity were only found for N78S (1.8-fold higher) and R138Q (4.2-fold lower) relative to wild-type oLEP. It is speculated that under artificial selection in farm animals, reduced affinity of leptin for its receptor may confer a selective advantage.

Key Words: leptin, polymorphism, ovine

T280 Effect of different aspiration pressure on the number and quality of ovine oocyte. A. Abedini*, H. Kohram, and R. Salehi, *Tehran University*.

This study was designed to characterize the effects of different aspiration pressure (20, 70, 110 mmHg) during oocyte collection on the number and quality of ovine oocytes. Ovine ovaries were collected exactly after slaughter and placed them in a 0.9% NaCl aqueous solution containing penicillin-streptomycin. Cumulus-oocyte complex (COCs) were aspirated almost from 300 ovaries by aspiration pump with a 20-g needle. After aspiration per ovary, with same needle was sucked TCM 199 that supplemented with penicillin-streptomycin. The oocytes were observed under microscope. COCs were categorized to 3 groups: A: denature oocytes, B: oocyte with damaged cumulus, C: qualify oocytes (had more than 3 layers with health cumulus layer). The data of oocytes were investigated separately in each group of oocytes with different aspiration pressure. The total numbers of oocytes and grade A, B, C oocytes per group (20, 70, 110 mmHg) were analyzed by ANOVA. Statistical differences showed that in group with 20 mmHg pressure, the number of oocytes was low but the number of grade C oocytes was more than other groups ($P < 0.05$). In 110 pressure treatment, the total number of oocytes was high but the quality was low. The percentage of grade A and B oocytes in 110 treatment was higher than other groups ($P < 0.05$). This results showed that the high pressure treatment destroyed the cumulus layer and decreased the qualify oocytes. In group with 70 pressure treatment the number and quality of oocytes were in average. The difference between the numbers of oocyte in 110 and 70 mmHg pressure was not significant however, the qualify oocyte was higher in 70 pressure treatment ($P < 0.05$). The results demonstrated that vacuum pressure during ovine oocyte aspiration affects the number and quality of oocytes. High pressure increase the number of oocytes harvested however reduced the qualify oocyte, while low pressure decrease the number of oocyte and increase the quality. To sum up, it seems that the average pressure (70 mmHg) could harvest the qualify oocytes with reasonable numbers.

Key Words: aspiration pressure, number and quality, ovine oocyte

T281 The effect of poly-L-lysine as a new cryoprotectant for ovine oocyte vitrification. N. Li*[1], T. Wuliji[1], A. Qi[1], S. H. Hyon[2], K. Matsumura[2], L. Shi[1], and W. Chen[1], [1]*University of Nevada, Reno*, [2]Kyoto University, Kyoto, Japan.

The objective of this study is to evaluate a polyampholyte, poly-L-lysine (PLL), as a new cryoprotectant for ovine oocytes vitrification. The PLL was experimented as an alternative cryoprotective reagents to the traditional dimethyl sulfoxide (DMSO) protocol. Recently, Matsumura et al. (2009) had demonstrated that PLL effectively protecting L929 stem cells during cryopreservation. Oocytes were screened and collected from fresh ovine tissue, then randomly distributed into 2 developmental stages, namely, germinal vesicle (GV) stage oocytes (immature) and metaphase 2 (M2) stage oocytes (mature). GV stage oocytes vitrification was carried out immediately upon collection, while M2 stage oocytes vitrification was made after 24h in vitro culture for oocyte maturation. Each developmental group was subjected to comparison of 2 different vitrification solutions: (1) PLL based formula (5% PLL for 45s, 10% for 25s) (2) DMSO based formula (10% DMSO, ethylene glycol, and holding medium for 45s, 20% for 25s), Therefore, following 4 groups comparison were conducted: Group I GV stage, vitrification solution (VS) (1); Group II M2 stage, VS (1); Group III GV stage VS (2) and Group IV M2 stage, VS (2). There are 5 replicated batches for each group, and each batch was processed on the same day under the same condition. The normality of developing oocytes was examined under microscope. Normal oocytes showed the characteristics of homogeneous cytoplasm and intact zona pellucida, while abnormal oocytes showed low density of granular cells. Under confocal microscope, the spindle and microtubules of normal oocytes are intact and dispersed within plasma uniformly; the abnormal oocytes displayed a reduced amount of microtubules. The group mean were compared by *t*-test procedure. The preliminary results showed that normal oocyte in group II(82.1) are significantly ($P < 0.05$) higher than that of group IV (58.0), the normal oocytes in group IV are significantly ($P < 0.05$) higher than group III (48.1). However, group I (53.6) and II did not differ. Although encouraging, the advantage of using PLL as an alternative cryoprotectant requires future investigation.

Key Words: poly-L-lysine, ovine oocyte, vitrification

T282 Administration of human chorionic gonadotropin (hCG) to embryo transfer (ET) recipients increased ovulation, progesterone,

and transfer pregnancy rates. L. D. Wallace*[1], C. A. Breiner[2], R. M. Breiner[1], and J. S. Stevenson[1], [1]*Kansas State University*, *Manhattan*, [2]*Cross Country Genetics North Inc.*, *Westmoreland, KS*.

We hypothesized that administration of hCG at ET would induce accessory corpora lutea (CL), increase circulating progesterone concentrations, and reduce early embryonic loss. At 2 locations, mature lactating (94%) and nonlactating (6%) purebred and crossbred Angus, Simmental, and Hereford recipients (n = 471) were assigned alternately to receive i.m. 1,000 IU hCG or 1 mL saline (control) at ET. Fresh or frozen-thawed embryos were transferred on d 5.5 to 8.5 (median = d 7) of the estrous cycle to recipients having a palpable CL (CL grade = 1 or 2). Recipients received a BCS of 1 to 9 at ET. Pregnancy diagnoses occurred by transrectal ultrasonography 28 to 39 d (median = d 36) and reconfirmed 58 to 77 d (median = d 74) post-estrus. At one location (n = 108), ovaries were examined to count the number of CL at pregnancy diagnoses. More ($P < 0.001$) pregnant hCG-treated cows (69.0%) had multiple CL than pregnant controls (0%). Serum progesterone (ng/mL) determined at both pregnancy diagnoses in pregnant cows was greater ($P \leq 0.05$) after hCG treatment than in controls (first: 8.1 ± 0.9 vs. 6.1 ± 0.8; second: 8.8 ± 0.9 vs. 6.6 ± 0.7), respectively. Transfer pregnancy rates (PR) were analyzed using logistic regression. Unadjusted PR at the first diagnosis was 62.0 vs. 55.6% for hCG vs. controls. At the second diagnosis, PR was 59.0 vs. 53.0%, respectively. Factors affecting PR were CL grade ($P = 0.12$), number of previous transfers ($P = 0.03$), and BCS ($P = 0.02$). Odds ratios indicated that greater PR occurred in recipients having a CL grade 1 vs. 2 (63.8 vs. 58.2%), fewer previous transfers 1 vs. > 1 (61.3 vs. 43.1%), and when BCS > 5 vs. ≤ 5 (67.1 vs. 54.0%). An interaction ($P = 0.11$) was detected between treatment and BCS in which hCG tended to improve PR in recipients having BCS ≤ 5 than in controls (60 vs. 48%), whereas no treatment effect occurred in recipients having BCS > 5 (65.5 vs. 68.5%), respectively. We concluded that hCG at ET increased incidence of accessory CL, increased progesterone in pregnant recipients, and tended to increase PR in thinner recipients (BCS ≤ 5).

Key Words: embryo transfer, hCG, pregnancy rates

T283 Effect of addition of cAMP regulators to bovine in vitro oocyte maturation medium. C. Burroughs* and G. Seidel, *Colorado State University*.

In vivo, the LH surge before ovulation stimulates resumption of oocyte meiosis, but in vitro, resumption occurs due to removal of the oocyte from inhibition in follicular fluid. The objective of this experiment was to create an in vitro system with greater resemblance to the in vivo situation to produce greater numbers of bovine blastocysts. The adenylate cyclase activator forskolin (100 μ*M*) and the phosphodiesterase inhibitors caffeine (2 μ*M*) and cilostamide (10 μ*M*), were added to maturation media to increase and maintain cAMP levels. Bovine oocytes were aspirated from abattoir-collected ovaries and immediately placed into medium containing forskolin and caffeine. Oocytes were incubated with different combinations of cAMP regulators during maturation as shown in Table 1 for all 6 replicates. All oocytes were moved to new medium at each time point. Half of the oocytes in each treatment were fertilized at 23 h of incubation and half at 28 h. Cleavage rates were recorded at 2.5 d post-fertilization and blastocyst rates at 7 d post-fertilization. Cleavage rates in treatment D were lower than the control (A) and those in C ($P < 0.05$, Table 1), indicating that prolonged exposure to cilostamide was detrimental to fertilization. There was no effect of time on cleavage rate, and no treatments had higher blastocyst rates per oocyte than the control ($P > 0.1$). Under the conditions used, there were no added benefits to blastocyst production from the treatments studied.

Table 1. Effects of cAMP regulators during in vitro maturation of oocytes

Trt	n	0-2h cult	2-6h cult	6-23/28h cult	Time of fert	Cleav %	Blast %
A	168	No add	No add	No add	23h	83.8±5.8	22.0±4.3
B	187	F+C*	No add	No add	23h	73.3±6.5	19.4±5.0
B	188	F+C	No add	No add	28h	75.6±10.2	11.3±3.5
C	181	F+C	Cilostamide	No add	23h	78.7±4.7	19.0±2.1
C	176	F+C	Cilostamide	No add	28h	87.2±2.4	18.0±3.1
D	187	F+C	Cilostamide	Cilostamide	23h	63.9±9.4	13.9±2.4
D	188	F+C	Cilostamide	Cilostamide	28h	62.7±6.1	11.9±2.0

*F+C = Forskolin+Caffeine.

Key Words: oocyte maturation, cAMP, bovine

T284 Testicular abnormalities in *Gallus gallus* var. *domesticus* males. J. R. Moyle*, S. M. Whipple, F. D. Clark, and R. K. Bramwell, *University of Arkansas*, *Fayetteville*.

In conducting research on testicular development on *Gallus gallus* var. *domesticus* males it was noticed that several the males had nodules on their testes. Further histological investigation showed that these nodules were composed of seminiferous tubules that were contained within the tunica albuginea of the testicular capsule. The seminiferous tubules within these nodules contained sperm as well as spermatids at various stages of development; however, no direct outlet of the sperm into the testes was identified or observed. These testicular nodules were found in all primary breeder males that were investigated (n = 8 flocks), with occurrences for individual males ranging from 42% to 93%. The flocks that were investigated consisted of commercial breeder flocks, individually caged males, as well as males used in pen trail. Nodules were also found in a pure line of French Mottled Houdan chickens, as well as a random bred broiler breeder line from the 1980s. These nodules occurred only on the left testes in 92% of males, with 1% only on the right, and 7% had nodules on both testes. The number of visible nodules on the testes ranged from 1 to as many as 18, with the size ranging up to 4.5mm. Using histological preparations these testicular abnormalities were detected in males that were 18 weeks of age, and had not been light stimulated. No conclusion about the affect of testicular nodules on fertility was apparent, as all of the flocks investigated had normal or higher fertility. Therefore, at this time the effects of testicular nodules, if any, are unknown.

Key Words: testes, males, broiler breeders

T285 Effects of hypothermic storage of striped bass (*Morone saxatilis*) sperm on intracellular calcium, reactive oxygen species formation, mitochondrial function, motility, and viability. H. D. Guthrie*[1], L. C. Woods III[2], and G. R. Welch[1], [1]*Animal Biosciences and Biotechnology Laboratory, Agricultural Research Service, USDA*, *Beltsville, MD,* [2]*Department of Animal and Avian Sciences, University of Maryland, College Park*.

Experiments were conducted to determine the effect of hypothermic 24 h storage of striped bass sperm cells on viability, intracellular Ca^{2+}[Ca^{2+}]$_i$, mitochondrial membrane potential ($\Delta\psi_m$), and reactive oxygen species (ROS) formation (oxidation of hydroethidine to ethidium) as determined by flow cytometry; motion activation; and ATP concentration as determined by Luciferin-Luciferase bioluminescence assay. Semen was stored for 1 or 24 h at 4°C in an O_2 atmosphere undiluted (raw); or diluted 1:4 (one volume semen with 3 volumes) with T350 (20 mM

TRIS base-NaCl, 350 mOsm/mL, pH = 8) or with seminal plasma (SP) in the presence of various treatments. Viability (% cells excluding propidium iodide) approached 100% after 1 h storage raw or in T350 and SP. After 1 h of storage Fluo-3 fluorescence (marker for $[Ca^{2+}]_i$) was detected in only 3% of sperm cells in raw and T350 or SP extended semen. In contrast to storage for 1 h, after 24 h the incidence Fluo-3 fluorescence intensity was increased in >50% of the viable cells in raw and in T350 or SP extended semen along with increased cell death; the presence of 1 mM EGTA prevented increased Fluo-3 fluorescence and attenuated cell death. Activation of sperm motility was 82% after 1 h in T350 and decreased to 30% after 24 h. However, activation failed in the presence of EGTA at 1 or 24 h. During storage $\Delta\psi_m$ and ATP did not change significantly between 1 and 24 h; however in the presence of EGTA ATP, but not $\Delta\psi_m$ decreased between 1 and 24 h. While ROS formation was induced by menadione treatment, there was no evidence of storage-induced ROS formation in the absence of menadione. The increased intracellular calcium found after 24 h indicates a storage-induced defect in the maintenance of cellular calcium homeostasis which may be detrimental to sperm activation.

Key Words: flow cytometry, Fluo-3, sperm viability

T286 Renin message is up-regulated in spermatogonia and testes of male mice in response to treatment with aflatoxin B1. K. J. Austin*, K. L. Speiser, A. M. Kaiser, R. R. Cockrum, and K. M. Cammack, *University of Wyoming*, *Laramie*.

Aflatoxin B1 (AFB1) has been shown to affect fertility in male mice and numerous livestock species. However, the exact genetic mechanisms associated with the disruption are not known. The objective of these experiments was to examine the genetic response to AFB1 and determine which male reproductive cell types are affected by treatment with AFB1. In previous experiments, male mice ≥4 wks of age were administered 50 µg/ kg BW AFB1 by IP injection daily for 45 d. Testes were collected and stored at −80°C until analysis. Mice were further characterized as being tolerant or intolerant to the effects of AFB1 based on TUNEL staining and the number of pups sired. An Affymetrix array was used to initially test for gene expression differences between tolerant and intolerant males; follow-up gene expression was assessed using real-time RT-PCR. Differences in gene expression were tested for effect of treatment (tolerant versus intolerant; control versus AFB1 treatment) using the GLM procedures of SAS. Messenger RNA for *Renin* was found to be upregulated ($P = 0.05$) in tolerant mice (n = 3) compared with intolerant mice (n = 3) by both microarray and real-time RT-PCR analyses. Further experiments using real time RT-PCR to analyze testicular RNA showed that *Renin* expression increased ($P = 0.02$) 10-fold in AFB1-treated mice (n = 8) compared with control (placebo) treated mice (n = 8). Spermatogonia treated with 0, 5, 10 or 20 µg/ mL AFB1 (n = 6 per treatment) resulted in a 10-fold upregulation of *Renin* mRNA at the 20 µg/ mL level, while Leydig tumor cells treated similarly showed no difference ($P > 0.05$) in mRNA for *Renin* in treated versus control cell cultures. These results demonstrate a genetic response to AFB1 in the testes and spermatogonia through upregulation of *Renin* and may lead to a better understanding of the mechanisms by which AFB1 disrupts fertility in male mice as well as livestock species.

Key Words: aflatoxin, *Renin*, spermatogonia

T287 Testicular development of breeder males reared on an accelerated growth schedule. W. D. Berry*, S. H. Oates, L. M. Stevenson, and J. B. Hess, *Auburn University Department of Poultry Science*, *Auburn, AL*.

Broiler breeders are reared using feed restriction to control body weight and delay sexual maturation. Earlier maturation of breeder males has not been explored with respect to effects on reproductive development. The objective of this study was to determine how rearing on a relatively accelerated growth schedule affects broiler breeder testicular development. In this study, male breeder chicks reared using a conventional feeding/growth schedule (CON) were compared with males reared on a growth schedule accelerated by 6 weeks (ACCEL). The ACCEL males were grown on a linear growth line designed to reach the CON 22-week body weight at 16 weeks. Male broiler breeder chicks in both treatments were started on a standard starter diet and full fed for 3 weeks. ACCEL male chicks were started 5 weeks after CON. The birds were placed in 3 replicates containing 14 chicks per rep at 4 weeks of age. Both treatments were then fed 15% protein grower diet for the remainder of the rearing period. The birds received 8 h light/day during rearing. The birds were transferred to breeder housing at 22 weeks of age (CON) or 17 weeks of age (ACCEL). Light was increased to 12 h/day to stimulate sexual maturation. Birds in both treatments were then fed to maintain the same body weight until termination of the experiment. Body and testes weights were recorded throughout the experiment. Testes samples were formalin fixed, sectioned, and stained for morphology. Testes areas and cell numbers were obtained from photomicrographs using Image J software. Body weights did not differ at photostimulation. Body weight uniformity was the same for the 2 treatments at photostimulation. However, ACCEL birds tended to be less uniform. Testes weight at initial sexual maturity was higher for ACCEL vs. CON (7.87 ± 0.67 vs. 7.16 ± 0.62). Sertoli cell and interstitial cell numbers as a percent of total cell numbers were not different between the treatments. It was concluded that accelerating sexual maturity by 6 weeks does not adversely affect testicular development of breeder males.

Key Words: breeder, testes, seminiferous

T288 Hypoxic conditions during the CAM development (E5-E12) effect on embryo development. S. Druyan*, *Institute of Animal Science, ARO The Volcani Center*, *PO Box 6, Bet Dagan, Israel*.

Hypoxia is a common situation that vertebrate face during fetal life. It plays an essential role in embryo development, inducing vasculogenesis, angiogenesis, hematopoiesis and chondrogenesis. Hypoxic conditions at different time points during embryonic development were found to affect both anatomical and physiological morphogenesis. The literature is unclear about the actual effect of hypoxic conditions on embryo development. Different levels of hypoxia were found to have conflicting effects on development, depending on time point and duration of exposure. It is still unknown whether chronic, alternating or acute hypoxia will induce some degrees of adaptation to hypoxia as a long lasting effect. Fine-tuning (critical period, level and duration) is required. This study was aimed to elucidate the effect of daily exposure to 17% O_2 for 6 or 12 hours during the chorioallantoic membrane (CAM) development on embryogenesis, angiogenesis and hematopoiesis. Data including hatch time, heart rate, oxygen consumption, embryo weight, hematocrit level and hemoglobin concentration were collected from E13 to hatch. Angiogenesis response was measured in the CAM from E6 to E13 by analyzing the blood vessels coverage area. The hypoxic exposure had a mild insignificant effect on embryo weight and relative yolk weight. However, hypoxic exposure was found to affect vascular area that was significantly higher in the 12h embryos compare to control (e.g. 24.7 mm^2 vs. 23.3 mm^2, measured on E12, $P \leq 0.01$). Oxygen consumption was similar for all 3 treatments although it was slightly lower in the 12h embryos. Heart rate was found to be relatively constant while hematocrit and hemoglobin concentration were affected by hypoxia on

several key developmental days (e.g. 41.6%, 41.9% vs. 38.6% for 6h, 12h and control embryos measured on E16, $P \leq 0.01$). These observations indicate that hypoxic exposure during the CAM development may improved its vascular system. Further exploration of this phenomenon may lead to an alternative management scheme to improve the quality of the neonatal chick, which is associated with superior performance during post hatch.

Key Words: hypoxia, embryogenesis, CAM

T289 Rumen fluid inhibits proliferation and stimulates expression of cyclin-dependent kinase inhibitors 1A and 2A in bovine rumen epithelial cells. A. Wang* and H. Jiang, *Virginia Polytechnic Institute and State University*, *Blacksburg*.

It has been known for decades that microbial fermentation within the rumen is critical to rumen development and maturation in young ruminants, but the underlying mechanism is largely unknown. In this study, we determined the effect of rumen fluid, which should contain all products from rumen fermentation, on growth of rumen epithelial cells in vitro. Rumen epithelial cells were isolated from newborn Holstein calves using the serial tryptic digestion procedure and were cultured in minimum essential medium supplemented with 10% fetal bovine medium. After 3 d of initial culturing, the cells were treated with 1% or 10% (v/v) rumen fluid from lactating Holstein cows or phosphate buffered saline (PBS). Addition of 10% rumen fluid to the culture medium for 72 h decreased the cell number by 36% ($P < 0.05$, n = 4), while that of 1% rumen fluid had no effect compared with addition of PBS. As revealed by DNA fragmentation analyses, 10% rumen fluid did not induce apoptosis in the cultured rumen epithelial cells (n = 4). Flow cytometric assays showed that 10% rumen fluid inhibited the transition of rumen epithelial cells from the G1 phase to the S phase during the cell cycle ($P < 0.05$, n = 3). Real-time RT-PCR analyses of mRNA for key cell cycle regulators indicated that 10% rumen fluid did not change the expression of cyclin D1, D2, D3, E1, or E2 mRNA or that of cyclin-dependent kinase inhibitor 1B or 2B mRNA ($P > 0.1$, n = 3), but caused nearly 3-fold increase in the expression of cyclin-dependent kinase inhibitors 1A and 2A mRNA in rumen epithelial cells ($P < 0.05$, n = 3). These mRNA data support the possibility that rumen fluid inhibits proliferation of rumen epithelial cells in vitro by increasing the expression of cyclin-dependent kinase inhibitors 1A and 2A. The result that rumen fluid inhibits proliferation of rumen epithelial cells in vitro suggests that the stimulatory effect of rumen fermentation on rumen development in vivo is mediated by indirect mechanisms.

Key Words: cattle, rumen fluid, rumen epithelial cells

T290 Short-term postpartum supplementation on hepatic gene expression in primiparous spring-calved beef cows on grazing conditions. I. Whole rice middlings. A. L. Astessiano*, C. López-Mazz, A. C. Espasandín, P. Soca, R. Pérez-Clariget, and M. Carriquiry, *School of Agronomy, UdelaR*, *Uruguay*.

The aim of this work was to evaluate the effects of short-term supplementation of beef cows on blood glucose and insulin concentrations and hepatic gene expression. The experiment was carried at the Experimental Station Bernardo Rosengurtt (Cerro Largo, 32°35′S, 54°15′W). Primiparous suckled crossbred cows (Hereford/Angus), blocked by calving date and body condition score (BCS) at calving, were at 64 ± 14 d postpartum, randomly assigned to 2 treatments: control (grazing of native pastures, 20 kg DM/animal/d; 8.5% CP, 63%NDF; n = 8; CON) and supplementation (2 kg DM/animal/d of whole rice middlings, 10%CP, 14%NDF, 9%EE; n = 8; SUP) for a 21 d. Glucose and insulin concentrations were measured at −2, 7, and 22 d of initiation of the nutritional treatment. Liver biopsies were collected at the end of the nutrition treatment (d 21). The amount of mRNA for growth hormone receptor (GHR), insulin-like growth factor-I (IGFI), IGF binding proteins-2 (BP2),-3 (BP3), insulin receptor (IR) and hypoxanthine-phosphoribosyltransferase (HPRT, endogenous control) were measured by SYBR Green real time RT-PCR. Means from mixed analyses were considered to differ when $P < 0.05$. Cow body weight and BCS did not differ between treatments. Insulin and glucose concentrations were not affected by nutritional treatment, but there was a trend ($P = 0.08$) for interaction between treatment and sampling day in glucose concentrations as glucose tended to increase from d 7 to 22 only in SUP cows. Expression of HPRT was similar between treatments. There were no differences in hepatic GHR, IGFI, and BP3 mRNA due to nutritional treatment. However, BP2 mRNA and BP2/BP3 mRNA ratio tended ($P < 0.10$) to be less in SUP than CON cows. The GHR mRNA was positively correlated with IGFI (r = 0.62, $P = 0.01$) and BP3 (r = 0.51; $P = 0.05$). Results could indicate that short-term postpartum supplementation with rice middlings could improve metabolic status of spring-calved cows at the initiation of the breeding period.

Key Words: liver, mRNA, somatotropic axis

T291 Short-term postpartum supplementation on hepatic gene expression in primiparous spring-calved beef cows on grazing conditions. 2. *Lotus subbliflorus* cv. Rincon. A. L. Astessiano*[1], R. Perez-Clariget[1], G. Quintans[2], P. Soca[1], and M. Carriquiry[1], [1]*School of Agronomy, UdelaR*, *Uruguay*, [2]*Instituto Nacional de Investigación Agropecuaria*, *Treinta y Tres, Uruguay*.

Primiparous suckled crossbred cows (Hereford/Angus) were used in a randomized block design to evaluate the effect of short-term supplementation on blood glucose and insulin concentrations and hepatic gene expression. The experiment was carried in INIA Treinta y Tres (Uruguay, 33°15′S, 54°28′W). Cows, blocked by calving date and body condition score (BCS) at calving, were at 48 ± 10 d postpartum, randomly assigned to 2 treatments: control (grazing of native pastures, 57 kg DM/ha/d, 12.8%CP, 55.9%NDF; n = 30; CON) and supplementation (123.8 kg DM/ha/d of grazing native pastures improved with *Lotus subbiflorous* cv. Rincon, 13.2%CP, 52.9%NDF; n = 30; SUP) for 23 d. Glucose and insulin concentrations were measured at −2, 12, and 26 d of initiation of the supplementation. Liver biopsies were collected at the end of the nutrition treatment (d 23). The amount of mRNA of growth hormone receptor (GHR), insulin-like growth factor I (IGFI), IGF binding proteins-2 (BP2),-3 (BP3), insulin receptor (IR) and hypoxanthine phosphoribosyltransferase (HPRT, endogenous control) were measured by SYBR Green real time RT-PCR. Means from mixed analyses were considered to differ when $P < 0.05$. Cow body weight (BW) and BCS were increased ($P < 0.05$) in SUP cows after 7 or 21 d of initiated the nutritional treatment, respectively. Calf BW increased at d 21 for SUP cows. Glucose concentrations along the period evaluated did not differ between treatments but insulin concentrations were greater ($P < 0.01$) in CON cows. Expression of HPRT mRNA was similar between treatments. Although GHR, IGFI, and BP2 mRNA were not affected by nutritional treatment, abundance of BP3 mRNA was greater ($P = 0.04$) and IR mRNA tended ($P = 0.07$) to be greater for CON than SUP cows. Short-term supplementation with improved pastures of suckled cows during the early postpartum did not improve hepatic expression of somatotropic axis genes.

Key Words: liver, mRNA, somatotropic axis

T292 Effects of glucose on suckling aggressiveness in newborn Holstein and Brown Swiss calves. M. D. DenBeste* and H. D. Tyler, *Iowa State University*, *Ames*.

To determine potential associations between suckling aggressiveness and glucose concentrations in newborn Brown Swiss (B) and Holstein (H)

calves, glucose concentrations were altered via intramuscular injection of insulin (1 mL) or an oral dose of glucose (25 mg) to 19 calves within 5.35 ± 2.72 min after umbilical cord rupture. Calves born from 19 H cows and heifers (9 carrying B embryos) were assigned to treatment randomly by alternating treatments based on birth order within breed. Initial blood samples were collected from calves within 3.25 ± 1.52 min and glucose and insulin treatments were administered within 5.35 ± 2.72 min after umbilical cord rupture. A second blood sample was obtained 57.85 ± 3.17 min after treatments were administered. Samples were analyzed to determine glucose, non-esterified fatty acids (NEFA), leptin, ghrelin, and glutamate (GLU) concentrations. Glucose, NEFA, leptin, ghrelin, and GLU were analyzed using the General Linear Model procedures of SAS. Calves were fed 2 quarts of colostrum replacer and suckling aggressiveness scores were given 1 – weakly, 2 – moderately, and 3 – aggressively. The FREQ procedure (CHISQ option) was used to determine the frequency of suckling aggressiveness scores within each breed. B calves suckled weakly ($P < 0.05$) when compared with H calves. NEFA, leptin, and ghrelin concentrations did not differ significantly ($P > 0.05$) between breeds, treatments, or suckling aggressiveness scores either at birth or post-treatment. Glucose concentrations only differed significantly ($P < 0.05$) between treatments post-treatment. Prior to treatment, B calves had lower concentrations of GLU ($P < 0.05$) than H calves and calves that subsequently suckled weakly had higher concentrations of GLU ($P < 0.10$) than calves that subsequently suckled more aggressively. Breed differences were still apparent in post-treatment samples. In conclusion, B calves suckled weakly when compared with H calves and altering glucose concentrations at birth had no effect on suckling aggressiveness. However, calves that suckled weakly had higher concentrations of GLU than calves that suckled aggressively.

Key Words: glucose, suckling aggressiveness, newborn calves

T293 Butyrate stimulates the cAMP/protein kinase A signaling pathway. A. Wang*, H. Si, D. Liu, and H. Jiang, *Virginia Polytechnic Institute and State University*, *Blacksburg*.

Butyrate is one of the major short chain fatty acids formed by microbial fermentation in the gastrointestinal tract. Butyrate is known as not only an important source of energy for ruminants, but also a signaling molecule, as it stimulates rumen development and inhibits growth of various types of cells in vitro. However, the signaling pathway induced by butyrate in cells is unknown. Here, we report that butyrate can activate the cAMP/protein kinase A (PKA) signaling pathway in the human epithelial colorectal adenocarcinoma cell line Caco-2 cells. The Caco-2 cells were cultured in minimum essential medium supplemented with 20% fetal bovine serum and were treated with 0.01, 0.1, 1, or 10 m*M* of butyrate or phosphate buffered saline (PBS) as a control for 30 min (for cAMP, ATP, protein phosphorylation, and PKA, phosphodiesterase, and adenylate cyclase activity assays) or 16 h (for luciferase assay). All experiments were repeated 3 or 4 times. Compared with PBS, 0.1 m*M* or higher concentrations of butyrate increased intracellular cAMP accumulation ($P < 0.05$, n = 4) and PKA activity ($P < 0.01$, n = 3). The same concentrations of butyrate also induced phosphorylation of the cAMP response element (CRE)-binding protein (CREB) ($P < 0.05$, n = 3) without changing its expression, and increased CRE-driven luciferase reporter gene expression ($P < 0.01$, n = 4). Moreover, butyrate at 0.1 m*M* or higher concentrations increased intracellular ATP levels ($P < 0.05$, n = 4), whereas it had no effect on the activity of phosphodiesterase or that of adenylate cyclase. Taken together, these data indicate that butyrate stimulates the cAMP/PKA signaling pathway in Caco-2 cells and that this stimulation may be due to increased ATP accumulation. This result suggests the possibility that butyrate affects rumen development or cell growth through the cAMP/PKA signaling pathway.

Key Words: butyrate, cAMP, protein kinase A

T294 The effect of forage availability on the somatotropic axis in free-ranging alaskan moose (*Alces alces*). A. A. Parillo*[1], J. P. Richmond[1], K. S. White[2], J. Crouse[3], B. W. Dale[4], and S. A. Zinn[1], [1]*University of Connecticut*, *Storrs*, [2]*Alaska Department of Fish and Game*, *Juneau*, [3]*Alaska Department of Fish and Game*, *Soldotna*, [4]*Alaska Department of Fish and Game*, *Palmer*.

To determine if components of the somatotropic axis reflect the availability of forage or nutritional status in adult moose (*Alces alces*), 3 distinct Alaskan populations of free-ranging moose [Gustavus (n = 42), Skwentna (n = 24), and Nelchina (n = 11)] were used. Forage availability, low (Gustavus), medium (med; Nelchina) or high (Skwentna) varied with population. Moose from each population were captured once in fall (October–November; high forage availability) and once the following winter (March; low forage availability). At capture, blood samples were collected via venipuncture to determine if forage availability influenced the somatotropic axis, and rump fat was measured to assess body condition. Concentrations of GH and IGF-1 were quantified by RIA using bovine and human antisera, respectively. Western ligand blots were used to quantify IGFBP-2 and −3. Rump fat was greater in fall than winter (2.4 ± 0.26 vs. 1.1 ± 0.24 cm; $P \leq 0.01$), but was similar across the 3 populations [1.68 ± 0.16 (low), 1.57 ± 0.27 (med) and 2.1 ± 0.18 (high) cm; $P \geq 0.17$]. Concentrations of GH averaged 3.4 ± 1.2 ng/mL and were not different between populations ($P \geq 0.15$) or season ($P \geq 0.12$). Average IGF-1 concentrations were greater ($P \leq 0.03$) in high than low (135.4 ± 17.6 vs 89.8 ± 17.1 ng/mL) forage availability and greater ($P \leq 0.01$) in fall [117 ± 20.01 (low), 138 ± 25.1 (med), and 220 ± 16.4 (high) ng/mL] than in winter [62.5 ± 14.2 (low), 42.2 ± 30.6 (med), and 50.6 ± 18.7 (high) ng/mL]. Conversely, IGFBP-3 was greater ($P \leq 0.01$) in low compared with high (72.1 ± 6.0 vs 43.4 ± 7.4 AU) forage availability, and greater ($P \leq 0.01$) in fall compared with winter (69.2 ± 4.4 vs 34.4 ± 4.6 AU). Similarly, IGFBP-2 was greater ($P \leq 0.01$) in low than high (47.1 ± 3.1 vs 24.4 ± 4.0 AU) forage availability, and was greater ($P \leq 0.01$) in winter than fall (36.9 ± 2.5 vs 32.0 ± 2.9 AU). Serum IGF-1 concentrations increased, whereas IGFBP-2 and IGFBP-3 decreased with greater forage availability. These components of the somatotropic axis may be useful indicators of nutritional status in free-ranging populations of Alaskan moose.

Key Words: somatotropic axis, moose (*Alces alces*), forage availability

T295 Effects of dietary probiotic supplementation and posthatching holding time on intestinal pH and microflora of male broilers. H. Unsal[1], A. G. Onol[1], M. Daskiran[2], O. Cengiz*[1], O. Tatli[1], and O. Sevim[1], [1]*Adnan Menderes University*, *Aydin, Turkey*, [2]*Johnson & Johnson Corporate Science and Technology*, *New Brunswick, NJ*.

A study was conducted to determine the effects of a dietary probiotic, a commonly used feed additive, and posthatching holding time (0, 12, 24, and 36 h post-hatching) on the intestinal pH and microflora of male broiler chicks. A 2 × 4 factorial design was implemented. Eight experimental groups were formed by two levels of dietary probiotic supplementation (Control and Protexin, 0.5 kg/ton) and four levels of posthatching holding time. Four posthatching holding times were 0 (chicks were given feed and water immediately after their arrival), 12, 24, and 36 hours. There were 4 replications for each treatment group and each replication consisted of 20 day-old birds. Chicks were received

from a commercial hatchery and transferred to the Experimental station within 2 hours after feather-sexing procedure. A corn-soybean meal based diet was used in the study. Water and feed were available for ad libitum consumption throughout the study and the experiment lasted 42 days. A significant decrease in day-10 intestinal pH ($P < 0.05$) was noted in groups with dietary probiotic supplementation (6.59 vs. 6.42). Dietary probiotic supplementation also numerically increased the number of colony forming units of lactobacilli at days 10 (7.35 vs. 7.60 cfu) and 21 (6.74 vs. 7.05 cfu) of the study. The number of colony forming units (cfu) of lactobacilli in groups with no feed and water restriction were either numerically or significantly (12 and 36 hour feed and water restriction treatments) higher (7.96 vs. 7.13, 7.28 cfu) than that of the groups with posthatching holding time prior to feeding ($P < 0.01$). Total bacteria count was similar among treatment groups during the experiment. In brief, this study indicated that early exposure to lactobacilli, which is found in either a dietary probiotic supplement or in feed naturally helps broiler chicks to develop a healthier gastrointestinal tract environment and microflora and this microflora may, in turn, inhibit pathogenic microorganisms in broiler gastrointestinal tract.

Key Words: broiler, post-hatching holding time, probiotic

T296 Maintenance energy requirements of gestating beef cows, rumen temperature, and plasma concentration of thyroxine and triiodothyronine. T. A. Pye*, B. H. Boehmer, and R. P. Wettemann, *Oklahoma Agricultural Experiment Station*, *Stillwater*.

Spring calving, Angus cows, (n = 32) were used to determine the effects of maintenance energy requirement (MR) on rumen temperature (RuT), and concentrations of thyroxine (T4) and triiodothyronine (T3) in plasma. Cows (4 to 7 yr of age) with an initial BCS of 4.4 ± 0.1 and BW of 556 ± 5.9 kg were individually fed a complete ration for 17 wk during 4–8 mo of gestation. After 2 wk on a diet calculated to supply MR (Model 1, NRC 1996) the diet was adjusted weekly until constant BW was achieved (regression analyses). BW was maintained for 31 d for 25 cows and the amount of feed consumed was actual MR. Blood samples were collected before and after consumption of feed on 2 d when cows consumed MR. Rumen temperature was recorded hourly, using rumen boluses (Smart Stock, LLC), for 4 consecutive days when cows consumed the MR diet and when cows consumed ad libitum roughage. Cows were classified based on MR as low (>0.5 SD less than mean, LMR), mod (±0.5 SD of the mean, MMR) and high (>0.5 SD greater than mean, HMR). Average MR was 84.04 (SD = 7.13) $Kcal \bullet kg^{-0.75} \bullet day^{-1}$. The difference in MR between the least efficient and the most efficient cow was 32%. Rumen temperature during maintenance and during ad libitum roughage was not influenced by MR. When cows were exposed to warmer temperatures (15°C) plasma T4 was not influenced by MR ($P = 0.92$). When exposed to cooler temperatures (−5°C), LMR cows had greater plasma T4 ($P = 0.003$) compared with HMR. Plasma T3 was not influenced by MR when cows were exposed cooler ambient temperatures ($P = 0.64$). When exposed to warmer temperatures, compared with LMR, HMR cows had greater plasma T3 ($P = 0.007$). During late gestation MR were associated with plasma concentrations of T3 and T4, but RuT was not influenced by MR. Thyroid hormone may be involved in the regulation of MR of beef cows during late gestation. Identification of cows with lower MR and greater efficiency could improve the profitability of beef production.

Key Words: beef cows, maintenance, thyroxine

T297 Effects of cobalt supplementation and vitamin B_{12} injections on energy metabolism of dairy cows. M. S. Akins*[1], S. J. Bertics[1], M. T. Socha[2], and R. D. Shaver[1], [1]*University of Wisconsin*, *Madison*, [2]*Zinpro Corporation*, *Eden Prairie, MN*.

The objective of this study was to determine metabolic responses of primi- and multiparous dairy cows fed different levels and sources (inorganic and organic) of cobalt or given weekly vitamin B_{12} injections. Forty-five primi- and multiparous cows 60 d prepartum were blocked by parity (1 or > 1) and expected calving date, and then randomly assigned to 1 of 5 treatments in a randomized complete block design. The treatments were: no supplemental Co (Control), 25 mg Co from Co carbonate (CoCarb), 25 mg (LcoGH) or 75 mg (HCoGH) Co from Co glucoheptonate, and Control with weekly 10 mg vitamin B_{12} injections. Cows were on trial until 150 DIM. Cobalt (ppm DM) in the lactating diet was 1.0, 1.9, 2.3, and 5.2 for Control and IB12, CoCarb, LCoGH, and HCoGH, respectively. Far-off, close-up, and lactating diets were 13.8, 15.1, and 18.0% CP and 48.8, 40.2, and 32.9% NDF (DM basis), respectively. Intake was not affected ($P > 0.10$) by treatment and was 19.4 ± 0.5 and 23.1 ± 0.8 kg DM/d for primi- and multiparous cows, respectively. Body weight and condition score and calculated energy balance were not affected by treatment ($P > 0.10$). Plasma glucose, non-esterified fatty acids, and β-hydroxybutyrate were not affected by treatment ($P > 0.10$). Effect of sampling day was significant ($P < 0.001$). Glucose decreased from 60 d prepartum (65 ± 1.1 mg/dL) to 30 DIM (55 ± 1.0 mg/dL), and increased at 90 DIM (60 ± 1.0 mg/dL); however, primiparous cows had a larger decrease at 30 DIM and smaller increase thereafter. Non-esterified fatty acids increased from 60 d prepartum (249 ± 39.8 mmol/L) to 1 DIM (724 ± 40.7 mmol/L), then decreased at 30 DIM (398 ± 40.1 mmol/L), with multiparous cows having a larger increase at 1 DIM. Beta-hydroxybutyrate increased from 60 d prepartum (4.2 ± 0.95 mg/dL) to 30 DIM (15.9 ± 0.95 mg/dL). Addition of Co above requirements or vitamin B_{12} supplementation did not improve energy metabolism of dairy cows.

Key Words: cobalt, vitamin B_{12}, dairy cow

T298 The relationship of tissue copper concentrations and genes involved in copper homeostasis in the cow, pig, and goat. H. So, E. Domby*, T. Engle, and H. Han, *Colorado State University*, *Fort Collins*.

Copper (Cu) serves as a cofactor for enzymes involved in a variety of biological functions. Copper transport/distribution within the cell is mediated by the expression of the copper transporter (CTR1), ATPase7A (ATP7A), ATPase7B (ATP7B) which helps Cu trafficking. Copper is also required for activity of lysyl oxidase like 1 (LOXL1) for the production of elastin and collagen in arterial tissue. Liver and pulmonary artery tissues tissue from 5 Angus crossbred steers, 6 Nubian goats, and 6 American Landrace pigs were collected. Liver and pulmonary artery samples were collected at the time of harvest and snap frozen. Liver and pulmonary artery Cu concentrations were determined via flame atomic absorption and gene expression was measured by real time PCR. Data were analyzed using PROC CORR of SAS. Liver Cu concentrations (ppm ± SE) were higher in cows (396.4 ± 109.1) and goats (181.4 ± 37.0) than in pigs (19.2 ± 3.5). All liver Cu concentrations were within normal ranges and considered adequate for each species. Liver Cu concentration was more variable in cows and goats compared with pig liver Cu concentrations. Real Time PCR revealed that goat liver *ATP7A* was positively correlated ($r^2 = 0.920$; $P < 0.003$) to liver Cu concentrations while cow and pig *ATP7A* was not correlated to liver Cu concentration. In the pig, liver *ATP7A* expression was positively correlated to *ATP7B* ($r^2 = 0.662$; $P < 0.049$). Pulmonary artery Cu concentration was highest in cows (14.9 ± 4.7), intermediate in pigs (8.9 ± 3.3), and lowest in goats (3.9 ± 1.1). Goat pulmonary artery Cu concentration was not correlated

to *CTR1* expression, however, *ATP7A* expression was positively correlated with *CTR1* ($r^2 = 0.897$; $P < 0.004$). In cow pulmonary artery, *LOXL1* expression was positively correlated to elastin expression ($r^2 = 0.912$; $P < 0.012$). Pulmonary artery Cu concentration was not correlated to gene expression of Cu homeostatic genes in the pig. This data indicates that genes involved in Cu homeostasis (*CTR1*, *ATP7A*, *ATP7B*, *LOXL1* and *elastin*) are differently regulated in different species. This may contribute to different responses to elevated pulmonary arterial pressure in different species.

Key Words: copper, liver, pulmonary artery

T299 Modification and validation of a bovine TNFα enzyme-linked immunosorbent assay with improved sensitivity. J. K. Farney*, L. K. Mamedova, and B. J. Bradford, *Kansas State University*, *Manhattan*.

Tumor necrosis factor α (TNFα) is an inflammatory cytokine that is involved in immune function and is proposed to play a role in metabolic disorders. Until recently, no bovine-specific antibodies were available for detection of TNFα. While some bovine-specific methods have been published recently, assays used for determining plasma TNFα concentration in bovine disease models often do not offer acceptable precision for measurement of basal concentrations in healthy animals. The objective of this work was to develop an effective, low-cost enzyme-linked immunosorbent assay (ELISA) procedure with improved sensitivity. A protocol developed for use with cell culture supernatant was modified for use with bovine plasma by optimizing antibody concentrations, incubation times and temperatures, and standard diluents. The coating antibody concentration was decreased from 10 μg/mL to 6.8 μg/mL, while the detection antibody concentration remained 2.5 μg/mL. Sample incubation was increased from 1 h at room temperature to an overnight incubation at 4°C, which increased the sensitivity of the assay. Multiple matrices were tested for dilution of standards and were assessed by determining recovery of bovine TNFα spiked into bovine serum and plasma. Standard curve matrices were fetal bovine serum (FBS), dialyzed FBS, lyophilized human serum (rehydrated), and phosphate-buffered saline (PBS) with 4% bovine serum albumin. Recoveries were < 50% when quantified with standards diluted in PBS, FBS, or dialyzed FBS. However, recoveries were acceptable in both bovine serum and plasma (85–120%) when quantified with standards diluted in lyophilized human serum. The modified bovine TNFα ELISA offers a detection range of 2 to 500 pg/mL. This detection limit is at least an order of magnitude lower than previously reported, and will allow for greater precision in determining basal TNFα concentrations in bovine plasma. The improved sensitivity of this ELISA will be critical to assessing current hypotheses concerning the metabolic effects of moderately elevated TNFα concentrations.

Key Words: Tumor necrosis factor alpha, bovine, ELISA

T300 Plasma cortisol, corticosteroid-binding globulin and free cortisol index in pre-and post-weaned pigs supplemented with omega-3 polyunsaturated fatty acid. H. G. Kattesh*, C. J. Kojima, M. P. Roberts, and G. M. Pighetti, *University of Tennessee*, *Knoxville*.

A dietary supplement of omega-3 polyunsaturated fatty acid (PUFA) has been shown to decrease corticosteroid-binding globulin (CBG) response to an LPS challenge in the post-weaned pig, suggesting a reduction in immune system activation and less of a need for the biologically active free form of cortisol. The aim of this study was to examine the effects of PUFA supplementation to lactating sows and their offspring on growth and indicators of stress in the pre- and post-weaned pig. Upon farrowing (d 0), sows received either a standard lactation diet (SC; n = 4) or SC supplemented (1.0% by weight) with a commercial PUFA source (SP) throughout lactation. At 11–14 d of age, pigs within sow-diet treatment group were creep-fed a diet similarly supplemented with or without PUFA. Pigs (n = 6/litter) were weaned at 21–24 d of age into 8 pens in a replicated 2 × 2 factorial design and fed a nursery diet with (PP; 12 SC and 12 SP) or without (PC) PUFA. Pigs were weighed (BW) and bled on d 14, 21 (before weaning), 22 and 28, for determination of plasma cortisol (CORT) and CBG concentrations, free cortisol index (FCI), and neutrophil: lymphocyte ratio (N:L). Pre- and post-weaning BW was not different ($P > 0.10$) among pigs regardless of treatment. On d 21, SP pigs exhibited a lower ($P < 0.01$) CORT (54.8 ± 7.2 vs. 90.0 ± 9.0 nmol/L) and higher ($P < 0.05$) CBG (9.1 ± 0.7 vs. 7.0 ± 0.5 mg/L) compared with SC pigs. The resultant FCI (nmol cortisol/mg CBG) was lower ($P < 0.001$) for the SP pigs. On d 22, CORT, CBG and N:L increased ($P < 0.001$) but returned to pre-weaning levels by d 28. No significant differences were found among the post-weaned treatment groups for any of the stress indicators measured. The results suggest that PUFA supplementation can reduce the amount of circulating free cortisol in the pig before weaning; however, this benefit is negated due to the stress of weaning.

Key Words: pig, PUFA, stress

T301 Characterization of omega-3 PUFA enrichment in laying hens. S. Nain* and R. A. Renema, *University of Alberta*, *Edmonton, AB, Canada*.

This study explored the effects of feeding linolenic acid and the time required to reach a plateau of omega-3 polyunsaturated fatty acid (ω-3 PUFA) concentration in blood plasma and egg yolk in laying hens fed Linpro, an extruded flax product. Additionally, the efficiency of long chain ω-3 fatty acid enzymatic conversion was also investigated. A group of 75, 65 week old Lohman White Leghorn layers divided into 3 groups (25/group) and subjected to either of one diet, Control diet, or low (Moderate) or high omega-3 diet (High) for 18 d. Diets had similar ME and CP concentrations, and contained 0, 7.5% or 15% Linpro, respectively. Baseline values were established for the BW, fatty acid composition in egg yolk and blood plasma before dietary treatment. Data was analyzed with Proc Mixed of SAS and broken stick analysis to determine ω-3 PUFA plateau using the NLIN procedure of SAS. Significance was assessed at the $P < 0.05$ level. The BW of the hens fed Moderate and High diets was reduced compared with Control birds during the study ($P = 0.003$). Dietary treatments did not affect egg production, egg weight, feed intake, or feed conversion. Total ω-3 PUFA in egg yolk achieved plateau of stationary phase at 343.7 mg/egg and 272.0 mg/egg in 6.6 and 5.9 d with High and Moderate diets respectively. In plasma the ω-3 PUFA concentration reached saturation in 7.2 d with 0.93 mg/ml and 0.67 mg/ ml with High and Moderate diets, respectively. Dietary LNA increased yolk LNA and led to increased long-chain ω-3 PUFA while reducing ω-6 PUFA in yolk and blood plasma. Moreover, Moderate and High diets resulted in 64% and 70% increases in yolk DHA, respectively, while in plasma the increase in DHA was only 13% and 8% in these groups, respectively. The calculated desaturase and elongase enzymatic activities for ω-6 PUFA (C20:4/C18:2) were negatively correlated with LNA ($r = -0.59$). Broken stick analysis indicated that High birds reached the target threshold of 300 mg of total ω-3 PUFA/egg in 5d. Individual hen effects on ω-3 PUFA absorption in this project suggest further work to optimizing egg enrichment through dietary strategies would be beneficial for the field of egg enrichment.

Key Words: LinPRO, egg yolk, plasma

T302 Effects of increased milking frequency on productivity of Holstein dairy cows. M. Dehghan-Banadaky*, M. Eslamizad, K. Rezayazdi, M. Moradi-Shahrbabak, and H. Bahrami, *Department of Animal Science, Campus of Agriculture and Natural Resources, University of Tehran*, *Karaj, Tehran, Iran*.

An experiment was conducted to determine the effects of different milking frequencies on the performance of Holstein cows. 105 multiparous and 15 primiparous Holsteins cows were assigned based on parity at calving to 1 of 3 treatments as follows: 1) milking 6 times per day in whole period (6x) ; 2) milking 6 times per day for 90 d and switching to 3 times subsequently (6x-3x); and 3) 3 times milking per day in whole period (3x). Milk production recorded every day for the first 60 DIM and on 2 consecutive days a week afterward. Cows were weighed after parturition and then weighed and scored for their body condition monthly; milk samples were taken monthly. Data until 150 DIM were statistically analyzed using the repeated measures option in Proc Mixed of SAS with cow as a random effect. Overall milk and fat corrected milk (FCM 3.5%) yield were higher on 6x and 6x-3x cows than 3x cows (41.03, 42.3; 40.11, 40.60 VS 37.97, 38.40 kg/d, respectively). Milk component concentration was not affected by treatment except solids non fat (SNF) that increased in 6x and 6x-3x group ($P < 0.05$). DMI was not different between treatment groups (23.04 and 23.12 vs. 22.45 kg/d for 6x, 6x-3x, and 3x cows respectively). 3x cows began to gain weight sooner than did 6x and 6x-3x cows but there were no significant differences between treatments for body weight change at the end of 150 DIM. These results indicate that increasing milking frequency to 6x, increased milk yield during early lactation, but did not have carryover effect after switching to 3x in 90 DIM. Relative to production and economical aspects, 6x until 90 DIM and then switching to 3x subsequently was preferred to other treatments.

Key Words: milking frequency, milk production, Holstein cows

T303 Effects of increasing milking frequency on blood metabolites of Holstein cows. M. Eslamizad, K. Rezayazdi, M. Dehghan-Banadaky*, H. Kohram, and R. Heydari, *Department of Animal Science, Campus of Agriculture and Natural Resources, University of Tehran*, *Karaj, Tehran, Iran*.

One hundred five multiparous and 15 primiparous Holsteins cows were assigned based on parity into 3 treatment groups immediately after calving. Treatments were: 1) milking 6 times per day in whole period (6x) ; 2) milking 6 times per day for 90 d and switching to 3 times subsequently (6x-3x); and 3) 3 times milking per day in the entire period (3x). Blood samples were taken from each cow at 15, 30, 60, 90, 120, 150 DIM, 3 h after morning meal for metabolic profiling. Data until 150 DIM were statistically analyzed using the repeated measures option in Proc Mixed of SAS with cow as a random effect. Blood glucose concentration was higher but blood nonesterified fatty acids (NEFA) and β-hydroxybutyric acid (BHBA) concentration were lower in 3x than 6x and 6x-3x cows ($P < 0.05$). Most of the differences were observed 30 initial days of the experimental period, indicating more severe negative energy balance in 6x and 6x-3x than 3x cows in fresh period. Phosphorous, blood urea nitrogen (BUN), triglycerides (TG), total protein, aspartate aminotransferase (AST) concentration were unaffected by treatments (Table 1). Overall, results suggest that metabolic health may be suppressed by increasing milking frequency in fresh cows. In respect to metabolic health aspects, 3x was preferred to other treatments.

Table1. Metabolic profiles of cows had different milking frequency

	Treatments				
Metabolites	6x	6x-3x	3x	SEM	P-value
Glucose (mg/dL)	64.36 a	63.44 a	69.02 b	1.910	0.02
NEFA (mmol/L)	0.44 a	0.38 ab	0.33 b	0.044	0.015
BHBA (mmol/L)	0.94 a	0.91 a	0.69 b	0.095	0.006
AST(unite/L)	71.14	63.07	64.61	3.830	0.14
TG (mg/dL)	12.46	12.45	13.77	1.831	0.48
Total protein (g/dL)	8.98	9.19	8.83	0.270	0.23
Phosphorous (mg/dL)	6.88	6.66	6.74	0.201	0.60
BUN (mg/dL)	21.27	21.84	21.13	1.150	0.64

a,b LSM within a row not sharing a common superscript differ ($P < 0.05$).

Key Words: milking frequency, Holstein cows, blood metabolites

T304 Effect of temperature-humidity index on test day milk yield of Iranian primiparous Holsteins. H. Farhangfar*[1], A. Arab[1], S. R. Miraee Ashtiani[2], A. Riasi[3], H. Rashid[4], and M. K. Akbari[4], [1]*Birjand University*, *Birjand, Iran*, [2]*Karaj University of Agriculture and Natural Resources*, *Karaj, Iran*, [3]*Esfahan Industrial University*, *Esfahan, Iran*, [4]*Agricultural Jihad Organisation*, *Mashhad, Iran*.

This research aimed to investigate the potential effect of temperature-humidity index (THI) on test day milk yield of Iranian Holsteins. The data were 95,510 moly test day milk records collected from 11,054 first parity Holstein cows calved from 1994 to 2008 in 76 herds of Mashhad, Iran. Milk records were augmented with climate information gathered by local climate stations. The climatic information was daily temperature (maximum, minimum and average) and relative humidity percentage over 2 decades data recording. THI was calculated based upon the formula which was pointed out by Aguilar et al. (J. Dairy Sci. 2009, 92:5702–5711). Response variable was monthly test day milk records for which there was an average 26.92 Kg (SD = 6.91 Kg) in the whole data set. A statistical linear model was used to evaluate the effects of some environmental factors. In the test day model, fixed effects of herd, year and month of milk recording, milking times, along with covariables of Holstein genes (linear), age at test day recording (linear and quadratic), days in milk (linear and quadratic) and THI (linear) were included. The model was fit with Mixed Procedure of SAS program. The results indicated that all environmental independent (categorical and continuous) variables included in the model had statistically significant ($P < 0.01$) influence on test day milk yield. The estimate of partial linear regression coefficient of test day milk yield on THI was found to be 7 gr THI-1 indicating that in average daily milk production increases as THI increases one unit until reaching the turning point in which it decreases due to heat stress. It can be therefore concluded that THI is needed to be taken into account in genetic evaluation of dairy cows as an animal model is applied to predict breeding value of the population under consideration.

Key Words: Iranian Holstein, temperature-humidity index, test day milk yield

T305 Application of mixed linear model to evaluate effects of temperature and relative humidity on lactation milk yield of Iranian primiparous Holsteins. H. Farhangfar*[1], H. Roshan[1], N. Emam Jomeh Kashan[2], and M. H. Fathi Nasri[1], [1]*Birjand University*, *Birjand, Iran*, [2]*Aboureyhan University*, *Tehran, Iran*.

The main aim of this research was to evaluate the effects of temperature and relative humidity on lactation milk yield of Iranian first parity Holstein cows. The data set comprised of 5,323 lactation milk records obtained from 5,323 primiparous Holsteins calved between 1994 and 2007 in 64 herds of Mashhad city, Iran. Total number of sires was 660. In the whole data set, averages of lactation milk yield and age at first calving were 7823 kg and 26.35 Months, respectively. Total lactation milk yield of individual cows was predicted based upon using Gompertz nonlinear function as applied by Fathi Nasri et al. (Journal of Agricultural Science 2008, 146:633–641). A mixed linear model was applied in which fixed effects of herd, year and month of calving, linear covariables of Holstein gene percentage, open days, days in milk, age at first calving (in month), temperature (in Centigrade) and relative humidity (%), and random effect of sire were included. Daily temperature and relative humidity information (obtained from local weather stations) were averaged over the course of the lactation for individual cows. The model was run using Mixed Procedure of SAS software. Results showed that herd, year and month of calving, Holstein gene percentage, age at first calving, days in milk and average temperature had significant ($P <$ 0.01) effects on lactation milk yield. Open days and relative humidity were found to be non-significant factors for lactation milk yield. For all the covariables with significant effect, positive partial regression coefficients were detected. The results indicated that total lactation milk yield increased by 36.65 kg as the average temperature increased by one centigrade. The findings of this research suggest that temperature information could be taken into account for analyzing milk records when a test day model is used.

Key Words: Iranian Holstein, temperature, Gompertz nonlinear function

T306 The association between days in milk, somatic cell counts, milk urea nitrogen, and percentage of milk fat and protein in dairy cows. S. R. Heidari Khormizi*, M. Dehghan Banadaki, and F. Farhang, *University of Tehran*, *Tehran, Karaj, Iran*.

Data concerning to days in milk, SCC, milk urea nitrogen, percentage of milk fat and protein from 5 commercial dairy herds in Iran were collected monthly from 2004 to 2007 to study relationship between them. Days in milk were grouped into 30-d increments with those greater than 420 d grouped into one category. Milk urea nitrogen was grouped by increments of 2 mg/dL with those less than or equal to 6 mg/dL grouped into one category, and equal to or greater than 26 mg/dL as a category. Univariate linear regression models were developed using Proc Mixed in SAS to test the relationship between days in milk (dependent variable) and other variables. The results of this study showed that DIM significantly affected SCC, milk urea nitrogen and percentage of milk fat and protein. In cows, SCC was at its minimum amount between 60 and 90 d after calving and reached maximum between 90 and 120 d of lactation. Significant differences in MUN were observed between herds ($P < 0.0001$), with a significant variability between test dates within herds. Significant effect of parity ($P < 0.0001$) and its interaction with DIM were also found. MUN increased at the beginning of the lactation, reached a maximum between 150 and 180 d postpartum, and then steadily decreased until the end of lactation. Percentage of milk fat and protein increased at >240 d postpartum. The results of this study suggest that days in milk is an important part in demonstrating milk composition changes.

Key Words: days in milk, somatic cell counts, milk urea nitrogen

T307 The association between milk urea nitrogen, milk yield, Somatic Cell Counts and parity in Holstein dairy herds. S. R. Heidari Khormizi*, M. Dehghan Banadaki, S. Hasanlou, and F. Fatehi, *University of Tehran*, *Karaj, Tehran, Iran*.

This study was conducted using data from Dairy Herd Improvement monthly tests to investigate the association between milk urea nitrogen concentration (MUN), milk yield, somatic cell counts, milk fat percentage, milk protein percentage, and order of lactation in 5 commercial dairy herds from Iran. Mean MUN for Holstein cows was 19.78 mg/dl. Mean MUN, categorized by 30-d increments of days in milk (DIM), paralleled changes in milk values and followed a curvilinear shape. Multivariate mixed linear regression (Proc Mixed in SAS) was used to determine the relationship between MUN (dependent variable) and independent variables: milk yield, somatic cell counts, milk fat percentage, milk protein percentage, and order of lactation. The results showed that the highest milk yield (32.65 ± 0.09 kg/d) was associated to higher milk urea nitrogen compare with cows with the lowest daily milk yield. The highest somatic cell counts (970.56×103 cell/ml) was associated to lower milk urea nitrogen compare with cows with the lowest milk urea nitrogen. As the milk protein percentage increased, MUN concentration decreased; Milk fat percentage also decreased so that the higher percentage of milk fat and protein (3.69 ± 0.01 and 3.31 ± 0.003 respectively) were found for cows with lower milk urea nitrogen. For cows, concentration of milk urea nitrogen was different among lactation groups 1, 2, and 3+. Milk urea nitrogen increased as parity decreased. It was concluded that milk urea nitrogen should be evaluated in association with milk yield, somatic cell counts, milk fat, milk protein, and parity.

Key Words: milk urea nitrogen, milk yield, dairy herds

T308 Control of acute postpartum metritis in lactating dairy cows at high risk of developing metritis following dystocia, stillbirth, twinning and/or retained placenta/fetal membranes with ceftiofur crystalline free acid sterile suspension (CCFA-SS). C. McLaughlin*, C. LaGrow, C. Daugherty, E. Stanisiewski, and M. Lucas, *Pfizer Animal Health*, *Kalamazoo, MI*.

Metritis is associated with significant economic loss due to treatment costs, reduced reproductive performance and premature culling. The objective of this multi-location clinical trial was to demonstrate that administration of 6.6 mg/kg BW dose of CCFA-SS once subcutaneously at the base of the ear reduces incidence of acute postpartum metritis compared with control cows. The study was a randomized block design with cows blocked on order-of-entry within herds without regard to parity to either saline treated (CON) or CCFA-SS. Daily observations were performed on d 1 to 14, rectal temperatures were recorded on d 0 to 14 and physical examinations were conducted on d 0–2, 7 ± 1, and 14. Twelve study sites, in CA (4), NY (2), IA (1), MI (2), FL (2) and TX (1) each enrolled at least 40 animals. Of the 494 animals enrolled (247 CON and 247 CCFA-SS), 54 were ineligible for analysis and 17 were removed from the study before d 14 for reasons unrelated to acute postpartum metritis. Cow was the experimental unit and the primary decision variable was incidence rate of metritis, defined during the d 14 physical exam as rectal temperature ≥39.5°C and a vaginal discharge score of 3 (not fetid; thin watery, serous; red, brown vaginal discharge), or a vaginal discharge score of 4 (fetid vaginal discharge), regardless of rectal temperature. Generalized linear mixed models were used. Incidence rate of metritis was lower for cows that received CCFA-SS than for CON (31.6 vs. 48.0%, $P = 0.0182$) with a difference of 16.4%. Mean rectal temperature over the first 6 d of study was lower ($P = 0.0015$) for CCFA-SS compared with CON cows. No detrimental effects attributable to the administration of CCFA-SS were observed. It

was concluded that CCFA-SS is safe and effective for control of acute postpartum metritis in lactating dairy cattle at high risk of developing metritis following dystocia, stillbirth, twinning and/or retained placenta/fetal membranes.

Key Words: metritis, dairy cow, ceftiofur

T309 Evaluation of ceftiofur crystalline free acid sterile suspension (CCFA-SS) administered to dairy cows exhibiting risk factors for acute postpartum metritis. E. Stanisiewski, C. Daugherty*, J. Hallberg, and M. Lucas, *Pfizer Animal Health*, *Kalamazoo, MI*.

The objective was to evaluate incidence of acute postpartum metritis in dairy cows after abnormal calving when given a single dose of CCFA-SS within 24 h following calving (day 0) at 6 commercial dairies. CCFA-SS was administered subcutaneously in the base of the ear. Response was compared with untreated controls (CON) that also exhibited abnormal calving. Abnormal calving was defined as dystocia, twins, retained membranes (≥12 h), stillbirth or any combination thereof. The study was a randomized block design with cows blocked on order of entry within herds without regard to parity to 1 of 2 treatments; CON or CCFA-SS (6.6 mg ceftiofur equivalents/kg). Untreated controls with normal calving (NTX) were included for observational purposes. Cow (122 NTX, 122 CON and 121 CCFA-SS) was the experimental unit. A generalized linear mixed model was used. Daily observations, including rectal temperatures, were performed on days 1 to 21 ± 2 along with physical examinations on Day 0–2, 7 ± 2, 14 ± 2 and 21 ± 2. A random subpopulation (about 50% of abnormal calving/at-risk cows) had samples collected from the uterus by swab on days 3 or 4, 7 ± 2, 14 ± 2 and 21 ± 2 for evaluation of bacteria present. The primary decision variable was incidence rate of metritis, defined as rectal temperature ≥ 39.5°C and fetid vaginal discharge. Cows with associated abnormal calving events that received CCFA-SS had lower ($P \leq 0.038$) incidence rates of metritis than CON at all 3 time points on study, with differences of 13.7 (day 7 ± 2), 16.8 (day 14 ± 2) and 14.9% (day 21 ± 2). Mean rectal temperature was lower ($P = 0.032$) in cattle over the first 6 d of study that received CCFA-SS compared with CON. Within day contrasts showed temperatures were 0.16 to 0.28°C lower ($P < 0.05$) in CCFA-SS cattle on study days 1, 2 and 3 compared with CON. Uterine cultures found *Escherichia coli* in 80% of samples during the first week postpartum. Incidence of acute postpartum metritis was reduced in dairy cows after abnormal calving when given a single dose of CCFA-SS within 24 h following calving.

Key Words: metritis, dairy cow, ceftiofur

T310 Evaluating reproductive outcomes in United States Holstein dairies. L. M. Moeller*[1], N. A. Michael[1], J. C. Dalton[2], and G. C. Lamb[3], [1]*ABS Global, Inc.*, *DeForest, WI*, [2]*University of Idaho*, *Caldwell,* [3]*University of Florida*, *Marianna*.

To assess reproductive management data were analyzed from 85 Holstein dairies in 4 regions of the US. Records of 231,288 cows and 649,495 matings from Region 1 (CA, ID, WA; n = 22 herds), Region 2 (KS, NM, TX; n = 15 herds), Region 3 (IL, MN, SD, WI; n = 35 herds), and Region 4 (IN, MI, NC, NY, OH, PA; n = 13 herds) were evaluated between August 2008 and August 2009. Analyses were conducted with PROC GLM to determine reproductive responses using herd as the experimental unit. Herd size ranged from 258 to 15,866 cows among all herds. Mean herd size was greater ($P < 0.01$) for Region 1 (5,809 ± 522) than Regions 2 (2,569 ± 632), 3 (1,240 ± 414) and 4 (1,704 ± 678). For all inseminations, the overall percentage of cows inseminated after estrus or ovulation synchronization with a fixed-time AI (TAI) protocol was 43.4%, and was greater ($P < 0.01$) for Region 3 (63%) than Regions 4 (46%), 1 (24%), and 2 (18%). The overall percentage of cows receiving an insemination after an observed estrus was 56.4%, and was greater for Region 1 (76%) than Regions 2 (82%), 4 (54%), and 3 (37%). Overall conception rates to first service TAI was 30.5% and was greater ($P < 0.01$) for Region 3 (33.6%) than Regions 1 (28.6%) and 2 (23.9%), whereas Region 4 (30.8%) was intermediate. Similarly, conception rates to cows inseminated after observed estrus was 34.9% and was greater ($P < 0.05$) for Region 3 (37.2%) than Regions 1 (33.6%), 2 (33.1%), and 4 (33.1%). Whole herd 21-d pregnancy rates (17.8%) and AI 21-d pregnancy rates (18.5%) were similar among regions. The mean percentage of cows that became pregnant, relative to the total number of cows eligible to become pregnant in the herd, was 76.9% and did not differ among regions. We conclude that regional differences in reproduction exist in US dairies, specifically in the percentage of cows that are inseminated at TAI and following detection of estrus. In addition, reproduction responses vary among region in terms of multiple measures of fertility, which may be attributed to protocol compliance, heat detection efficiency, and differences in herd size.

Key Words: estrous synchronization, fertility, reproduction

T311 The effect of soy isolate source in milk replacer on growth and health of calves fed milk replacer. R. C. Musser*, B. L. Miller, T. J. Earleywine, and T. E. Johnson, *Land O'Lakes, Inc.*, *Webster City, IA*.

Forty-eight (48) Holstein bull calves with an average initial weight of 44.2 kg were employed in a 42 d trial to evaluate 3 different sources of soy isolate in milk replacer (MR). Calves were allotted to treatment based upon weight and blood gamma globulin status. Calves were fed a 25% protein / 20% fat MR powder to provide 681 g DM feeding rate daily in 2 feedings. Calves were offered one feeding (340 g) per day during the week of weaning. Each MR contained soy isolate protein from one of 3 different sources-A, B and C-and were medicated (0.28 g neomycin:0.14 g oxytetracycline/kg). Soy isolate sources replaced 37.5% of the milk protein. Calf starter (20% CP as-fed) was fed throughout this 42-d trial. The Mixed procedure of SAS was used to analyze data. Source C was inferior ($P < 0.05$) in total weight gain, MR intake, starter intake and feed efficiency when compared with the other soy isolate sources. Soy isolate sources differ in ability to support calf performance.

Table 1. Soy Isolate Source

Item	A	B	C	SE
BW gain, kg	19.0[b]	17.7[b]	6.0[a]	1.239
MR (DM), kg	23.3[b]	22.9[b]	21.1[a]	0.526
Starter (DM), kg	14.9[b]	13.6[b]	8.9[a]	0.447
Feed/Gain	2.12[a]	2.12[a]	5.29[b]	0.372

[a,b] Means within a row differ ($P < 0.05$).

Key Words: calf, milk replacer, soy isolate

T312 Non-dietary risk factors for lameness and their consequences in dairy cows. I. Guasch[1] and A. Bach*[1,2], [1]*Deparment of Ruminant Production, IRTA*, *Caldes de Montbui, Spain*, [2]*ICREA*, *Barcelona, Spain*.

Forty-three herds (4,366 cows; herd average milk yield 26 ± 2.8 kg/d) located in the Northeast of Spain feeding exactly the same ration were included in a survey aimed at determining non-dietary risk factors for lameness and potential consequences of lameness on herd performance. The survey was conducted within a 2-mo time span and each herd

was visited at least twice. All cows (dry and lactating) were evaluated using a 5-point locomotion scoring system by the same observer for lameness. Management parameters were gathered through a direct interview with the herd manager. Reproductive data were derived from historical records collected for an entire year. Daily milk yield and composition during the 2 mo before and the month that the farm visit took place was collected from the milk processor. Data were analyzed using linear regression analysis. Overall, average lameness (locomotion score ≥4) prevalence was 18 ± 9.0%. No relationship was found between cubicle dimensions and lameness incidence. The frequency of bedding the cubicles (cushioning) was negatively correlated with lameness. Herds that moved cows between pens in groups of several animals had a lower incidence of lameness (14.2 ± 1.97%) than those that moved cows individually (21.6 ± 1.88%). Herds with an average age at first calving (AFC) > 27 mo had a greater lameness prevalence (20.8 ± 2.09%) than those with and AFC <27 mo (14.79 ± 1.71%). Herds producing more than 27 kg/d had a lower lameness incidence (12.9 ± 2.35%) than those producing less than 27 kg/d (20.3 ± 1.64%). Herd milk efficiency (normalized for fat and protein) ranged from 1.03 to 1.52 kg of milk/kg of DMI and tended ($P = 0.06$) to decrease as lameness prevalence increased. Heat detection rate ranged from 26.5% to 72.3%, and decreased as lameness incidence increased. Management aspects such as moving cows in groups, AFC, and frequency of bedding are highly associated with lameness prevalence. Lameness may decrease herd profitability by, among other factors, compromising reproduction through poor heat detection and tending to reduce milk efficiency.

Key Words: lameness, housing, management

T313 Associations between several aspects of heifer development and dairy cow longevity. A. Bach*[1,2], [1]*ICREA*, *Barcelona, Spain*, [2]*Department of Ruminant Production, IRTA*, *Caldes de Montbui, Spain*.

A data set from 8,549 heifers born between 2003 and 2006 including growth rates since birth until first calving, age and BW of insemination, and incidence of diarrhea and respiratory problems (RP) was used to evaluate potential associations between these factors and cow longevity. All heifers were raised in a contract heifer operation (Rancho Las Nieves, Mallen, Spain) and returned to their herds of origin (133 herds in total) before calving. Dates of death were provided by the Subdirección General de Explotaciones y Sistemas de Trazabilidad de los Recursos Agrícolas y Ganaderos from the Ministry of Environment, and Rural and Marine Areas of the Spanish Government. At the time of analysis, 3,138 animals out of the 8,549 considered had died. Age and BW before first calving was 727 ± 41.2 d and 661 ± 43.8 kg, respectively, with an overall ADG between 10 d of life and first calving of 873 ± 117.3 g/d. Average longevity for the 3,138 heifers that had died was 1,395 ± 407 d, with 10.4% of total cullings (or deaths) occurring within the first 50 DIM, and 30.9% of total cullings (or deaths) that did not complete the first lactation. Data were analyzed using a mixed-effects model accounting for the random effect of the farm of origin (and fate), year of calving, and their interaction. The number of RP that heifers experienced was the most significant parameter affecting longevity. Heifers that never incurred an RP had an average longevity of 1,606 ± 126 d, and this number progressively ($P < 0.001$) decreased to 1,511 ± 129 d in those that had experienced 4 or more RP. Heifers that completed the first lactation grew at a greater ($P < 0.05$) rate (875 ± 1.4 g/d) and were bred with a greater ($P < 0.05$) BW (62.9 ± 0.16% of calving BW) than those that never finished it (861 ± 3.85 g/d and 60.9 ± 0.26% of calving BW, respectively). The consideration of these results, especially recurrences of RP and rate of growth, when making decisions on heifer management has the potential to improve overall future herd profitability by increasing cow longevity.

Key Words: longevity, heifer, development

T314 Effects of heat stress and Niashure (NI) supplementation on winter acclimated lactating cattle. S. Rungruang*[1], R. P. Rhoads[1], L. H. Baumgard[1], M. DeVeth[2], J. L. Collier[1], and R. J. Collier[1], [1]*University of Arizona*, *Tucson,* [2]*Balchem Corp, New Hampton, NY*.

A replicated design with 24 multiparous high producing dairy cows (40 ± 1.4 kg/d) was utilized to evaluate a dose range of dietary NI (0, 4, 8, or 12 g/d) in winter acclimated lactating dairy cows on body temperature indices, sweating rate, feed intake, water intake, production parameters and blood niacin concentrations under thermoneutral (TN) and heat stress (HS) conditions. Temperature Humidity Index (THI) values for TN never exceeded 65 while THI values during HS were above 72 (stress threshold) for 12 h/d. The HS environment increased skin, rectal and vaginal temperatures, respiration rate, sweating rate and water intake and decreased feed intake (4 kg/d, $P < 0.01$), milk yield (3.4 kg/d, $P < 0.01$) and milk protein (0.18 g/100 mL, $P < 0.01$). Sweating rate increased during HS (13 g/m^2 h, $P < 0.01$) compared with TN, but this increase was 10-fold lower than reported in summer acclimated cattle. NI supplementation had no effect on sweating rate, dry matter intake, milk yield and composition in either environment. Dietary NI increased blood ($P < 0.07$) and milk ($P < 0.02$) niacin concentrations in a linear manner. Heat stress reduced blood (7.82 vs. 6.63 ug/mL, $P < 0.01$) but not milk niacin concentration. Reduced blood niacin concentration was partially corrected by dietary NI. Dietary NI linearly increased water intake ($P < 0.02$) in both environments but the increase was greater during HS conditions ($P < 0.03$). Dietary NI also increased skin temperature in both environments ($P < 0.01$) from both shaved and unshaved skin in a dose-dependent manner ($P < 0.01$) but the increase was greatest from shaved skin ($P < 0.04$). This suggests skin blood flow was enhanced with increasing NI dose. Results indicate that HS decreased blood niacin concentration in lactating dairy cows and that NI supplementation partially restored blood niacin concentration during HS. Dietary NI increased water intake and skin temperature. There may be seasonal differences in sweating rate responses to HS and NI.

Key Words: niacin, heat stress, cattle

T315 A preliminary investigation of individual variation in N excretion by lactating dairy cows. P. Gregorini*, P. Beukes, A. Romera, C. Clark, and D. Clark, *DairyNZ*, *Hamilton, Waikato, New Zealand*.

Dairy systems are under pressure to reduce their environmental footprint, and N excreted from cows is a primary concern. Three data sets were separately analyzed to explore the animal variability in N excretion, and associations among genetic merit, live weight, DMI and N excretion parameters. This was a preliminary step in evaluating the potential for genetic selection for reduced urinary N (UN) and milk urea N (MUN) concentrations. Data sets consisted of cows fed a) Total mixed ration (TMR), b) Grazing fresh pasture (GR), and c) fresh pasture indoors (IG). Data sets contained 372, 144 and 90 measurements, respectively. Cows in GR and IG were identified by profit-based genetic evaluation in relation to ability to breed efficient replacements (BE) and produce efficiently (PE). Data sets were analyzed using mixed models. Cow variance components were estimated using models that included treatment and period as fixed effects and cow and period within cow as random effects. Associations among the UN, MUN, BE, PE, DMI, and live weight were determined using random coefficient regression for TMR. For GR and IG, pooled within-treatment regression was used. Analyses

indicated a significant ($P < 0.001$) cow variance component for MUN (13 ± 3.9 m*M*/L) in TMR, MUN (7.7 ± 1.8 m*M*/L) and UN (1.2 ± 0.4 g/L) in GR, and UN (7.8 ± 1.0 g/L) in IG, with greater variation between cows than within-cow for each data set. In TMR, UN was positively associated ($P < 0.01$) with live weight and N intake. In GR, UN was negatively associated with PE ($P < 0.05$), but not BE. Live weight was positively associated ($P < 0.01$) with UN. With IG, genetic merit, neither live weight nor DMI was associated with MUN. None of the experiments were designed to study within- and between-cow variation in UN or MUN specifically, so caution must be applied when drawing inferences from these analyses. However, the analyses indicate consistent individual cow variation, suggesting a need for further research to explore the possibility of genetic selection for variation in N excretion.

Key Words: N excretion, dairy cow, genetics

T316 Repeatability coefficients for dry matter intake and efficiency of nitrogen utilization for milk production in lactating Holstein cows challenged with low N diets. N. B. Kristensen*, T. Hvelplund, M. R. Weisbjerg, P. Lund, and P. Løvendahl, *Aarhus University*, *Tjele, Denmark*.

Data from 63 cows fed 4 different diets varying in nitrogen (N) content in a multiple Latin square design with 2 tests, 8 blocks per test, 4 experimental periods of 14 d, and 4 treatments within block were used to estimate repeatability coefficients for dry matter intake, milk production traits, and efficiency of nitrogen utilization for milk production (ENU). Cows were blocked according to parity and days in milk. Diets were composed of corn silage, rolled barley, grass clover silage, and N adjusted by substituting soyhulls and cane molasses for soybean meal (120, 80, 40, and 0 g/kg DM) with a fixed proportion of soyhulls to molasses of 4 to 1. Diets contained 167, 150, 134, and 121 g crude protein/kg DM for the 4 soy levels, respectively. The study included 24, 25, and 14 cows of 1st, 2nd, and +3rd parity and cows were in average (mean ± SD) 160 ± 28, 180 ± 47, and 136 ± 30 d in milk by the first sampling period for the 3 parities, respectively. Repeatability coefficients were estimated in a linear mixed model containing the fixed effects of treatment, treatment × test, and experimental period × test and the random effect of block × test as well as random intercept, linear- and quadratic effects of treatment with subject = the individual cow. Repeatability coefficients were calculated as the variance component estimate for intercept / intercept + residual. The following repeatability estimates were obtained: dry matter intake, 0.77; milk yield, 0.57; energy corrected milk, 0.38; fat yield, 0.55; protein yield, 0.39; ENU, 0.52. Including BW and BW x treatment as fixed effects in the model reduced the estimates for energy corrected milk, 0.18 and protein yield, 0.093, however, the estimate for ENU (0.55) did not decrease, suggesting that ENU is a trait of the individual cow without being a function of its body weight. The estimated high repeatability coefficient for ENU further suggests a possibility for genetic improvement of N efficiency of dairy cows.

Key Words: repeatability coefficients, nitrogen utilization, dairy cows

T317 Metabolic profile and postpartum health in early lactating Holstein cows in southern Brazil. T. A. Frigotto[1], S. O. Juchem[2], R. D. Ollhoff[3], I. R. Barros Filho[1], P. Schmidt[1], and R. Almeida*[1], [1]*Universidade Federal do Paraná*, *Curitiba, PR, Brazil*, [2]*University of California*, *Davis*, [3]*Pontifícia Universidade Católica do Paraná*, *Curitiba, PR, Brazil*.

Objectives of the study were to describe the concentrations of serum metabolites and the occurrence of diseases in a group of parturient cows from commercial dairy herds. Two high-producing dairy herds in the county of Arapoti, Brazil, were monitored from April to July of 2009, resulting in data collection from 105 dairy cows (73 multiparous and 32 primiparous). Blood was withdrawn on d 1, 2, 5, and 10 after calving, and serum analyzed for non-esterified fatty acids (NEFA), β-hydroxybutyrate (BHBA), and calcium (Ca). Continuous data was analyzed as repeated measures, whereas dichotomous data was analyzed with Fisher exact test. The statistical model included the fixed effects of herd, parity, time, and appropriate interactions. Concentration of NEFA in serum decreased ($P < 0.01$) as DIM increased (d1 = 0.73; d5 = 0.62; and d10 = 0.51 mmol/L). Concentrations of NEFA were similar ($P > 0.05$) between herds, but multiparous cows had higher ($P < 0.05$) concentrations of NEFA than primiparous cows (0.71 vs. 0.53 mmol/L). Concentrations of BHBA were highest ($P < 0.05$) at d5 (d1 = 0.45; d5 = 0.59; d10 = 0.43 mmol/L). There was no ($P > 0.05$) difference on BHBA concentrations between first-lactation and mature cows. Concentrations of Ca in serum were similar ($P > 0.05$) between farms (10.5 vs. 10.7 mg/dL) and parity (10.7 vs. 10.6 mg/dL). The incidence of dystocia, displaced abomasum, clinical hypocalcemia, mastitis and subclinical ketosis were similar ($P < 0.05$) between herds and parity. Incidence of retained placenta was higher in primiparous cows from herd A ($P > 0.05$) than herd B (50 vs. 15%), but similar within multiparous cows (28.6 vs. 23.7%). Multiparous cows from herd A had higher incidence of metritis than herd B (28.6 vs. 5.1%; $P = 0.02$). Primiparous cows had higher incidence ($P < 0.01$) of udder edema than multiparous cows (40.6 vs. 11.0%). Milk production was similar between primiparous cows across herds (31 vs. 31 kg/d), but multiparous cows from herd A produced more milk from 14 to 56 DIM (46.5 vs. 39.7 kg/d). Parity and DIM are important sources of variation when monitoring metabolic parameters and evaluating disease incidence of transition cows.

Key Words: NEFA, BHBA, calcium

T318 Factors affecting the bulk tank milk quality collected by a dairy industry of Minas Gerais state, Brazil, from 2002 to 2008. C. A. V. Paiva, A. F. Cunha, M. O. Leite, R. Rodrigues, C. F. A. M. Pena, A. M. Q. Lana, M. Houri Neto, L. M. Fonseca, M. R. Souza, and M. M. O. P. Cerqueira*, *Federal University of Minas Gerais state*, *Belo Horizonte, Minas Gerais, Brazil*.

Objectives were to determine the bulk tank milk quality in compliance with the Brazilian Ministry of Agriculture standards (IN51) and the effect of total bacterial count (TBC) and somatic cell count (SCC) on protein, fat, and solids nonfat solids (SNF) content, as well as on the milk powder yield. A total of 60,243 milk samples were collected on farms in the state of Minas Gerais, Brazil, from 2002 to 2008. The TBC and milk composition and SCC were performed using Bactocount IBC and CombiSystem 2300 (Bentley Instruments Inc.). The results were analyzed by Chi-squared . From 2002 to 2008, the volume of milk (%) in compliance with IN51 increased 11.58% for TBC and 1.4% for protein while it decreased 3.33% for SCC, 2.05% for fat, and 4.07% for SNF. The frequencies of samples (%) in compliance with IN51 regarding TBC, SCC and contents of fat, and NFS were higher ($P < 0.05$) during the dry (72.88, 92.63, 96.27, and 90.65, respectively) than the rainy season (66.55, 90.35, 91.26, and 89.49, respectively). For protein, these frequencies were similar ($P > 0.05$) during the dry (97.72%) and rainy seasons (97.52%). The seasonal variations influenced the bulk tank milk quality. TBC and SCC varied more and had lower means during the dry (5.12 logCFU + 1/mL and 5.41 log SCC + 1/mL, respectively) than the rainy season (5.16 log CFU + 1 and 5.44 log SCC + 1/mL, respectively). Means (%) of fat, protein and SNF were higher during the dry (3.81, 3.30, and 8.82, respectively) than the rainy

season (3.61, 3.26, and 8.79, respectively). Seasonality influenced fat and protein and at the rainy season, SCC and TBC may have decreased the milk solids. Milk powder yield was higher in the dry season due to the highest solids content of milk. However, the total production of kg of solids was lower due to the lower volume of milk collected in that season. Indeed, seasonality influenced all the studied parameters and it may have affected milk powder yield.
Financial support: FAPEMIG

Key Words: milk, quality, factors

T319 Evolution of milk production and premium payment for total bacterial count, somatic cell count, fat and protein contents in a dairy industry of Minas Gerais state, Brazil. C. A. V. Paiva, A. F. Cunha, M. O. Leite, R. Rodrigues, C. F. A. M. Pena, L. M. Fonseca, A. M. Q. Lana, M. Houri Neto, M. R. Souza, and M. M . O. P. Cerqueira*, *Federal University of Minas Gerais state*, *Belo Horizonte, Minas Gerais, Brazil*.

Objectives were to characterize milk quality parameters in the state of Minas Gerais, Brazil, from 2002 to 2008. A total of 60,243 raw bulk tank milk samples were collected and analyzed for total bacterial count (TBC), SCC, fat and protein. Results were tabulated according to year and then related to the volume of milk produced and value paid to the producers according to a system of payment for quality established by the local industry. Descriptive analyses were performed to report results. For all 4 parameters used in the payment for milk quality (TBC, SCC, fat and protein contents), the value paid to the producer increased. However, not all parameters followed the same pattern. TBC and SSC followed distinct trajectories. The volume of milk that received premium payment for TBC increased 27.18% between 2005 and 2008, and the average premium payment for TBC increased 3.15% in the same period. In relation to SCC, the volume of milk that received a premium payment decreased 27.52% between 2005 and 2008, but the premium payment for SCC increased 58.89% in the same period. The average fat content decreased, whereas the protein content increased in the period evaluated. The volume of milk that received premium payment for fat content was reduced 0.92% between 2005 and 2008, but the average premium payment for fat content increased 14.38% in the same period. The volume of milk that received premium payment for protein content increased 61.86% between 2005 and 2008. The average premium payment for protein content increased 69.60% between 2005 and 2008. It is necessary to monitor and to evaluate the parameters used in the payment of milk quality so that it has, in fact, a continuous improvement of the productive processes and the economic index.

Key Words: milk, quality, payment system

T320 Comparison of different methods of rearing management in Holstein dairy calves. F. Niazi, H. Amanlou, E. Qashqayi*, and E. Mahjoubi, *Zanjan University*, *Zanjan, Iran*.

Milk consumption, dry feed intake, body weight (BW) gain and occurrence of diarrhea were studied in male Holstein calves fed milk either through conventional or step-down (STEP) methods. A completely randomized design was used in this study. In conventional method, the calves (n = 9) were fed colostrum and then milk at the rate of 10% of BW for the entire period of 45 d. In STEP method, the calves (n = 9) were given colostrum and then milk for 25 d at the rate of 20% of BW in 2 meals and another calves (n = 9) in 3 meals for 25 d, which was reduced (between d 26 to 30) to 10% of BW for the remaining 15 d. The calves fed through conventional and STEP methods were weaned gradually by milk diluting with water between d 46 and 50. Feed intake and BW of the calves were monitored until 90 d of age. The STEP calves consumed more milk than conventionally fed calves during the pre-STEP (d 1 to 30) and post-STEP (d 31 to 50) periods ($P < 0.01$). Consumption of starter in calves provided milk using conventional method compared with STEP-fed calves was greater during the pre-STEP period and there was no significant difference during the post-STEP and postweaning (d 51 to 90) periods. Body weight gain (8.5, 18.7 and 21.3 kg/30 d, $P < 0.001$, respectively) and feed efficiency (0.37, 0.49 and 0.55, $P < 0.001$, respectively) of calves were greater in those on the STEP method during the pre-STEP period than on the conventional method and were numerically higher during post-STEP and post-weaning. There was no significant difference in occurrence of diarrhea in calves fed milk through conventional method compared with STEP-fed method. Increasing number of milk meals tended to increase body weight gain (65.4 vs. 70.7 kg/90 d, $P < 0.17$). In conclusion, STEP milk feeding may prevent the problems of depressed solid feed intake associated with ad libitum milk feeding and of poor BW gain with conventional milk feeding in dairy calves.

Key Words: weaning, starter, Holstein bull calves

T321 Differences between expanding and non-expanding Wisconsin dairy farms. J. M. Janowski and V. E. Cabrera*, *University of Wisconsin*, *Madison*.

A survey was administered (September 2009 to January 2010) to a sample of 1,000 randomly selected Wisconsin dairy producers to discern differences between those planning to expand and those not planning to expand their operations. A total of 300 dairy producers (30%) across 33 counties in Wisconsin completed the survey. Results indicated 33% of dairy producers planned to expand their dairies in the future. The majority planned to grow their herds from within. Significant differences between dairy producers and their operations were found regarding producer age, producer experience, farm herd size, and land per cow. Low net profit was the top issue hampering growth and modernization for producers planning to expand. Most producers not planning to expand were satisfied with their current operation size and did not feel expansion was necessary. Producers planning to expand cited an increase in net farm income as their most important motivation, while producers not planning to expand wanted to keep the farm at its best size given available labor. Dairy producers planning to expand were interested in receiving more information about financial planning, profitability measures, and financial efficiency. Producers not planning to expand were interested in topics regarding reproduction and financial efficiency. Results provide evidence toward development of risk management and financial management programs tailored for expanding and non-expanding dairy producers.

Table 1. Characteristics of expanding and non-expanding dairy operations

	Planning to expand (n = 78)	SD	Not planning to expand (n = 222)	SD	P-value
Producer age (yr)	47.08	10.70	51.19	10.70	0.01
Producer experience (yr)	25.33	12.99	29.15	12.14	0.04
Farm herd size (#)	247.35	362.97	82.11	117.03	0.00
Farm land per cow (ha/cow)	0.94	1.06	1.73	2.18	0.00

Key Words: expansion, modernization, survey

T322 Effect of heat stress on pregnancy rate of dairy cows using artificial insemination or embryo transfer in commercial dairy farms of central Mexico (Aguascalientes). R. Lozano[1], E. Gonzalez-Padilla[2], C. Vazquez[2], C. F. Arechiga*[3], and J. M. Silva[3], [1]*Instituto Nacional de Investigaciones Forestales, Agricolas y Pecuarias*, *Pabellon, AGS, Mexico*, [2]*Universidad Nacional Autonoma de Mexico*, *Mexico, D.F.*, [3]*Universidad Autonoma de Zacatecas*, *Zacatecas, Mexico.*

Objective of present study was to evaluate the effect of heat stress on pregnancy rates of Holstein cows using artificial insemination or embryo transfer in commercial dairies from central Mexico (Aguascalientes, Mexico). The study was carried out in 2 commercial dairy herds during 2 seasons of the year: Warm (May 1 to August 17) and Temperate (January 15 to March 27). Cows included in the study were randomly allotted into 2 groups: 1) artificially inseminated (n = 682) and 2) embryo-recipient cows (n = 107). Days in milk (DIM), milk estimated production to 305 d (P305D); and the index temperature-humidity (THI) were recorded during both seasons. Data was evaluated through descriptive statistics. Pregnancy rate was evaluated in recipient cows and analyzed through a first-order multiple logistic regression analysis. DIM of cows in study (86.7 ± 2.8) were similar for both times and reproductive techniques ($P > 0.05$). P305D in recipient cows (9,261.8 ± 192.3) was higher than the observed in cows that were inseminated (8,397.9 ± 84.9; $P < 0.01$). As expected, THI was higher during warm season (76.7 ± 0.3) compared with temperate season (70.3 ± 0.3; $P < 0.05$). Pregnancy rate decreased during the warm season (21.1%) compared with the temperate season (35.9%; $P < 0.01$) for both AI and ET. Pregnancy rates were similar using artificial insemination (32.9%) and embryo transfer (24.9%; $P > 0.05$). Embryo transfer did not improve pregnancy rate over artificial insemination of Holstein cows exposed to heat stress conditions present during the summer in central Mexico (Aguascalientes).

Key Words: heat stress, embryo transfer, pregnancy rate

T323 Calculating field nutrient removal rates to comply with General Order for Existing Milk Cow Dairies from California's Central Valley Regional Water Quality Control Board. J. M. Heguy*, B. M. Karle, P. L. Price, and D. Meyer, *University of California, Davis*.

The Dairy General Order requires dairy operators to document total weight of nutrients removed from fields where manure is applied. A detailed protocol requires sub-sampling (n = 8) from each 16.19 ha, with additional composites made to represent morning and afternoon harvest periods for dry matter (DM). Analysis of forage DM forms the basis for all nutrient removal calculations. A single composite sample for each field is prepared for nutrient analyses. Field observations indicated the detailed sampling protocol was not generally followed at dairies. The objective of this study was to determine if differences exist in calculating DM removal based on various intensities of sub-sample and composite collection. Weights were obtained and samples collected for each truckload (TL) of forage harvested from 3 fields after unloading at the silage pit. Each sample was sealed in a plastic bag and placed on ice. Dry matter was determined for each sub-sample by drying 25–40 g, in triplicate, in a 55°C oven for 24 h, then weighing the dry residual. DM is dry weight divided by wet weight. Actual field DM removal was determined by summing TL × DM for all samples from the field. Field DM removal totals were calculated using 3 composite sampling models (sequence, interval, and period). Sequence values are the average of sample DM within each hour of harvest. Interval values are the average of every 10th sample. Period values represent averages of samples collected in am or pm on each day. Mean ± standard deviation (SD) sequence DM percent ranges were 27.23 ± 1.43 to 29.62 ± 1.64; 21.21 ± 1.45 to 24.57 ± 2.04; and 27.88 ± 1.03 to 31.71 ± 1.81, for Dairy 1, 2 and 3, respectively. Mean ± SD interval DM percent ranges were 27.26 ± 0.90 to 29.06 ± 2.19; 22.49 ± 1.57 to 23.36 ± 1.28; and 29.04 ± 2.40 to 30.65 ± 2.10, for Dairy 1, 2 and 3, respectively. DM percent of am/pm composites were: Dairy 1 (27.74 ± 1.51/29.00 ± 1.62); Dairy 2 (23.72 ± 1.78/22.53 ± 1.39/22.86 ± 1.43); and Dairy 3 (29.71 ± 2.05/31.97 ± 2.18).

Key Words: regulation, sampling, forage

T324 Association of production level and calving season with reproductive function of Holstein cows from an intensive dairy production system of central Mexico (Aguascalientes, Mexico). P. Hernandez-Briano[1], C. F. Arechiga*[1], J. I. Aguilera-Soto[1], M. A. Lopez-Carlos[1], M. Rincon[1], J. M. Silva[1], C. A. Medina-Flores[1], and R. Lozano[2], [1]*Universidad Autonoma de Zacatecas*, *Zacatecas, Mexico*, [2]*Instituto Nacional de Investigaciones Forestales, Agricolas y Pecuarias*, *Pabellon, Ags, Mexico.*

Objective of present study was to determine factors influencing productive and reproductive function of Holstein cows in an intensive dairy productive system in central Mexico (Aguascalientes, Mexico). Effects of calving season (CS) and milk production level (MPL) on number of services (NS), interval from calving to conception (ICC) and interval from calving to next calving (ICNC) of Holstein cows (n = 363) from January 1st 2008 to March 29th 2009 was evaluated. Data was analyzed by SAS proc GLM as fixed effects of CS, parity (PAR), milk production level (MPL), age of cow and interactions. High-producing Holstein cows (above 20 kg/d; elevated MPL x = 9,644 kg/lactation), required a higher NS (3.4 vs. 2.6), a greater ICC (174.2 vs. 130.9 d), and a greater ICNC (446.9 vs. 401.2 d), compared with low-producing Holstein cows (below 20 kg/d; x = 6,410 kg/lactation). According to CS, it was found that cows calving during cool season of the year and bred during the summer presented a greater NS (3.7 vs. 2.8), a greater ICC (187.2 vs. 140.9 d) and a greater ICNC (467.9 vs. 412.7 d) in comparison to cows calving during the hot season of the year. Probably, due to inseminations carried out during the hot months of the year. Moreover, 2 years-old cows (PAR 1), presented a lower ICC compared with cows with PAR 2 and/or greater ($P < 00.5$). In conclusion, a high MPL, CS and PAR compromised significantly productive and reproductive parameters of Holstein cows from an intensive dairy in Central Mexico (Aguascalientes, Mexico).

Key Words: dairy cow, milk yield, heat stress

T325 Bacterial survival rate in sanitizing teat dips for dairy cows. S. Retz and S. I. Kehoe*, *University of Wisconsin-River Falls*, *River Falls*.

It is common practice to apply a teat dip before and after milking to prevent mammary infections from occurring in dairy cows. Teat dips commonly contain a sanitizer and emollient to reduce bacterial invasion and keep teat skin from drying and cracking. Many dairies use a dip cup which has a container attached where the teat dip is kept to apply pre and post milking. The person milking squeezes the container to fill the cup and then dips the cows. To save teat dip, multiple cows are dipped using the same fluid. Because the fluid contains a sanitizing agent, few people are concerned about bacterial transfer. Therefore, our objective was to determine whether there were any bacteria surviving after dipping multiple cows. One teat dip container and cup were cleaned and filled with 0.1% iodine teat dip. Teat dip was used on 2 cows and then swabbed on a Minnesota Easy Culture System II triplate (Minneapolis, MN). This process was redone a total of 6 times over 4 random days. Results showed a numerically increasing trend ($P < 0.09$) for growth of gram-positive species by sampling time (7.98, 8.69, 19.69, 43.13, 21.41,

and 18.96 cfu). Growth of streptococcus and gram-negative species were not significant however increased numerically (0.39, 0.39, 0.96, 1.25, 1.10, and 1.53 cfu for streptococcus spp. and 0.32, 0.14, 0.61, 1.75, 0.32, and 1.04 cfu for gram-negative spp.). It can be concluded that there is some survival of bacteria as well as further growth. These results indicate that more research is needed to determine other variables such as type of teat dip.

Key Words: teat dip, cows, bacteria

T326 Stage of lactation alters production responses of cows subjected to feed restriction. V. Bjerre-Harpøth, N. C. Friggens, V. M. Thorup, K. L. Ingvartsen, and K. M. Moyes*, *Aarhus University*, *Tjele, Denmark*.

Our objective was to determine the effect of stage of lactation on production responses of cows during feed restriction (FR). Forty-seven healthy Holstein dairy cows in early (E; n = 14; 0–90 DIM), mid (M; n = 15; 91–220 DIM) and late (L; n = 18; 221–355 DIM) lactation were used. Of these, 26 cows were primiparous and 21 cows were multiparous. At the beginning of the study, all cows were fed a standard TMR for ad libitum intake. After 8-d, all cows were FR to provide ~40% of NE_L requirements based on body weight, milk production and composition by supplementing the standard TMR with 60% wheat straw. After 4-d of FR, cows returned to full feed. At each milking, milk yield was recorded and composite milk samples were collected automatically and analyzed for % fat, protein, and lactose and concentration of BHBA and MUN (m*M*). For each cow, the change in each variable was calculated as average [before] – [during] FR. The MIXED procedure of SAS was used to determine the effect of stage of lactation on production responses during FR. Stage of lactation did not affect ($P > 0.05$) changes in fat and MUN but changes in lactose and daily milk yield (kg/d) were greater ($P < 0.05$) in E (0.18 ± 0.02 and 11.6 ± 1.3, respectively) than M (0.08 ± 0.02 and 8.9 ± 1.2, respectively) or L cows (0.13 ± 0.02 and 8.9 ± 1.1, respectively). Changes in protein were greater in both E (0.24 ± 0.03) and M cows (0.28 ± 0.03) than L cows (0.07 ± 0.02). However, greater changes in BHBA (log[m*M*]) were observed in M (0.13 ± 0.06) and L cows (0.06 ± 0.06) than E cows (−0.33 ± 0.06). One week after FR, all cows returned to production levels similar to those observed before FR. Our results show that cows in early lactation respond differently to feed restriction than cows in mid or late lactation. These results provide insight into the homeorhetic mechanisms controlling the partitioning of nutrients of dairy cows during early lactation and should be beneficial for our understanding of how to maintain animal health and productivity throughout the lactation cycle.

Key Words: cow, stage of lactation, feed restriction

T327 The effects of dietary ThermalCare-R (TCR) on body temperature indices, production and metabolism in heat-stressed lactating cows. R. P. Rhoads*[1], M. V. Skrzypek[1], S. S. Block[2], and L. H. Baumgard[3], [1]*University of Arizona*, *Tucson,* [2]*Archer Daniels Midland, Decatur, IL,* [3]*Iowa State University, Ames*.

Multiparous Holstein cows (n = 22; 115 ± 5 DIM, 582 ± 41 kg BW) housed in climate chambers were individually fed a TMR consisting primarily of alfalfa hay and steam flaked corn. Cows were randomly assigned to 1 of 2 treatments: a diet containing TCR(a fermentation material and botanical product for heat stress, n = 11, 45.4 g/d) or control diet (n = 11). Trial length was 21d consisting of a 7d thermal-neutral (TN) period (18°C, 20% humidity) followed by 14d of heat stress (HS; cyclical daily temps ranging from 31.1 to 38.9°C and 20% humidity, maximum heat was at 1300 h). TCR feeding had little or no effect on body temperature indices during TN conditions. During HS and compared with controls, TCR-fed cows tended to have a reduced rectal temperature at 1300 h (40.29 vs. 40.11°C; $P = 0.08$) and a higher shaved rump skin temperature at all time points (37.35 vs. 37.67°C; $P < 0.01$). TCR-fed cows also had an increased respiration rate at all time points during HS (78 vs. 83 BPM; $P < 0.02$). Overall, TCR-fed cows tended to consume less feed (21.9 vs. 22.5 kg/d; $P = 0.06$) but the decrease during HS was not as severe in TCR-fed cows compared with controls (4.8 vs.6.0 kg/d; $P < 0.05$). Cows fed TCR had an overall (independent of environment) increase in milk fat content (3.96 vs. 3.67; $P < 0.01$) and tended to have increased milk protein levels compared with controls (2.78 vs. 2.71; $P = 0.07$). Overall TCR-fed cows produced more milk (0.5 kg/d; $P < 0.05$) and the difference became larger when evaluated on a FCM and ECM basis. During HS, both groups had a similar milk yield reduction (6.1 kg/d). TCR-fed cows had improved feed efficiency (12%; $P < 0.01$) and both groups lost a similar amount of BW (21.5 kg) during HS. During HS, plasma NEFA levels did not change but glucose levels decreased (5%; $P < 0.05$), PUN increased (27%) and TCR-fed cows had overall increased PUN levels (12.7 vs. 11.6 mg/ml; $P < 0.01$). Feeding TCR improved some body temperature indices and production variables in heat-stressed cows.

Key Words: heat stress

T328 Effect of increased omega-3 fatty acids on production and reproduction in high producing lactating cows during cool season and hot season conditions. T. Colburn*[1], K. D. Murphy[1], C. Walhof[2], and A. V. Grove[3], [1]*Virtus Nutrition, LLC*, *Corcoran, CA*, [2]*Valley Veterinarians, Inc.*, *Tulare, CA*, [3]*AG Research, LLC*, *White Sulphur Springs, MT*.

High-producing cow diets contain large quantities of polyunsaturated fatty acids, primarily omega-6 fatty acids. This results in a high omega-6:omega-3 ratio of fatty acids flowing to the small intestine. This elevated ratio may reduce optimal production and reproduction. We hypothesize that increasing dietary omega-3 fatty acids will result in improved production and reproductive parameters in lactating cows during cool season and hot season conditions. Five hundred multiparous Holstein cows were used to evaluate the effect of 2 omega fatty acid nutrition programs on milk yield and conception rates during 2 periods (summer vs. rest of year). Cows were randomly assigned to either control or treatment diets. All cows were supplemented with 113 g omega-6 fatty acid supplement from −21 d prepartum to 21 d postpartum. From 22 to 150 d postpartum, control cows received 225 g calcium salts of long chain fatty acids and cows in the treatment group received 113 g calcium salts of long-chain fatty acids and 113 g of primarily polyunsaturated omega-3 eicosopentanoic (EPA) and docosohexanoic (DHA) calcium salts of fatty acids. Diets were balanced to be isonitrogenous, isolipidic and isocaloric. Peak milk production was greater ($P = 0.02$) in cows in the treatment vs. control groups 51.4 vs. 50.1 kg/d, respectively. Treatment diet tended ($P = 0.06$) to increase conception rate for the 1st insemination during the period covering the entire year, 45.6% for cows consuming the treatment diet and 30.7% for the control cows. Conception rates tended to be associated ($P = 0.07$) with time of year for cows inseminated for the combined 1st and 2nd insemination times, 36.7% during the summer vs 29.4% for the rest of the year. Modifying dietary concentrations of omega-6 and omega-3 fatty acids had positive effects on production and reproduction in lactating cows.

Key Words: dairy cow, calcium salts of fatty acids, omega-3

T329 Effect of thermal stress, cistern size, and milking frequency on plasma mineral concentrations in Holstein dairy cows. R. Ben Younes[1], M. Caccamo*[2], I. Schadt[2], M. Ayadi[3], T. Najar[1], M. Ben M'Rad[1], and G. Caja[4], [1]*Institut National Agronomique de Tunisie*, *Tunisia*, [2]*CoRFiLaC, Regione Siciliana*, *Ragusa, Italy*, [3]*Institut Superieur de Biologie appliqué de Médenine*, *Tunisia*, [4]*Universitat Autònoma de Barcelona*, *Bellaterra, Spain*.

The study was carried out in 2006, in North Tunisia using 28 Holstein cows (169 ± 16 DIM) producing in average 18.0 ± 5.1 L/cow/d. Cows were classified according to udder cistern size, using a randomized block design, by ultrasonography to large-cisterned (47 cm^2 ± 17; LC) and small-cisterned (23 cm^2 ± 8; SC). The experiment was conducted in 4 times, April 5 (T1), July 18 (T2), August 18 (T3), and September 18 (T4). In each test day temperature and relative humidity data were registered hourly and cows′ blood was sampled from the jugular vein to determine serum concentrates of minerals (P, Fe, Ca, Mg, K, Na, Cl). In T1 and T2, cows were daily milked twice (2X). Immediately after T2, within each group, cows were randomly assigned to 2 levels of milking frequency: 2 times per day (2X) and 3 times per day (3X). To evaluate the effects of period and cistern size, only 2X events were considered. To assess effects of milking frequency, only T3 and T4 were considered. Mean THI values were 62 ± 2, 79 ± 2, 84 ± 2, and 77 ± 1 in T1, T2, T3, and T4, respectively. The concentration of each single mineral was affected by test day ($P < 0.02$), but neither by cistern size nor milking frequency. Minerals concentration least squares means in T1, T2, T3, and T4, respectively, are reported in Table 1. Some minerals, such as Fe, P, Mg, and K, seemed to be lowered through heat stress only after a certain period of exposure to stress. Heat stress should be considered especially for the nutrition of the close-up dry cows group and of cows within 72 h of calving.

Table 1. Least squares means of minerals concentrations

Minerals	T1	T2	T3	T4
P (mg/L)	64.29^{a}	64.75^{ab}	56.50^{bc}	51.89^{c}
Fe (mg/L)	1.03^{a}	0.98^{a}	1.01^{a}	0.81^{b}
Ca (mg/L)	89.27^{a}	69.17^{c}	79.79^{b}	66.64^{c}
Mg (mg/L)	22.27^{a}	22.04^{a}	22.93^{a}	19.75^{b}
K (mmol/L)	4.91^{a}	4.89^{a}	4.76^{ab}	4.59^{b}
Na (mmol/L)	140.94^{a}	133.04^{b}	136.73^{b}	127.17^{c}
Cl (mmol/L)	101.67^{a}	94.48^{b}	97.75^{b}	89.87^{c}

Superscripts within rows differ by $P < 0.05$.

Key Words: heat stress, plasma minerals, temperature humidity index

T330 Body growth of pregnant Holstein heifers reared on pasture or conventional diet. R. R. Peters*[1], S. W. Fultz[2], J. W. Semler[3], and R. A. Erdman[1], [1]*University of Maryland*, *College Park*, [2]*University of Maryland Extension*, *Frederick*, [3]*University of Maryland Extension*, *Boonsboro*.

Interest in grazing to reduce feed costs and increase profitability has increased in Maryland. To develop internal expertise, grazing work was initiated at our research unit. Study objective was to compare body growth of pregnant Holstein heifers on pasture (P) vs. conventional (C) diets. Between June 10 and Dec. 1, 2009, heifers were alternately assigned to either P or C diets based on date of pregnancy confirmation. One month before predicted parturition date, animals were moved to maternity pens. Both P (n = 16) and C (n = 15) fed heifers were located in adjacent areas. Heifers fed conventional TMR included corn and rye silage, grass hay, and a monensin supplemented grain mix. Pasture reared heifers received no supplemental feed or minerals. Unimproved permanent pasture consisted primarily of endophyte-infected tall fescue. Heifers were rotated daily to a new paddock of approximately 0.1 to 0.3 ha, based on available DM. Measurements included body weight (BW), whither height (WH), hip height (HH), and body condition score (BCS) taken every 2 wk. Data collected for heifers on study for at least 70 d was fitted by quadratic regression to generate growth curves by individual animal. First derivatives of regression equations were used to estimate average growth rates for BW, WH, and HH. Equations of Heinrichs and Hargrove (J. Dairy Sci. 70:653–660, 1987) were used to compare actual growth rates to standard expected growth rates for heifers of this age and breed. Heifers on P had reduced ($P < 0.001$) ADG and BCS while skeletal growth rates (WH, HH) were similar to C. We conclude that P could be used without effect on skeletal development but it did have an impact on BW gain and BCS.

Table 1.

Growth Measure	Pasture	Conventional	SEM	P value
ADG, kg/d	0.42	1.11	0.034	0.001
Expected ADG, kg/d	0.58	0.59	0.025	0.773
WH gain, cm/d	0.041	0.050	0.004	0.376
Expected WH gain, cm/d	0.037	0.036	0.002	0.942
Mean HH gain, cm/d	0.062	0.044	0.001	0.320
BCS	2.87	3.11	0.044	0.001

Key Words: pasture, heifer growth

T331 Postpartum reproduction and NEFA changes during early lactation in Holsteins, Jerseys and their crosses. K. L. Brown*, B. G. Cassell, M. L. McGilliard, M. D. Hanigan, and F. C. Gwazdauskas, *Virginia Polytechnic Institute and State University*, *Blacksburg*.

One hundred sixty-three cows in first and second (n = 111) lactation were sampled to determine if reproduction and NEFA differed between breeds. Thirty-four cows were Holstein-Jerseys (HJ) crosses, 49 were Jersey-Holsteins (JH) crosses, 51 were Holsteins (HH), and 29 were Jerseys (JJ). Blood samples were collected weekly for 10 wk postpartum. Statistical analyses were by MIXED models. Season were cold (November to May) and hot (June to October). Days open were affected by breed and year-season ($P < 0.019$). The days open for HH were 151.1 ± 8.4 d and not different for HJ (133.7 ± 14.1 d), or JJ (127.1 ± 12.6 d), but different from JH (116.5 ± 7.9 d). Services per conception (s/c) were affected by breed ($P < 0.019$). HH had more s/c (2.1 ± 0.1) than JH (1.7 ± 0.1). NEFA were affected by parity ($P < 0.002$), year-season, week, and breed by parity interaction ($P < 0.05$). NEFA were higher in parity 2 (0.50 ± 0.02 mEq/L) than parity 1 (0.43 ± 0.02 mEq/L). NEFA were generally higher in the cold season vs. the hot season, except for yr 3 hot season. NEFA for wk 1 was 0.74 ± 0.02 mEq/L, 0.60 ± 0.02 mEq/L in wk 2, 0.54 ± 0.02 mEq/L in wk 3, 0.50 ± 0.02 mEq/L in wk 4, 0.48 ± 0.02 mEq/L in wk 5, 0.39 ± 0.02 mEq/L in wk 6, 0.36 ± 0.02 mEq/L in wk 7, 0.33 ± 0.02 mEq/L in wk 8, 0.28 ± 0.03 mEq/L in wk 9 and 0.39 ± 0.10 in wk 10. The breed by parity effect showed HH in parity 2 had 0.56 ± 0.03 mEq/L, which was higher than parity 1 (0.44 ± 0.03 mEq/L; $P < 0.0001$). HH parity 2 NEFA was higher ($P < 0.0001$) than HJ parity 1 (0.39 ± 0.03 mEq/L) and JH parity 1 (0.43 ± 0.03 mEq/L; $P < 0.001$) and parity 2 (0.45 ± 0.03 mEq/L). HH parity 2 NEFA was higher than JJ parity 1 (0.45 ± 0.04; $P < 0.02$). HJ parity 1 and 2 were different (0.48 ± 0.03 mEq/L; $P < 0.002$). Even though breed by week interaction was not significant slices analysis revealed differences in wk 1 ($P < 0.03$) and wk 2 ($P < 0.04$). Change in NEFA during the first 2 wk postpartum was most dramatic. Reproductive measures appear more

affected by breed, while week postpartum, season, parity and breed had greater impacts on NEFA.

Key Words: crossbreds, NEFA, reproduction

T332 The effect of feed sorting on intakes of fiber and phosphorus in dairy cows. A. C. Huisman, R. L. Kincaid*, J. J. Michal, K. A. Johnson, and C. T. Gaskins, *Washington State University*, *Pullman*.

This study examined the impact of diet sorting on intake of NDF and P by lactating cows fed one of 2 TMRs that were fed for 10% refusals. Holstein cows (n = 24; 114 DIM) were fed a control TMR (CTMR; 27.3% alfalfa haylage, 25.4% alfalfa hay, 6.4% whole cottonseed, 36.4% concentrate, and 4.5% dried distillers grains and soluble) or a TMR in which 40% of the alfalfa hay DM was replaced by bluegrass straw (BGSTMR). After 3 wk the diets were switched and cows fed for another 3 wk. Fresh diet was delivered 1X/d with frequent pushups. Feed sorting by pen was assessed by comparing particle size distribution of fresh feed and 24 h refusals for 2 consecutive days for each treatment and period. Actual intakes of NDF and P were determined from the nutrient concentration in each particle size fraction for both fresh diet and refusals. Total fecal P excretion was estimated using ADL values. Analysis of data was performed using PROC GLM of SAS and the model included the effects of treatment, period, and treatment by period. Cows sorted ($P < 0.05$) against the long fraction (23 percentage unit increase in refusals) and for the short fraction (53 percentage unit decrease in refusals) for both treatments. Although sorting occurred, the % NDF in the consumed diet did not differ from the formulated diet (34% vs. 33% for formulated and consumed CTMR, and 36% vs. 35% for formulated and consumed BGS TMR, respectively). Similarly, the % P (0.41%) in the consumed diet did not differ from the formulated diet for either treatment. The feces contained 0.69 and 0.67% P and total fecal P excretion was 75 and 76 g/d, respectively, for the 2 treatments. However, comparison of particle size fractions of fresh feed to 24-h refusals does not consider within day variation of nutrient intake. In summary, feed sorting had no effect on daily intakes of NDF and P of cows fed these alfalfa-based diets.

Key Words: sorting, fiber, phosphorus

T333 Effect of Tasco on core body temperature of dairy cows exposed to heat stress. L. B. Pompeu[1], J. E. Williams*[1], D. E. Spiers[1], R. L. Weaber[1], M. R. Ellersieck[1], K. M. Sargent[1], N. P. Feyerabend[1], H. L. Vellios[1], and F. Evans[2], [1]*University of Missouri*, *Columbia*, [2]*Acadian Seaplants*, *Darmouth, Nova Scotia, Canada*.

Previous research in our laboratory revealed Tasco (*Ascophyllum nodosum*) temporarily lowers core body temperature (Tc) in rats and steers fed diets with endophyte-infected tall fescue during heat challenge. The present study determined the impact of Tasco on Tc in dairy cows exposed to elevated ambient temperature (Ta). Holstein cows (n = 32; DIM 107 ± 43; parity 2.7 ± 1.5) were assigned to treatments (trt) using a randomized complete block design, with 8 cows per trt. The study was divided into 3 periods: Period 1 (7 d) was adaptation to the Calan gate system; in Period 2 (28 d) trt were: Control-1 (C-1); Control-2 (C-2); 0.25% Tasco (0.25T); 0.50% Tasco (0.5T); in Period 3 (28 d) C-2 changed to 0.50% Tasco (C-.5T) to evaluate length of feeding Tasco. Each cow had a telemetric temperature transmitter (SmartStock, Pawnee, OK) placed in the reticulum, to record Tc every 20 min. Ta was continuously recorded (Hobo, Onset Computer Corp., Bourne, MA). Daily feed intake and milk production were collected for each cow. For Periods 1, 2 and 3 the average maximum Ta was 29.6, 28.0 and 31.0°C, respectively. In Period 2, no differences ($P > 0.10$) were found between C-1 and C-2 for any parameter, so they were combined for this period (C). Tasco trt had no effect ($P > 0.10$) on milk production, even with occasionally lower ($P < 0.05$) DMI for 0.25T compared with C and 0.5T. In Periods 2 and 3, there was a trend ($P < 0.10$) for a higher Tc for 0.5T compared with other trt. Linear regression of Tc vs Ta showed that, in Period 2, 0.25T had a slower increase in Tc with the rise in Ta during the day compared with C, while in Period 3, both 0.25T and 0.5T had a slower increase in Tc compared with C-1 and C-.5T ($P < 0.05$). In this same study, for Period 3, 0.25T had a slower increase in rump and ear surface temperature than C-1 and C-.5T as Ta increased. These results revealed that 0.25T maintained lower Tc, rump and ear temperature with increasing Ta.

Key Words: Tasco, heat stress, dairy cows

T334 An update of bulk tank milk quality in California. N. Silva-del-Río*[1] and C. Collar[2], [1]*University of California Cooperative Extension*, *Tulare County,* [2]*University of California Cooperative Extension, Kings County.*

Information about bulk tank milk (BTM) quality parameters can be used by dairy producers to compare their milk quality to industry wide benchmarks, and to define achievable goals for their operations. The objective of this study was to describe BTM quality for the California dairy industry. Individual herd information on somatic cell count (SCC), standard plate count (SPC), laboratory pasteurization count (LPC) and coliform count (Coli) from Oct-08 to Sep-09 were provided by a large dairy cooperative in California. All the milk loads shipped by each dairy were sampled weekly (ranging from 1 to 7 loads per week per dairy). Only herds with BTM samples collected throughout the 12 mo period were included in the final data set (n = 537) which comprised a total of 56,455 BTM observations. BTM samples below the regulatory threshold set by the California Department of Food and Agriculture (CDFA) were: 99.4% for SCC (<600,000 cell/mL), 96.5% for SPC (<50,000 CFU), 96.1% for LPC (<750 CFU/mL), and 93.0% for Coli (<750 CFU/mL). BTM quality parameters were described with Proc Univariate of SAS. Season effects (S1 = Jan-Mar, S2 = Apr-Jun, S3 = Jul-Sep, S4 = Oct-Dec) of log-transformed data were evaluated using Proc Mixed of SAS with repeated measurements on herd. Description of BTM quality parameters for the top 25% herds, the bottom 25% herds and the median counts are presented in Table 1. There was a significant effect of season on each of the BTM quality parameters ($P < 0.001$). SCC were lower in S2 than S1-S3-S4. SPC were higher for S1 than S2-S3-S4. However, SPC and Coli were higher in S1-S4 than in S2-S3. Overall, during the study period, California BTM quality was within acceptable parameters.

Table 1. SCC, SPC, LPC and Coli counts in California BTM, top 25% herds, bottom 25% herds and median counts from Oct-08 to Sep-09

	SCC (cell/mL)	SPC (CFU/mL)	LPC (CFU/mL)	Coli (CFU/mL)
25% top herds	<156,698	<2,969	<43	<25
25% bottom herds	>252,679	>5,729	>129	>63
Median	202,208	3,534	74	39

Key Words: bulk tank milk quality, dairy, California

T335 Determination of variation in dairy cows response to heat stress using radiotelemetry. L. B. Pompeu, J. E. Williams, D. E.

Spiers*, R. L. Weaber, and M. R. Ellersieck, *University of Missouri*, *Columbia*.

Summer heat is a major problem for dairy cattle, which have an elevated body heat production. At air temperature (Ta) above thermoneutrality, reduction in feed intake and milk production occur along with increased core body temperature (Tc). However, individual animals vary in response to heat stress, which can provide large variance between groups. To evaluate different levels of animal response to heat stress, a study was performed utilizing 15 Holstein cows, housed in a free-stall barn, during June and July (2008). A telemetric temperature transmitter (SmartStock, Pawnee, OK) was placed in the reticulum of each cow to record Tc. Ta was recorded using Hobo loggers (Onset, Bourne, MA). Feed intake and milk production were collected daily. A period of progressively increasing heat stress (9 d) was chosen to be analyzed (max Ta: 29.7°C, min Ta: 20.7°C). Tc and milk production relationships to Ta were assessed by quadratic and linear regressions, respectively, to separate cows into sensitive (S; n = 5) and non-sensitive (NS; n = 5) groups based on R^2. Five cows showed an intermediate response and were removed from analysis. For the analysis, hours 1000 to 1500 were used to assess the major rise in Tc during the day. A 1-h lag in Tc and 1-d lag for milk production were utilized for better correlation with Ta. Linear regression of Tc vs. Ta showed a difference between regression coefficients and slopes of S ($R^2 = 0.68$; slope = 0.12) and NS ($R^2 = 0.54$; slope = 0.08). Daily max, min, and mean Ta were tested against milk production, with min Ta yielding the best correlation. Milk production also showed a large difference with the linear fit and slope of S ($R^2 = 0.75$; slope = −0.71) being larger than NS ($R^2 = 0.27$; slope = −0.25). The greater slopes of sensitive animals indicate a larger response to Ta compared with non-sensitive animals, indicating variations in responses between animals among the same group of cows. Thus, to evaluate heat strain, it is essential to analyze animals separately by their level of response.

Key Words: heat stress, dairy cow, core temperature

T336 Corn silage management practices on California dairies. N. Silva-del-Río*[1], J. M. Heguy[2], and A. Lago[3], [1]*University of California Cooperative Extension*, *Tulare County,*[2]*University of California Cooperative Extension, Stanislaus and San Joaquin Counties,*[3]*APC Inc., Ankeny, IA.*

The aim of this study was to obtain information on current corn silage feed management practices in California's Central Valley. In summer 2009, a feed management survey was mailed to dairy producers in Tulare, Stanislaus, and San Joaquin; the first, third and seventh largest dairy counties in California, respectively. Producers received an envelope containing an invitation letter to participate in the study, a one-page survey, and a pre-paid return envelope. Response rate was 16.9% (120/710). Herd size ranged from 160 to 6,600 cows (median = 950). Corn silage in California was more frequently stored in piles (85.0%) and on concrete (75.0%), versus bunkers or dirt. Dairies reported top surface spoiled forage: <7.5 cm (25%), 7.5 to <15 cm (53.9%), 15 to <23 cm (15.7%), ≥23 cm (4.9%). Only one producer indicated that silage was not covered. A total of 54.7% (n = 55) of dairies covered silage with oxygen barrier (OB) technology. Top surface spoiled forage was reported to be < 15 cm in 89.3% of silages covered with OB technology and in 64.0% of silages covered with conventional plastic material. Bacterial inoculants of various types were used in 54.0% of corn silages. Most respondents (73.4%) considered that silage faces were maintained smooth, but only 5 producers used face shavers. The entire width of the silage face was removed daily in 41.7% of dairies, and of those, 27% removed less than 15 cm depth per day. Of dairies that did not remove the entire width of the silage face (1/2 face-24.0%, 1/3 face-26.9%, 1/4 face -7.4%), 15.0% advanced less than 15 cm depth per day. Determination of silage dry matter (DM) was conducted at least once a month in 52.3% of dairies. Only 8.3% of dairies determined DM weekly, or more often. Most dairies delegated DM determination to an outside nutrition consultant (86.6%). A total of 25.0% of dairies suspected mycotoxins in 2008. Top surface spoiled forage was discarded by 70.4% of dairies suspecting mycotoxins, and by 55.8% of those that did not suspect mycotoxins. Although dairy owner and manager responses are subjective, results indicate areas where corn silage management can be improved, such as removal rate, surface spoilage, and pile size.

Key Words: corn silage, dairy, survey

T337 Interaction of breed and quantity of milk replacer on the performance of dairy calves. C. J. Cobb* and M. A. Ballou, *Department of Animal and Food Sciences, Texas Tech University*, *Lubbock*.

Objective was to determine the influence of breed and quantity of milk replacer fed on the performance of dairy calves. Forty-two bull calves (n = 20 Holstein and n = 22 Jersey, 2 ± 1 d old) in a 2 × 2 factorial arrangement were observed through 11 weeks of age. Holstein and Jersey calves on the lower plane of nutrition were fed a 20% protein and 20% fat milk replacer at a rate of 454 g / d. Holstein calves on the higher plane of nutrition were fed a 28% protein and 20% fat milk replacer at a rate of 810 and 1,180 g / d for wk 1 and wk 2 – 6, respectively. Jersey calves on the higher plane of nutrition were fed a 28% protein and 25% fat milk replacer at a rate of 568 and 680 g / d for wk 1 and wk 2 – 6, respectively. At wk 7 all milk intakes were reduced to 50% to stimulate starter consumption. Calves were weaned when consuming 900 g/d of starter. There were breed × plane of nutrition × time interactions ($P < 0.01$) for milk refusal, starter intake, and total energy intake. Holstein calves fed the lower plane of nutrition had greater starter intakes from wk 4 through wk 8 than Holsteins fed the higher plane of nutrition. Plane of nutrition did not influence starter intake in Jersey calves. Calves fed the higher planes of nutrition had greater total energy intakes before weaning; however, after reducing milk intakes at wk 7 there was no difference within breed. There was an interaction of plane of nutrition and time ($P < 0.01$) on average daily gain; whereas calves fed the higher planes of nutrition had greater gains from wk 1 to 6, but were not different from the calves fed the lower planes of nutrition from wk 7 to 11. Utilization of energy for body weight gain was greater for calves fed higher planes of nutrition ($P < 0.01$) and Holsteins ($P < 0.02$) from wk 1 to 6; however, from wk 7 to 11 the opposite was observed for plane of nutrition ($P < 0.05$) and breed ($P < 0.01$). These data indicate under the current higher plane of milk feeding schemes both Holstein and Jersey calves performed well; however, the amount of milk replacer fed to Jersey calves may be able to be increased during the pre-weaning period.

Key Words: breed, calf, performance

T338 Evaluation of mannanoligosaccharides route of administration for dairy calves: Performance and rumen development. J. T. Silva[1,2], L. S. Ferreira[1,2], and C. M. M. Bittar*[1,2], [1]*University of Sao Paulo/ESALQ*, *Piracicaba, SP, Brazil*, [2]*CNPq*, *Brasília, DF, Brazil*.

The objective of this study was to evaluate the route of administration of mannanoligosaccharides (MOS) for dairy calves and its effects on performance and plasma parameters indicative of rumen development. Following birth, 24 male Holstein calves were used in a completely randomized design and assigned to the following treatments: 1) Control; 2) MOS (4 g/d Bio-Mos, Alltech Biotech.) via starter feed (MOSF); 3) MOS (4 g/d Bio-Mos, Alltech Biotech.) via milk replacer (MOSR). The animals were housed in individual hutches, with free access to water, and fed 4L/d of milk replacer (18.5% CP, 22.5% fat, 12.5% solids; Nattimilk, Auster Animal Nutrition) until weaning at 6 weeks; calves also received a 23% CP starter feed ad libitum. Fecal scores were evaluated daily. Calves were weighted and growth measurements and blood samples for glucose, urea-N (PUN) and β-hydroxybutyrate (BHBA) were taken weekly until the eighth week of age. There was no significant ($P > 0.05$) effect of treatment or treatment × age interaction for average starter feed intake (737.4; 842.6; 798.6 g DM/d for C, MOSF and MOSM, respectively), weight gain (352.2; 411.3; 409.6 g/d for C, MOSF and MOSM, respectively) or body growth (heart girth: 1.63; 1.74; 1.75 cm/week; hip width: 0.43; 0.4; 0.36 cm/week for C, MOSF and MOSM, respectively). However, there was an age significant effect for all parameters ($P < 0.0001$). Fecal scores were not affected by treatments; animals presented scores considered as diarrhea (>2.0) only during the second week of life. Plasma concentration of glucose (81.4; 82.7; 86.7 mg/dL for C, MOSF and MOSM, respectively), PUN (13.7; 14.6; 14.0 mg/dL for C, MOSF and MOSM, respectively) or BHBA (0.203; 0.177; 0.163 mmol/L for C, MOSF and MOSM, respectively) were also not affected ($P > 0.05$) by treatment or the interaction treatment × age. However, PUN and BHBA concentrations were significant increased with age ($P < 0.05$), suggesting adequate rumen development. For the general and nutritional management imposed, there were no benefits of providing MOS via liquid or solid diet.
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Key Words: additives, early weaning, fecal score

T339 Impact of solids level of colostrum replacer formulations on immunoglobulin absorption in calves. J. M. Campbell*[1], J. C. Gawthrop[2], A. W. Riad[2], L. E. Russell[1], J. D. Crenshaw[1], and J. Q. Quigley[1], [1]*APC, Inc.*, *Ankeny, IA*, [2]*CalfCare*, *North Manchester, IN*.

The objective was to determine if varying level of solids in a single feeding of colostrum replacer (CR) containing IgG derived from bovine serum fractions affected 24-h serum IgG, serum total protein, and the ability of calves to achieve adequate passive transfer. Forty-eight heifer or bull calves were randomly assigned to 1 of 4 treatments that included receiving a single feeding of CR containing 155 g of IgG reconstituted to 17.4, 20.2, 24.1, or 29.7% solids. Sex was equalized among treatments. All CR were blended, individually packaged, and irradiated before feeding. Colostrum replacers were reconstituted in warm water, mixed using a hand blender, and fed with an esophageal feeder at 1 h of age. Acquisition of passive immunity was assessed by measuring 24-h serum IgG, serum total protein, apparent efficiency of absorption (AEA) of IgG, and the ability to prevent failure of passive transfer (FPT). Data were analyzed as a completely randomized design with BW as a covariate when appropriate. Percentage of calves with FPT was analyzed by chi-squared analysis. Linear contrasts were used to produce linear analysis. As level of solids of the blended CR increased from 17.4 to 29.7%, there was a tendency ($P < 0.10$) for increased 24-h serum IgG, while serum total protein was increased ($P < 0.05$). No treatment differences ($P > 0.10$) were noted in AEA or percent FPT. In conclusion, a range of solids level from 17.4 to 29.7% offered in a single feeding of CR containing 155 g IgG from bovine serum fractions can be fed to calves without impacting AEA or FPT.

Key Words: calves, immunoglobulin, colostrum replacer

T340 Effect of yeast β-glucan and antibiotics on growth and intestinal microflora in early-weaning calves. Y. Zhou, Q. Diao*, Y. Tu, and Q. Yun, *Feed Research Institute, Chinese Academy of Agricultural Sciences*, *Beijing, China*.

This experiment was conducted to investigate the effect of yeast β-glucan and bacitracin zinc on growth performance and intestinal microflora in rectum of early-weaning calves. Twenty neonatal healthy Holstein male calves were randomly allotted to 4 treatments, each treatment contained 5 replicates with one calf per replicate. All calves were fed with diets supplemented with 0 (Treatment A), 75mg/kg yeast β-glucan (Treatment B and C), 60mg/kg bacitracin zinc (Treatment D). The experiment lasted

for 28 d. On d 21, calves of Treatment A, B and D were challenged orally with *Escherichia coli* (O141:K99). Average daily feed intake (ADFI), average daily gain (ADG) and intestinal tract bacterial communities were determined. Comparing with Treatment A, the ADG of calves in Treatment B increased by 26.17% and 24.93% in the 2 phases before the *Escherichia coli* challenged ($P < 0.05$), the ADG of calves in Treatment B and D increased by 30.38% and 30.81% after the *Escherichia coli* challenged($P < 0.05$).As for the F/G, which in Treatment B and D were significantly lower than that in Treatment A ($P < 0.05$). The amount of *Escherichia coli* in rectum was rapidly increased after the challenge, compared with Treatment A, the amount of *Escherichia coli* in rectum at 12h and 24h in Treatment B and D were significantly decreased ($P < 0.05$), and the amount of Lactobacillus was significantly decreased in the Treatment D ($P < 0.05$). PCR-DGGE of 16S rDNA was used to investigate the similarity index, the band number in Treatment C was significant higher than that in Treatment A and D ($P < 0.05$).The degree of similarities of treatments ranged from 50% to 75%. According to the results, β-glucan could improve the growth of claves and adjust the structure of intestinal microflora, thus using β-glucan in calves feed may decreased the usage of antibiotics.

Key Words: calves, yeast β-glucan, intestinal microflora

T341 Effects of forage quality traits and access to calf starter on selection between forages in milk-fed calves. N. B. Kristensen*, M. R. Weisbjerg, and M. Vestergaard, *Aarhus University*, *Tjele, Denmark*.

The present study aimed to investigate how milk-fed calves selected among 4 different grass-clover forages [1st cut silage (F1), 1st cut hay (F2), 2nd cut silage (F3), and 4th cut silage (F4)] and how access to calf starter affected forage selection. Sixteen Holstein bull calves (20 ± 2 d of age) offered 4.84 kg/d of skim-milk based milk-replacer (12.3% DM) were randomly allocated to no starter (CON) or ad libitum access to a barley-based calf starter (START). Calves were housed in individual pens and offered the 4 forages ad libitum. Calves were harvested at 59 ± 2 d of age. Data on DMI and effect of starter on relative intake of individual forages were analyzed using the MIXED procedure in SAS by a model containing the fixed effects of block, time (day on trial), calf starter treatment, and the interaction between treatment and time. Calf by treatment was designated as a random effect and time considered a repeated measure. Friedman′s test computed using the FREQ procedure was used to evaluate selection between forages. The forages had the following nutrient and fermentation product contents: DM (48 ± 1, 88 ± 1, 41 ± 2, and 47 ± 2%), pH (5.33 ± 0.13, 6.01 ± < 0.01, 4.23 ± 0.01, and 4.34 ± 0.02), DL-lactic acid (17 ± 3, not detectable, 69 ± 2, and 89 ± 3 g/kg DM), and acetic acid (4.6 ± 0.7, 0.7 ± 0.2, 14.6 ± 0.6, and 13.0 ± 0.4 g/kg DM) for F1, F2, F3, and F4, respectively. The intake of the individual forages differed ($P < 0.01$) by source being 57 ± 3, 29 ± 3, 4 ± 1, and 10 ± 2% of total forage intake for F1, F2, F3, and F4, respectively. Only intake of F4 was affected by calf starter (START: 14 ± 2% vs. CON: 6 ± 2%, $P = 0.02$). Forage intake tended ($P = 0.09$) to be lower with START compared with CON, but total daily intake of calf starter + forage did not differ ($P = 0.47$) between treatments (39 d average being 714 and 771 ± 55 g DM/d for CON and START, respectively). Young milk-fed calves showed strong preference for lightly fermented grass-clover silage compared with both hay and more fermented silages, and the preference pattern was unaffected by the access to a barley-based calf starter.

Key Words: milk-fed calf, forage quality, feed intake

T342 Performance of calves fed an all-milk or enzymatically modified plant protein containing milk replacer with and without a specific amino acid profile. F. Soberon*, A. M. Severy, and M. E. Van Amburgh, *Cornell University*, *Ithaca, NY*.

The most nutritionally effective milk replacers (MR) are produced from all milk proteins. Supplementing non-milk protein MR with amino acids (AA) might help overcome some of the performance limitations previously observed with the use of plant proteins. The objectives of this study were to compare the performance of calves fed an all-milk containing MR compared with a MR with 50% of the protein replaced by a proprietary formulation of enzymatically modified plant proteins (EPP) as formulated or with a specific AA profile calculated from body composition and efficiency of use data. Eighty calves (20 per treatment, TRT) were assigned, as they were born, by 24 h of age. Calves were blocked by birth weight and sex and assigned to one of 4 TRT: Control: all milk protein MR (Excelerate milk replacer, Milk Specialties Global (MSG), Carpentersville, IL); TRT 1: Control plus AA supplied by added crystalline AA; TRT 2: EPP containing MR formulated at 28% CP and 15% fat containing proprietary EPP protein (MSG, Carpentersville, IL) representing approx. 50% of the MR protein; TRT 3: EPP containing MR with supplemental AA. All MR were formulated to be isocaloric and isonitrogenous. Significance was declared at $P < 0.05$. Calves were fed only MR to d 28, offered grain from d 29 to 42, and then weaned in a step-down manner over 7 d. Growth and starter intakes were measured until d 70. ADG (kg/d) data are reported in the table. Calves fed the all-milk containing MR had greater ADG up to weaning ($P < 0.05$) whereas post-weaning, increased starter intake in calves fed TRT 2 and 3 negated the growth advantage. Calves fed TRT 1 demonstrated greater hip height by d 49 compared with calves fed TRT 2 and 3 ($P < 0.05$) and the difference remained until d 70. Prior to weaning performance was greater in calves fed milk protein base MR.

Table 1.

TRT	Day 28	Day 49	Day 70
Control, kg/d	0.72[a]	0.74[a]	0.73[a]
TRT 1, kg/d	0.74[a]	0.73[a]	0.71[a]
TRT 2, kg/d	0.63[b]	0.66[b]	0.70[a]
TRT 3, kg/d	0.59[b]	0.63[b]	0.69[a]

Values with different superscripts within column differ $P < 0.05$.

Key Words: amino acids, calves, milk replacer

T343 Measurement of adaptive and innate immune function in calves raised under traditional and accelerated growth regimens. B. A. Hengst*[1], L. M. Nemec[1], R. R. Rastani[2], and T. F. Gressley[1], [1]*University of Delaware*, *Newark*, [2]*Milk Specialties Global Animal Nutrition*, *Carpentersville, IL*.

This study compared conventional and accelerated milk replacer feeding regimens on growth, respiratory and digestive health, vaccination response, and neutrophil mRNA levels. Holstein calves (10 male and 5 female) were randomly assigned to a 10-wk study on d 2 of life. Treatments were control (CON; n = 8) and accelerated (ACC; n = 7) milk replacer feeding programs. CON calves were fed a 20% crude protein (CP)/20% fat milk replacer (Advance Calvita Supreme; Milk Specialties Global, Carpentersville, IL) at 1.25% birth body weight (BW) from wk 1 to 6 and 0.625% birth BW during wk 7. A 28.5% CP/15% fat milk replacer (Advance Excelerate; Milk Specialties Global, Carpentersville, IL) was fed to ACC calves at 1.5% birth BW during wk 1, 2% current BW from wk 2 to 6, and 1% current BW during wk 7. All calves were

given milk replacer twice daily during wk 1 to 6, once daily during wk 7, and were weaned completely during wk 8. Calf starter intake was measured daily through wk 8. BW and wither height were measured weekly. Fecal scores (1 = firm to 4 = liquid) and respiratory scores (1 = normal; 2 = abnormal) were recorded twice daily. Neutrophils were isolated from blood at wk 1, 3, 5 and 8. Quantitative PCR was used to measure neutrophil mRNA levels of 7 functionality genes including the adhesion factor *L-selectin* (CD62L). Adaptive immune function was measured by vaccinating calves against ovalbumin at wk 1, 3 and 5 and measuring anti-ovalbumin IgG production at wk 1, 3, 5 and 8. There was no treatment effect on wither height, respiratory score, or anti-ovalbumin IgG production. BW during wk 4 to 10 was greater for ACC than CON calves ($P < 0.01$). Calf starter intake was greater for CON than ACC calves during wk 4 to 7 ($P < 0.01$), with no difference during wk 8. CON calves had firmer feces than ACC calves (fecal score 1.4 vs. 1.7, $P = 0.02$). Neutrophil *L-selectin* mRNA levels were 51% greater in ACC than CON calves ($P = 0.03$). Feeding calves a 28.5% CP/15% fat milk replacer in an accelerated feeding regimen increased growth and may enhance innate immune function, as indicated by the increased neutrophil mRNA levels of *L-selectin*.

Key Words: dairy calf, immune function, milk replacer

T344 Effects of hay intake on calves fed high volumes of milk. M. A. Khan*[1], D. M. Weary[1], D. M. Veira[2], and M. A. G. von Keyserlingk[1], [1]*University of British Columbia*, *Vancouver, BC, Canada*, [2]*Agriculture and Agri-Food Canada*, *Agassiz BC, Canada*.

Research to date has suggested that access to forage before weaning can limit rumen development in calves fed restricted amount of milk, but no research has addressed the role of forage on calves fed at higher planes of nutrition. This study compared performance and rumen development of calves provided high volumes of milk with and without access to hay. At d 3 of age, individually housed calves were randomly assigned to treatment (either ad libitum access to chopped grass hay or no forage; n=15 calves per treatment, 10 heifers and 5 bulls). All calves were provided ad libitum access to water and starter throughout the study. All calves were offered 8 L/d of milk from a nipple bottle from d 3 to 35, 4 L/d from d 36 to 53 and 2 L/d for the next 3 d before weaning at d 56. Solid feed intake and growth were monitored from d3 to d70. At d 70 males from both treatments were slaughtered and rumen pH and weight of ruminal contents with and without digesta measured. Overall DMI from solid feed did not differ between treatments before weaning. After weaning calves provided hay consumed less starter but more total DM (starter plus hay) than calves that had no access to forage. Over the experimental period (d 4 to 70), calves fed hay gained approximately 6 kg more than did control calves (58.14 ± 1.83 vs. 52.04 ± 2.03 kg, respectively; $P < 0.05$). Hip and wither height, heart girth and body barrel at d 35, 56 and 70 did not differ between treatments. Rumen and reticulum weights with (7.99 ± 0.69 vs.12.77 ± 1.29 kg; $P < 0.05$) and without digesta (1.60 ± 0.09 vs. 1.89 ± 0.05 kg; $P < 0.05$) were heavier in calves fed hay. Mean rumen pH was higher in calves fed hay compared with those fed no forage (5.49 ± 0.08 vs. 5.06 ± 0.04; $P < 0.002$). In conclusion, providing hay before weaning resulted in increased weight gain, rumen weight and rumen pH in calves fed high volumes of milk.

Key Words: solid feed, forage, weaning

T345 Influence of milk replacer feeding program on pre- and post-weaning performance and health of dairy calves. D. Carlson*[1], B. Ziegler[2], D. Schimek[2], M. Raeth-Knight[3], G. Golombeski[3], J. Linn[3], D. Ziegler[4], and H. Chester-Jones[4], [1]*Milk Products LLC*, *Chilton, WI*, [2]*Hubbard Feeds, Inc.*, *Mankato, MN*, [3]*University of Minnesota*, *St. Paul*, [4]*University of Minnesota, Southern Research and Outreach Center*, *Waseca*.

Holstein heifer calves (n = 100, 2–4 d of age) were assigned randomly to 1 of 4 milk replacer (MR) programs to evaluate the effect of MR feeding rate and crude protein (CP) intake on calf performance and health during pre- (d 1–42) and post-weaning (d 43–56) periods. Treatments (TRT) were: 1) 20% CP, 20% fat MR fed at 0.57 kg/d (as-fed powder weight) from d 1–35 and 0.28 kg/d from d 36–42 (CON); 2) 20% CP, 20% fat MR fed at 0.68 kg/d from d 1–14, 0.45 kg/d from d 15–35, and 0.23 kg/d from d 36–42 (TRT 2); 3) 24% CP, 18% fat MR fed at 0.68 kg/d from d 1–14, 20% CP, 20% fat MR fed at 0.45 kg/d from d 15–35 and 0.23 kg/d from d 36–42 (TRT 3), and 4) 28% CP, 16% fat MR fed at 0.68 kg/d from d 1–14, 20% CP, 20% fat MR fed at 0.45 kg/d from d 15–35 and 0.23 kg/d from d 36–42 (TRT 4). Calves were fed MR twice daily from d 1–35, and once daily from d 36–42. Calves were housed in individual calf pens within a naturally ventilated barn with curtain sidewalls, were fed a texturized calf starter (18% CP), and had access to fresh water. Average daily gain (ADG) during d 1–14 was greater ($P < 0.05$) for TRT 2, 3, and 4 versus CON, and TRT 4 had greater ($P < 0.05$) ADG than TRT 2 and 3. For d 15–28, ADG was lower ($P < 0.05$) for TRT 2, 3, and 4 compared with CON. Milk replacer feeding program did not affect ADG from d 29–56, 1–42, or 1–56. Calf starter intake was similar for d 1–14, whereas TRT 4 had greater ($P < 0.05$) starter intake than CON with TRT 2 and 3 being intermediate for d 15–28. For d 29–42, TRT 3 and 4 had greater ($P < 0.05$) starter intake than CON with TRT 2 intermediate. Health parameters did not differ among groups. Under the conditions of this study, increasing MR feeding rate and feeding 28% CP MR resulted in greater ADG from d 1–14, but reducing MR feeding rate and CP intake on d 14 resulted in depressed ADG from d 15–28.

Key Words: calves, milk replacer, feeding rate

T346 The effect of feeding dairy heifers diets with and without supplemental phosphorus for 18 months on growth, reproductive efficiency and lactation performance. D. W. Bjelland*[1], N. M. Esser[1], K. A. Weigel[1], P. C. Hoffman[1], and W. K. Coblentz[2], [1]*University of Wisconsin*, *Madison,* [2]*USDA-ARS Dairy Forage Research Center, Marshfield, WI.*

The phosphorous (P) requirements for dairy heifers (0.20–0.35%) and endogenous levels (0.20–35%) of P in feeds fed to dairy heifers are similar, suggesting that the need for supplemental P in dairy heifer diets may be minimal. Because long-term studies are unavailable, 183 Holstein heifers and 182 backcross Holstein × Jersey heifers were fed diets with (SP = 0.38% of dry matter (DM)) and without (NP = 0.28% of DM) supplemental phosphorus from 4 to 22 mo of age in a replicated pen design. Heifers were evaluated for body weight (BW), external bone/frame growth, dystocia, calf BW, reproductive efficiency, and first lactation performance. Data were analyzed using a mixed model with effects of season of birth, age of dam, pen number as a heifer, sire, sire birth year, and days in milk. No breed × diet interactions were observed. Heifers fed NP had similar average daily gain from 170 to 410 (0.86 vs. 0.83 kg/d) and 410–650 (0.85 vs. 0.86 kg/d) d of age as compared with heifers fed SP. At 22 mo of age, heifers fed NP were wider at the hip but did not differ in BW, hip height, body length, heart girth, cannon bone circumference or pelvic area as compared with heifers fed SP. As heifers, services per conception (1.45 vs. 1.39), age at pregnancy (451 vs. 452 d), and age at first calving (726 vs. 727 d) were not different between heifers fed NP or SP. At parturition, heifers fed NP or SP had similar dystocia scores and calves were similar in BW. Complete first

lactation data (305 d) were available for 333 primiparous cows, and cows fed NP as heifers produced similar milk (8702 vs. 8714 kg), fat (330 vs. 328 kg) and protein (274 vs. 277 kg) as cows fed SP as heifers. Days open (152 vs. 160 d), days in milk at first breeding (76 vs. 76 d), and services per conception (1.82 vs. 1.85) were also similar for primiparous cows fed NP or SP as heifers. Data suggest there was no growth, reproductive or lactation benefit to feeding dairy heifers diets containing 0.38% P as compared with 0.28% P.

Key Words: dairy heifers, phosphorous, lactation performance

T347 The effect of *Megasphaera elsdenii* NCIMB 41125 (Me) on performance of pre-weaned dairy calves. F. M. Hagg*[1], C. M. Muya[2], and P. H. Henning[1], [1]*MS Biotech*, *Centurion, South Africa*, [2]*ARC-Irene*, *Centurion, South Africa*.

Dairy farmers often aim to wean calves as early as possible. They are usually weaned upon reaching a target starter diet intake, so that rapid increase in feed intake becomes an important attribute. Field observations suggest that dosing pre-weaned calves with Me, as a DFM, has a positive effect on their well-being and performance. The objective of this study was to determine if dosing calves with Me could reduce weaning time by increasing the rate at which intake of dry feed increases in pre-weaned calves. Forty pre-weaned Holstein dairy calves entered the trial 14 d after birth, as they became available. The first calf was randomly allocated to one of the 2 treatments and all subsequent calves were alternately allocated to one or the other treatment. Me-treated calves received a single oral dose of Me (50 mL, 10^8 cfu/mL) on d 14. Control calves received no Me but were treated similar in all other respects. Commercial calf starter (18% CP) was fed ad lib while milk supply was restricted. Water was supplied ad lib. Feed, water and milk intake were measured daily while calves were weighed once per week. Calves were weaned upon reaching a DMI of 1.0 kg/d. Four additional calves, 2 each for treatment and control, and handled similar to the others, were slaughtered 72 h after dosing for rumen and colon samples to measure Me using Q-PCR. Me-treated calves had a greater ($P = 0.11$) rate of increase in DMI (37.0 vs. 28.6 g/d) and greater ($P = 0.02$) water intake (3.2 vs. 2.4 kg/d). Milk intake (3.46 and 3.51 kg/d) and ADG (480 and 437 g/d), for Me and control respectively, did not differ ($P = 0.63$ and $P = 0.44$) significantly. Me treatment decreased ($P = 0.21$) the number of days from birth to weaning (40 d vs. 44 d) and Me-treated calves had 67% less mortalities than the untreated calves. Me-treated calves had greater Me levels than controls in both rumen (1.4×10^9 vs. 1.6×10^6 genomes/mL) and colon (1.4×10^7 vs. $<1 \times 10^3$ genomes/mL). These results suggest that dosing calves with *Megasphaera elsdenii* NCIMB 41125 establish the organism in the GIT and may benefit calves through increased DMI and earlier weaning.

Key Words: *Megasphaera elsdenii*, dairy calves, early weaning

T348 Influence of nonmedicated additives as alternatives to antibiotics on calf health, growth, and intestinal development. S. I. Kehoe*[1], D. B. Carlson[2], and E. O. Hardwick[1], [1]*University of Wisconsin-River Falls*, *River Falls,* [2]*Milk Products, Inc., Chilton, WI.*

Many producers use medicated milk replacers to prevent scours in dairy calves, however, a commonly added level of neomycin and oxytetracycline is no longer approved. The objective of this trial was to determine whether a milk replacer with a blend of nonmedicated additives would have similar benefits to a milk replacer with added neomycin and oxytetracycline. Twelve bull calves were purchased from a local farm 3 separate times and were fed one of 3 treatments for a 5 week period. All treatments used a 20% fat, 20% crude protein milk replacer with either no additives (C), a blend of nonmedicated additives (NM; animal plasma, yeast cell wall extracts, inulin, and a direct-fed microbial), or neomycin and oxytetracycline (MED; 400 g/ton of neomycin; 200 g/ton of oxytetracycline). Two calves from each treatment were slaughtered during their second day of scouring and intestinal tissues were collected for morphological analyses. The surviving calves were fed until 3 weeks of age when they were moved to indoor individual pens and grain starter was offered. Weekly growth parameters were recorded and blood was analyzed for blood urea nitrogen (BUN) and glucose concentrations. Results indicate there were no significant differences between treatments for BUN, glucose, and serum protein. Feed intake was also not significant (C 652.4g, NM 759.4g, MED 687.5 g) however, hematocrits were highest for C compared with NM and MED (65.9 vs. 57.5 and 56.3%, respectively; $P < 0.005$). Fecal scores were significantly higher for C than NM and MED (1.9 vs. 1.5 and 1.5, for C, NM and MED, respectively). Intestinal weights and lengths were not significant except for colon weight which was lower for NM than for MED or C ($P < 0.02$). Although not statistically analyzed, fecal results indicate C had the highest density of *E. coli*. Growth parameters were also not significant; however, heart girth was lower in C compared with NM and MED (32.7 vs. 33.1 and 33.5, respectively; $P < 0.005$). These results indicate that nonmedicated additives may have some effect in reducing diarrhea and dehydration, and promoting some growth.

Key Words: calves, milk replacer, health

T349 Pre- and post weaning performance and health of calves fed milk replacers and calf starters with or without yeast supplementation (Nupro) and growth performance from 9 to 25 weeks of age. H. Chester-Jones*[1], J. Tricarico[2], D. Ziegler[1], K. Dawson[2], P. Groenewegen[2], M. Raeth-Knight[3], and G. Golombeski[3], [1]*University of Minnesota Southern Research and Outreach Center*, *Waseca,* [2]*Alltech Inc., Nicholasville, KY,*[3]*University of Minnesota Southern Research and Outreach Center, St. Paul.*

One hundred seven (2- to 4-d-old) individually housed Holstein heifer calves (39.1 ± 0.68kg) were randomly assigned to 1 of 4 treatments to evaluate the effect of supplementing natural yeast (NuPro; NP) in milk replacer (MR) and calf starter (CS) on performance and health pre- (d 1–42) and post-weaning (d 43–56). All calves were fed a 20:20 MR (CP:fat) containing 12.5% solids and an 18% CP starter. Nursery treatments were: 1) 0% NP in calf MR and CS (CON); 2) 5% NP in MR and 0% in CS (NPMR); 3) 0% NP in MR and 2.5% NP in CS (NPCS); and, 4) 5% NP in MR and 2.5% NP in CS (NPMRCS). Milk replacers for all treatments was fed at 0.57 kg/d (as-fed powder weight) twice daily from d 1 to 35 and at 0.28 kg/d 1X daily from d 36 to 42. Calf growth up to 25 wk of age was also monitored in all calves receiving the above nursery treatments when they were housed in group pens (7 calves/pen) and fed a common grower diet from 9 to 25 weeks of age. Pre-weaning ADG tended to be higher ($P = 0.08$) for CON calves than those fed the other treatments. Post weaning gain was lowest for NPMR and NPMRCS calves ($P < 0.05$). Overall 56 d ADG was highest for CON calves ($P < 0.05$). There were no pre- weaning and overall 56 d differences in CS and total DMI. Pre-weaning feed/gain (FG) was higher for NPMR vs. NPMRCS calves ($P = 0.04$). Post weaning FG was lower ($P < 0.05$) for CON and NPMR vs. NPCS calves. There were no differences in pre-weaning scouring days across treatments. There were no effects of nursery feeding programs on calf growth when fed a common diet from 9 to 25 wk of age. Under the conditions of this study supplementing nursery programs with a natural yeast supplement did not enhance individual or group fed heifer calf performance.

Key Words: calf performance, feeds, yeast supplementation

T350 Pre- and post weaning performance and health of calves fed milk replacers and calf starters with or without essential oils. H. Chester-Jones*[1], T. Steiner[2], M. Watkins[3], D. Taylor[3], D. Ziegler[1], M. Raeth-Knight[4], and G. Golombeski[4], [1]*University of Minnesota, Southern Research and Outreach Center*, *Waseca*, [2]*BIOMIN Holding GmbH*, *Herzogenburg, Austria*, [3]*BIOMIN America Inc.*, *San Antonio, TX*, [4]*University of Minnesota*, *St. Paul*.

One-hundred thirty (2- to 4-d-old) individually fed Holstein heifer calves (40 ± 0.73 kg BW) were randomly assigned to 1 of 5 treatments to evaluate the effect of supplementing essential oils (Biomin P.E.P.) in milk replacer (MR) and calf starter (CS) on performance and health pre-(d 1–42) and post-weaning (d 43–56). Treatments were: 1) Medicated MR and a 18% CP (as-fed) texturized calf starter with rumensin (0.033 mg/kg; CON); 2) Non-medicated MR and CS with no additives (NM); 3) Non-medicated MR with PEP (0.88 g/kg) and CS with no additives (NMPEP); 4) Non-medicated MR and CS with PEP (0.41 g/kg; CSPEP); and 5) Non-medicated MR and CS with PEP (MRCSPEP). A 20:20 (CP:fat) milk replacer containing 12.5% solids, was fed at 0.57 kg/d (as-fed powder weight) twice daily from d 1 to 35 and at 0.28 kg/d 1X daily from d 36 to 42. Pre-weaning ADG was higher ($P < 0.05$) for CON and NMPEP calves vs. those fed NM and MRCSPEP. Post weaning ADG was higher ($P < 0.05$) for CSPEP vs. CON and NM calves. Overall ADG was lower ($P = 0.02$) for NM calves vs. NMPEP, CSPEP and MRCSPEP calves. Calves fed NMPEP had higher ($P = 0.04$) overall ADG than MRCSPEP calves. Total calf starter and DMI for NMPEP calves tended to be higher vs. those fed NM ($P < 0.07$) and MRCSPEP ($P < 0.09$). There were no treatment differences in total DMI. Pre-weaning feed/gain (FG) was lowest for CON and NMPEP vs. other treatments. Post weaning FG was similar ($P > 0.05$) across all treatments. There were no treatment differences in scouring days or health costs. In this study, feeding a non-medicated MR with PEP and a CS without additives resulted in similar calf performances compared with a medicated MR and CS with rumensin. There were no benefits of offering non-medicated MR without PEP and CS with PEP or a combination of non-medicated MR and CS with PEP.

Key Words: calf performance, milk replacer, calf starter

T351 Pre- and post weaning performance and health of calves fed texturized calf starters with different levels of monensin and affect on growth from 9 to 25 weeks of age. H. Chester-Jones*[1], B. Ziegler[2], D. Schimek[2], D. Ziegler[1], M. Raeth-Knight[3], G. Golombeski[3], and J. Linn[3], [1]*University of Minnesota Southern Research and Outreach Center*, *Waseca*, [2]*Hubbard Feeds Inc.*, *Mankato, MN*, [3]*University of Minnesota Southern Research and Outreach Center*, *St. Paul*.

One-hundred twenty three (2- to 4-d-old) individually fed Holstein heifer calves (40.3 ± 0.77kg) were randomly assigned to1 of 4 treatments to evaluate pre- (d 1–42) and post weaning (d 43–56) calf performance and health when fed 18% CP (as-fed) texturized calf starters (CS) with varying monensin levels. All calves in the nursery were fed a medicated 20% fat:20% protein milk replacer at 0.284 kg in 1.99 L water (12.5% solids) 2X daily for the first 35 d and 1X daily from d 36 to weaning at 42 d. Calf starters were fed free choice from d 1 and calves had access to fresh water. The formulated CS monensin treatment levels were 1), none; 2), 33 mg/kg; 3), 49.5 mg/kg; and, 4) 66 mg/kg. Monensin level did not affect ($P > 0.05$) pre- and post weaning ADG which averaged 0.69 kg/d for 56 d. Overall starter intake decreased linearly ($P = 0.02$) with increasing dietary monensin. Feed/gain was similar ($P < 0.05$) across CS fed (average 1.9 kg/kg gain). There were no health differences across treatments. Calves were transitioned to grower pens (7 heifers/pen) and performance was monitored from 9 to 25 wk of age. Calves were limit-fed a common 16% CP grain mix containing monensin (42.9 mg/kg d1–84, and 71 mg/kg d 85–112) fed at 2.72 kg for 56 d then 2.27 kg for an additional 56 d with free choice hay. Overall 112 d ADG in the grower period linearly increased ($P = 0.06$) for calves fed increasing monensin levels in the nursery. Under the conditions of this study increasing monensin levels in the CS during the nursery phase did not affect daily gain but starter intake decreased. Calves fed increasing levels of monensin in the nursery tended to show performance compensation when fed a common diet in group pens.

Key Words: calf performance, calf starters, monensin levels

T352 Effect on feed sorting of adding plain or flavored water to a TMR for heifers. A. Mereu[1], A. Puddu[2], I. R. Ipharraguerre*[1], and A. Bach[2,3], [1]*Lucta SA*, *Barcelona, Spain*, [2]*IRTA-Ruminant Production*, *Caldes de Montbui, Spain*, [3]*ICREA*, *Barcelona, Spain*.

The impact on feed sorting of adding plain or flavored water to a TMR was evaluated using 24 Holstein heifers (315 ± 24 kg of BW) in a replicated 3 × 3 Latin square design with 14-d periods. Once daily, heifers were fed individually for ad libitum intake a TMR (16.5% CP, 33.8% NDF) composed of 40% ryegrass hay and 60% concentrate. Treatments resulted from the addition of plain (WET; 55.8% DM) or flavored water (FLAV; 53.7% DM) to the ryegrass hay of a control diet (DRY; 90.2% DM). A flavor combined with a sweetener (Luctarom SFS-R) was mixed with tap water and applied to the hay at 250 g/ton of diet. Dietary particle size distribution was measured with the Penn State Particle Separator determining 4 fractions (long, medium, short and fine) at 0, 6, 12 and 24 h after feeding during the last 2 d of each period. Data were analyzed using a mixed model with animal (period) treated as random variable and treatment, period and their interaction treated as fixed effects. There were no significant differences on DMI. Both ADG and G:F were numerically greater for FLAV (1.41 kg/d and 0.18, respectively) when compared with WET (1.19 kg/d and 0.15, respectively) and DRY (1.34 kg/d and 0.17, respectively). Six hours after feeding, FLAV heifers reduced ($P < 0.05$) the preferential consumption of fine particles (<1.18 mm) compared with DRY and WET. At 24 h post-feeding, heifers in the DRY group consumed proportionally less ($P < 0.05$) long particles (>19 mm) and tended ($P < 0.15$) to consume a larger proportion of fine particles when compared with those receiving the WET and FLAV rations. Findings from this study indicate that plain or flavored water addition to the TMR can contribute to limit the sorting of long particles by heifers. Furthermore, flavor addition can enhance hay palatability and thereby minimize the preferential consumption of fine particles within the first 6 h post-feeding.

Key Words: sorting, palatability, flavor

T353 Effect of including corn distillers dried grains in calf feeds. F. X. Suarez-Mena*[1], A. J. Heinrichs[1], T. M. Hill[2], H. G. Bateman II[2], J. M. Aldrich[2], and R. L. Schlotterbeck[2], [1]*The Pennsylvania State University*, *University Park*, [2]*Nurture Calf Research, Provimi North America*, *Lewisburg, OH*.

A series of 5 trials were conducted to determine the effect of distillers dried grains with solubles (DG) in calf diets. Trial 1 compared 0 and 49% DG in 18% CP starters (as-fed basis) fed to calves initially 2 to 3 d old for 56 d. Digestibility was estimated during d 52 to 56 using chromic oxide. Trial 2 compared 0 and 39% DG in 16% CP growers fed to calves from 8 to 12 wk of age from 28 d. Trial 3 compared 0, 10, and 20% DG in 18% CP starters fed to calves initially 2 to 3 d old for 56 d. Trial 4 compared 0 and 20% DG in 16% CP growers fed to calves from 8 to 12 wk of age from 28 d. As DG increased in all the

experiments, ADF, NDF, and fat increased and calculated metabolizable energy (ME) was similar but not equalized. In Trials 1 and 3, calves (48 calves/trial) housed in individual pens were fed a 26% CP, 17% fat milk replacer powder and weaned at 28 d. Trials 2 and 4 used calves (48 calves per trial) housed in group pens (6 calves/pen) that had been weaned from 28 d before the trials start. Trial 5 (18 calves) had same treatments as Trial 3, with calves killed at 35 d to determine DG effects on rumen development. All trials were completely randomized designs. Calf was the experimental unit (EU) in Trials 1, 3 and 5, and pen was the EU in Trials 2 and 4. In Trial 1, ADG was 6% greater and dry matter digestibility was 10% greater ($P < 0.05$) for calves 0% vs. 49% DG. In Trial 2, ADG (9%), feed efficiency (10%), and hip width change (19%) were greater ($P < 0.05$) for calves 0% vs. 39% DG. In Trial 3, performance measures did not differ among starter treatments. Calf ADG were numerically 4% greater ($P > 0.50$) in calves fed 0% vs. 10 or 20% DG. In Trial 4, ADG (4%), feed efficiency (5%), and hip width change (19%) were greater ($P < 0.05$) for calves fed 0% vs. 20% DG. Thus, these results suggest that high levels of distillers in calf starters and growers reduce calves growth.

Key Words: corn distillers dried grains with solubles, calf digestion, rumen development

T354 Determination of oro-sensorial preferences of protein ingredients in weaned calves. C. Montoro*[1], I. Ipharraguerre[2], and A. Bach[1,3], [1]*Ruminant Production, IRTA*, *Caldes de Montbui, Barcelona, Spain*, [2]*Lucta S.A.*, *Barcelona, Spain*, [3]*ICREA*, *Barcelona, Spain*.

The objective of this study was to determine oro-sensorial preferences among common protein feed ingredients used to manufacture calf starters. A total of 15 assays involving 160 calves were conducted to rank calf oro-sensorial preferences for wheat distillers dried grains (DDG), corn gluten meal (CGM), peas, rapeseed meal (RSM), soybean meal (SBM) and sunflower meal (SFM). To minimize the effect of feed texture, all ingredients were ground at 3 mm. In each assay, 20 naive calves were offered a choice ad libitum of 2 ingredients and feed consumption was monitored every 30 min for 6 h. Each group of calves was used in 2 different assays which were conducted 3 and 5 d after weaning. No calf was presented twice with the same ingredient. Oro-sensorial preferences were calculated as the mean difference in feed consumption every 30 min over a 6-h period. Feed preferences were determined using a mixed-effects model. The most preferred protein ingredients were soybean meal and DDG, whereas CGM was the least preferred. Soybean meal was the most preferred ingredient in all assays and consumption was clearly greater than for the others ingredients (Table 1). On the other hand, CGM was the least preferred ingredient in all assays. Results indicate that SBM and DDG should be the preferred protein sources and CGM should be avoided when formulating starters for calves.

Table 1. Ingredient (Ingr) dry matter intake (DMI) per assay (g/30 min)

Ingr 1	DMI 1	Ingr 2	DMI 2	P-value	Ingr 1	DMI 1	Ingr 2	DMI 2	P-value
DDG	67.77	CGM	11.54	<0.0001	CGM	5.71	PEA	78.02	<0.0001
DDG	53.73	PEA	40.90	0.138	CGM	2.06	SBM	159.38	<0.0001
DDG	4.06	SBM	157.17	<0.0001	CGM	2.08	RSM	20.33	<0.0001
DDG	59.04	SFM	29.13	<0.0001	CGM	3.21	SFM	145.08	<0.0001
DDG	49.60	RSM	13.98	<0.0001	PEA	2.31	SBM	63.08	<0.0001
RSM	1.83	SBM	93.04	<0.0001	PEA	8.10	RSM	10.06	0.570
RSM	1.90	SFM	29.08	<0.0001	PEA	12.79	SFM	15.19	0.703
SFM	26.08	SBM	150.50	<0.0001					

Key Words: palatability, preferences, intake

T355 Effect of dietary supplementation of exogenous polysaccharide-degrading enzymes on blood metabolites and rumen fermentation and nutrient digestibility for Holstein heifers. C. Y. Guo*, Q. Y. Diao, N. F. Zhang, and Y. Tu, *Chinese Academy of Agricultural Sciences*, *Beijing, China*.

The objective of this job was to investigate the effect of supplementation poly-saccharide-degrading enzymes (EPDE) to TMR diets on their blood metabolites and rumen fermentation and nutrient digestibility for 12 weeks to 24 week Holstein heifers. The treatments were as follows: control (no EPDE), EPDE sprayed onto and mixed with the daily ration (EF, 20.0 g/d). Feed samples were collected once weekly, feed refusals and fecal samples were collected twice weekly. Ruminal fluid was collected from rumen tube. Plasma was collected by centrifugation at 1800xg for 30 min and stored at −20°C until it was analyzed. We chose to measure serum total protein and plasma urea nitrogen (PUN) to evaluate protein metabolism and triglyceride concentrations as indices for fat metabolism. Data were analyzed using the general linear model ANOVA procedures of SAS. The results show that enzyme treatment increased the concentration of soluble reducing sugars ($P < 0.05$) and decreased NDF content ($P < 0.05$) in the treated feed. Compared with control, ruminal fermentation was affected by EF ($P < 0.05$), ruminal VFA patterns were changed. Ruminal carboxymethylcellulase (CMCase) and xylanase activities were not affected by treatment. In a digestion trial, heifers were fed EPDE 20g/heifers per day, and total faces were collected. Compared with control, enzyme treatment increased the apparent digestion of DM ($P < 0.05$), acid detergent fiber ($P < 0.05$). Crude protein in the diet tend to increase numerically. The results of evaluate lipid metabolism and protein metabolism showed that add EPDE to diet have no significant effect on PUN, total albumin, total cholesterol, triglyceride. But numerically, supplement of EPDE decreased total albumin and total cholesterol in plasma and increased the concentrate of blood glucose in plasma. In conclusion, adding EPDE to diets could improve feed nutrition digestibility, especially enhance NDF and ADF digestibility (DM basis), change ruminal fermentation, and have no effects on lipid metabolism and protein metabolism.

Key Words: exogenous enzymes, Holstein heifers, rumen fermentation

T356 Relationships between chewing behavior, digestibility and digesta kinetics parameters in calves fed restricted and ad libitum levels of oat hay. R. S. Dias[1], H. O. Patino[2], S. López[3], E. Prates[2], K. Swanson*[1], and J. France[1], [1]*University of Guelph*, *Guelph, Ontario, Canada*, [2]*Universidade Federal do Rio Grande do Sul*, *Porto Alegre, Rio Grande do Sul, Brazil*, [3]*IGM, CSIC-Universidad de León*, *León, Spain*.

The objective of this study was to elucidate relationships between chewing behavior, digestibility and digesta kinetics parameters in steers fed restricted and ad libitum levels of oat hay. Four male Herefords with an average initial weight of 136 kg were used in an experiment conducted as a Latin square with 4 treatments and 4 periods. Animals were fed 4 levels of oats hay DM (*Avena strigosa* L.) namely: 1.5, 2.0, 2.5% BW/day and ad libitum representing the treatments T1, T2, T3 and T4, respectively. Chewing behavior, digestibility, and digesta kinetics measurements were recorded. Most of the measured parameters were better related to OM intake scaled by metabolic weight. Rumination and eating chewing rate (chews/min/g OM/kg$^{0.75}$) decreased with increased OM intake whereas total chewing and total time spent on each chewing activity increased. Calculated total energy expended by chewing activity was 4.2, 4.4, 5.2 and 5.3%, of ME intake for T1, T2, T3 and T4 respectively. Digestibility of OM, DM, ADF, NDF, hemicellulose and

cellulose decreased with increased OM intake. Retention time (h) was strongly related to OM intake (g/kg$^{0.75}$/day) (r = – 0.85), OM digestibility (r = 0.84) and with ruminating (r = 0.81) and eating chewing rate (r = 0.80) highlighting the relationship between chewing behavior and the digestive process. Fractional outflow rate from the reticulo-rumen and that from the cecum-colon were positively related to total chews, indicating that decrease in particle size facilitates particle flow through the digestive tract. In conclusion, the results of this study show that animals fed a restricted diet altered their chewing behavior when eating and ruminating by increasing chewing rate (chews/min/g OM/BW$^{0.75}$), which was also related to retention time and digestibility.

Key Words: chewing behavior, digestibility, digesta kinetics

T357 Effect of different feeding regimens on growth performance and health of Sahiwal calves during pre-weaning period. S. A. Bhatti*[1], M. F. Ahmed[1], D. McGill[2], M. Sarwar[1], M. Afzal[3], E. Ullah[1], M. A. Khan[4], M. S. Khan[1], R. Bush[5], and H. M. Warriach[2], [1]*University of Agriculture*, *Faisalabad, Pakistan*, [2]*EH Graham Centre (NSW Industry and Investment and Charles Sturt University)*, *Wagga Wagga, Australia*, [3]*Pakistan Agricultural Research Council*, *Islamabad, Pakistan*, [4]*Livestock Production Research Institute*, *Bahadurnagar, Okara, Pakistan*, [5]*University of Sydney*, *Camden, Australia*.

The objective of the study was to examine the growth potential of Sahiwal calves using recommended feeding practices (milk/milk replacer with concentrates and forage) in a clean environment. For this purpose, Sahiwal calves (n = 48; 24 of each sex 3 ± 2 d of age born in January/February 2009) were maintained in raised individual pens until weaning at d 84. Four groups each of 12 animals (6 of each sex) were offered liquid feed as either whole cow′s milk or a commercial milk replacer (MR; reconstituted to specification; Sprayfo) to 10% of their body weight (traditional recommendation in Pakistan) from d 3 ± 2 and solid feed as either a starter ration (SR; prepared at the University CP = 20%, TDN = 72%) plus Berseem hay (H; Egyptian Clover; CP = 21% TDN = 63%) or H only ad libitum from d 7. The milk or MR was withdrawn gradually from d 56 until weaned completely by d 84 but not the solid feed. The data were analyzed using repeated measure analysis by MIXED procedures of SAS. Calves offered milk grew faster than those offered MR (357 ± 8 vs. 162 ± 8; $P < 0.05$) and displayed higher weaning weights (51.6 ± 0.7 vs. 35.2 ± 0.7; $P < 0.05$). Similarly calves offered SR plus H grew faster (311 ± 8 vs. 208 ± 8 g/d; $P < 0.05$) and developed higher weaning weights (48.7 ± 0.7 vs. 38.1 ± 0.7 kg; $P < 0.05$) than those fed H alone. Male calves offered milk plus SR and H showed the highest growth rate and weaning weights (459 ± 16 g/d and 62.9 ± 1.4 kg, respectively). The lowest growth rate and weaning weights were observed in female calves given MR and H only (108 ± 16 g/d and 28.6 ± 1.4 kg, respectively). Calves offered the MR showed a greater incidence of calf scours than those offered the milk (88 vs. 42%, respectively). The feeding of whole milk in combination with starter ration and hay resulted in superior growth rates, higher weaning weights, and healthier calves than the other feeding regimens.

Key Words: calf nutrition, milk replacer

T358 The effect of feeding different dilution levels of milk replacer to calves once or twice daily, with or without yeast culture. M. F. Ortega*, H. M. Rodriguez, and M. Vélez, *Zamorano University*, *El Zamorano, Honduras*.

Conventional feeding in the tropics for calves (2L of milk/milk replacer twice daily) was compared with a lower intake (3L once daily). Effects of live yeast culture (YC; YEA SACC ^{1026}, Alltech, Inc.) addition were investigated when added to these feeding strategies. A study was conducted using 40 male and female newborn calves assigned randomly to a 2 × 2 factorial design to determine the effects on growth in terms of average daily gain (ADG), and initial/final body weight (BW). The treatments consisted of 2 levels of milk replacer: 3 L once a day (3L) or 4 L split in 2 feedings daily (4L). The amount of milk replacer (20% CP and 15%Fat) as such was similar (450 g/d), but diluted in the 3L or 4L treatment with (Y) or without (NY) YC addition. Calves were weaned at 60 d. BW was measured every 30 d until they were 120 d. The statistical analysis of this experiment was performed using the MIXED procedure of SAS. 3L or 4L calves had similar initial body weight (37.37 and 37.42 ± 1.37 kg, respectively; $P = 0.98$), but calves assigned to the Y treatment were significant smaller than NY (34.03 and 40.76 ± 1.37 kg, respectively; $P < 0.01$). Final weights of animals at 120 d followed the same pattern as initial weight. ADG at 60 d of 3L was similar to 4L calves (0.37 and 0.39 ± 0.03 kg/d, respectively, $P = 0.50$), but Y calves had a lower ADG than NY (0.31 vs. 0.44 ± 0.03 kg/d; $P = 0.006$). There were no effects of milk replacer or YC addition on ADG at 120 d (0.44 ± 0.02 kg/d). These results suggests that there is no difference between the diluted levels of milk replacer (3L or 4L) on ADG when grain was offered ad libitum, and that YC-calves had a lower ADG at 60 d but similar ADG after 120 d.

Key Words: calves, milk replacer, yeast culture, average daily gain

T359 Utilization of yeast (*Saccharomyces cerevisiae*) in dairy calf diets. J. A. De Freitas*[1], M. S. Schoten[1], D. R. Fronchetti[1], A. F. Garcez Neto[1], and J. C. De Souza[2], [1]*University Federal of Parana*, *Palotina, Parana, Brazil*, [2]*University Federal of South Mato Grosso*, *Aquidauana, Mato Grosso do Sul, Brazil*.

There are few farms that give priority to calf rearing. Most of farms justify that the economic impact of investments in calf rearing does not provide significant profits. However, feed management practices that can improve animal performance, prevent enteric diseases (diarrhea) and reduce production costs are of great interest. Among the practices used in food nutrition, the inclusion of some substances (additives) in the diet may be responsible for improving digestibility, nutrient absorption and thus in the feed conversion. The aim of this study was to assess the influence of 3 levels of yeast (*Saccharomyces cerevisiae*) in the Holstein calves diet on the weaning weight (W60), weight gain from birth to weaning (WG), average daily gain from 0 to 60 d (ADG), concentrate feed conversion (CFC) and diarrhea incidence (ID). Twenty-one Holstein calves were randomly assigned to 3 treatments consisting of different levels of yeast in the diet (0, 5 and 10 g/animal/day). Immediately after birth, animals were separated from their mothers and transferred to individual pens where they received 5 L of colostrum for 3 d. After that period, the calves received 8 L of colostrum/day divided in 3 meals. The yeast was mixed with the milk of the first meal. From the 2nd week animals had ad libitum access to concentrate feed containing 18% crude protein and 75% TDN. The amount of concentrate ingested was controlled daily. The animals were weighed and had their height measured at birth and every 15 d (0, 15, 30, 45 and 60 d). The data were analyzed by PROC REG of SAS. It was found a quadratic effect of the treatments for WG (kg), ADG (kg) and CFC variables. The equations and their respective coefficient of determination were: WG = 394167 + 3.8178x - 0.3802x^2 ($r^2 = 0.25$), ADG = 0.6567 + 0.0642x - 0.006387x^2 ($r^2 = 0.55$) and CFC = 0.4317 + 0.0482x + 0.0046x^2 ($r^2 = 0.55$). The addition of yeast culture in the calf diet improved feed conversion into increased growth.

Key Words: additives, ruminant nutrition, nutrition efficiency

T360 The effects of feeding fermented soybean meal in calf starter on growth and performance of dairy calves. T. L. Wolfswinkel*[1], H. D. Tyler[1], J. E. Cunnick[1], T. Waugh[2], J. Sewell[2], and A. Chestnut[3], [1]*Iowa State University*, *Ames,* [2]*Nutra-Flo Protein and Biotech Products, Sioux City, IA,* [3]*Vigortone Ag Products, Brookville, OH.*

The use of soybean meal in animal diets is primarily limited to adult animals due to the inefficient digestibility of soy proteins by young animals and the susceptibility of young animals to antinutritional compounds in soybeans that are either not properly processed or undercooked. The objective of this study was to evaluate the suitability of fermented soybean meal for use in dairy calf starter diets in place of soybean meal. The experiment was conducted using 66 dairy bull calves that were randomly assigned to either the control diet, containing soybean meal (SBM) as the primary source of protein in the starter diet, or the treatment diet, containing fermented soybean meal (FSBM) in place of soybean meal as the primary source of protein in the starter diet. Measured parameters included weekly weight gains, total weight gained, attitude, appetite, fecal scores, and immunological parameters that included mitogen proliferation, CD4, CD8, CD45RO, and B-cell counts which were measured by flow cytometry. None of the measured growth and health parameters were significantly different between the calves on the control and treatment diets. Weaning age was older for calves on the fermented soybean meal in comparison to the soybean meal based starter diet ($P = 0.0422$). Immunological data showed no differences in the development and responsiveness of the immune system between groups of calves receiving different treatments. This data suggests that growth and performance of calves fed fermented soybean meal based starter diets are similar to those fed soybean meal based diets.

Key Words: fermented soybean meal, calves, immune system development

T361 In vitro methane production from increasing levels of corn- or wheat-based dried distillers grains with solubles. M. Hünerberg*[1], L. Holtshausen[2], T. A. McAllister[2], K. A. Beauchemin[2], and E. Okine[1], [1]*University of Alberta*, *Edmonton, AB, Canada*, [2]*Agriculture and Agri-Food Canada*, *Lethbridge, AB, Canada*.

Increasing dietary fat levels have shown to depress ruminal methane (CH_4) production, but the reduction may depend upon the dietary forage to concentrate ratio. The objective of this study was to compare in vitro CH_4 production from wheat- or corn-based dried distillers grains with solubles (WDDGS, CDDGS). The WDDGS (4.9% crude fat) and CDDGS (11.5% crude fat) replaced barley silage as substrate at levels of 0, 20, 40, 60 or 100% (DM basis). Each treatment, dried and ground through a 1-mm screen, was incubated (n = 5) in Ankom bags in 125-mL sealed batch culture flasks (0.3 g substrate + 40 mL of anaerobic medium and 10 mL of inoculum). The inoculum was obtained from cows fed a high forage (65% of diet DM) diet. Gas pressures arising from substrate fermentation were measured at 3, 6, 12 and 24 h post inoculation. Pressure values, corrected for gas released from 3 negative controls (no substrate) were used to generate volume estimates. Gas samples collected at the same 4 time points were analyzed for CH_4 concentration. Disappearance of DM and VFA concentration in incubation liquid were measured at 24 h. Production of CH_4 increased linearly (r^2 = 0.98) for CDDGS from 15.2 to 33.3 mL CH_4/g of DM loss at 20 and 100% DDGS, respectively. Production of CH_4 was greater ($P < 0.01$) for WDDGS (averaging 32.6 ± 0.3 mL/g DM loss) than for CDDGS at 20, 40 and 60% of inclusion rates. The percentages of propionate in fluid were greater ($P < 0.01$) for CDDG (22.3, 21.3 and 20.3% of total VFA) than for WDDGS (19.4, 19.4 and 19.5% of total VFA) at 20, 40 and 60% of inclusion. The results suggest: (i) in vitro CH_4 production as per unit of DM loss is lower at lower DDGS inclusion rates (ii) including CDDGS, most likely as response to its higher fat content, produced less CH_4 per unit of DM loss then including WDDG at up to 60% of dietary DM.

Key Words: methane, dried distillers grains with solubles, in vitro

T362 The impact of DDGS on presence of ruminal bacteria, ruminal protozoa and yeast during in vitro fermentation. E. Castillo-Lopez*, J. L. Miner, and P. J. Kononoff, *University of Nebraska-Lincoln*, *Lincoln*.

Changes in ruminal microbial populations is of interest because of their role in feed degradation and metabolizable protein supply to the animal. The objective of this experiment was to evaluate the effect of dried distillers grains and solubles (DDGS) on presence of ruminal bacteria, protozoa and yeast during in vitro fermentation. Treatments were, CONTROL (50% grass hay and 50% rolled-corn), LOW DDGS (33% grass hay, 33% rolled-corn and 33% DDGS) and HIGH DDGS (100% DDGS). Substrates were incubated in rumen inoculum and replicated 3 times. At 0 and 48h fermentation a pellet was isolated from each sample, then bacterial, protozoal and yeast crude protein was estimated by real-time PCR. To do so, microbial markers were designed from the 16S rRNA, 18S rRNA and the second chromosome; for bacteria, protozoa and yeast. Data were analyzed as a 3 × 2 factorial design to test the effects of 3 treatments, 2 time points and interaction between treatment and time. Treatment did not ($P = 0.31$) affect the estimates of bacterial crude protein and averaged 206, 200 and 171 (SEM = 16.08) mg/g DM for the CONTROL, LOW DDGS and HIGH DDGS. However, treatment affected ($P < 0.05$) the estimate of protozoal crude protein and averaged 46, 27 and 6 (SEM = 3.74) mg/g DM for the CONTROL, LOW DDGS and HIGH DDGS. In addition, treatment did not affect ($P = 0.25$) the estimate of yeast crude protein and averaged 0.05, 0.09 and 0.19 (SEM = 0.06) mg/kg DM for the CONTROL, LOW DDGS and HIGH DDGS. Fermentation time did not affect ($P = 0.66$) the estimates of bacterial crude protein and were 197 and 189 (SEM = 12.38) mg/g DM at 0 and 48h. However, time affected ($P < 0.05$) the estimates of protozoal crude protein and were 14 and 39 (SEM = 3.14) mg/g DM at 0 and 48h and the interaction of treatment by time was significant ($P < 0.05$). Furthermore, time did not affect ($P = 0.66$) the estimates of yeast crude protein and were 0.09 and 0.12 (SEM = 0.04) mg/kg DM at 0 and 48h. With real-time PCR, it was possible to estimate the variation of ruminal bacterial, protozoal and yeast crude protein. Level of DDGS may affect the in vitro microbial growth.

Key Words: bacteria, protozoa, real-time PCR, yeast

T363 Effects of low dose of *Saccharomyces cerevisiae* on metabolism by ruminal microbes in dual flow continuous culture fermenters. M. Ruiz-Moreno*[1], M. D. Stern[1], and J. Sullivan[2], [1]*University of Minnesota*, *St Paul,* [2]*Lallemand Animal Nutrition - North America, Milwaukee, WI.*

Effects of *Saccharomyces cerevisiae* (SC) on rumen fermentation were evaluated using a dual flow continuous culture system. Eight fermenters were inoculated with ruminal fluid from a dairy cow in early lactation on d 1 of a 10-d experimental period. Fermenters were provided with 75 g of DM/d of a pelleted diet formulated for a high lactating dairy cow (40 kg milk/d, 3.8% fat, 3.7% protein). Two levels of SC (Levucell, SC20, Lallemand) at 0 or 2 mg/fermenter/day (SC0 and SC2, respectively) were infused twice a day at 0900 and 2100 h to the fermenters in a completely randomized arrangement of treatments. The latter concentration would be equivalent to supplementing 0.5 g/d of SC to a dairy cow. Apparent and true organic matter degradability were not affected ($P > 0.05$) by SC averaging 55.6 vs. 56.0 and 65.5 vs. 64.7% for SC0 and SC2, respectively. Similarly, no differences were obtained ($P > 0.05$) in NDF and ADF digestibility (51.1 vs. 49.4% and 50.3 vs. 48.1% for SC0 and SC2, respectively). Total VFA concentrations were not affected ($P > 0.05$) by treatments (140.2 and 140.8 m*M* for SC0 and SC2, respectively). There was a trend ($P < 0.1$) for a higher branched chain VFA (isobutyrate, isovalerate and 2-methylbutyrate) concentration in SC0 compared with SC2 (2.34 vs. 1.82 m*M*, respectively). The addition of SC resulted in a lower ($P < 0.05$) NH_3-N concentration and NH_3-N flow (6.28 vs. 3.85 mg/100 mL and 0.19 vs. 0.12 g/d for SC0 and SC2, respectively), without affecting ($P > 0.05$) CP degradation and efficiency of microbial protein synthesis (35.7 vs. 29% and 29.1 vs. 25.8 g of N/kg OM truly digested for SC0 and SC2, respectively). Average and minimum pH of fermenters did not differ between treatments ($P > 0.05$) but a trend ($P < 0.1$) for a lower maximum pH was obtained at 5.78 vs. 5.71 for SC0 and SC2, respectively. A low dose of SC may benefit NH_3-N metabolism, without having any negative effects on in vitro rumen fermentation.

Key Words: *Saccharomyces cerevisiae*, rumen, continuous fermenters

T364 Effects of copper and zinc on in vitro ruminal fermentation of total mixed ration using goat inoculum. J. F. Vázquez-Armijo[1], R. Rojo*[1], D. López[1], A. Z. M. Salem[1], and J. M. González-Alvarado[2],

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One in vitro experiment was conducted to examine the effects of supplemental copper (Cu) and zinc (Zn) on ruminal parameters, in vitro dry matter degradability (IVDMD), gas production (GP) and metabolizable energy (ME) (MJ kg^{-1} DM). Total mixed ration was incubated in vitro for 96 h with 4 different supplemental treatments (Control, Cu (860 ppm), Zn (224 ppm), Cu-Zn (860–224 ppm)) provided as mineral premixed. Added Zn increased fraction B (ml g^{-1} DM), but added Zn-Cu treatment decreased fraction B. Supplemental treatments did not alter the initial delay before gas production begins (L) and IVDMD (g^{-1} DM). Added Cu tended to increase the amount of GP (ml g^{-1} DM) at 24, 48 and 96 h (GP_{24}, GP_{48}, and GP_{96}, respectively) of incubation. Cu treatment was the highest value for the fraction the rate of gas production (K) and ME, while Zn was the lowest values. In conclusion, the addition of Cu to in vitro ruminal fermentation was found to increase gas production volume and efficient use of energy.

Table 1. In vitro ruminal fermentation parameters of total mixed ration with different supplemental treatments

Parameters	Control	Zn	Cu	Zn-Cu	SEM	P-value
B	273.57^{bc}	334.90^{a}	288.80^{b}	241.63^{c}	10.78	0.004
K	0.014^{c}	0.008^{d}	0.037^{a}	0.019^{b}	0.003	<0.001
L	0.87	1.32	1.78	0.68	0.19	0.153
GP_{24}	69.35^{c}	58.51^{c}	169.39^{a}	90.72^{b}	13.22	<0.001
GP_{48}	140.68^{bc}	114.03^{c}	237.07^{a}	153.22^{b}	14.11	<0.001
GP_{96}	202.61^{b}	182.96^{b}	291.02^{a}	210.02^{b}	12.84	<0.001
IVDMD	724.30	714.16	707.07	703.33	4.09	0.309
ME	15.14^{c}	14.40^{c}	21.94^{a}	16.59^{b}	0.90	<0.001

Different superscripts in the same row differ (P<0.05).

Key Words: gas production, minerals, goats

T365 Effects of high rates of extruded flaxseed fed to dairy cows on n-3 fatty acids enrichment in milk-fat and the interaction with milk fat content and yield. U. Moallem*[1], M. Zachut[1,2], H. Lehrer[1], L. Livshitz[1], and A. Arieli[2], [1]*Agriculture Research Organization*, *Bet Dagan, Israel*, [2]*Faculty of Agriculture, Hebrew University*, *Rehovot, Israel*.

The objectives were to examine the effects of high rates of dietary extruded flaxseed (EF) containing high proportion of C18:3n-3 on fatty acids (FAs) composition in milk fat, and the interaction with milk fat content and yield. Multiparous Israeli-Holstein dry cows (256 d pregnant) were assigned to 2 treatments: (i) control (n = 22) were fed a dry cow diet and postpartum (PP) lactating cow diet, and (ii) EF (n = 22) supplemented prepartum with 1 kg/d per cow of EF providing 141 g/d of C18:3n-3, and PP to 100 d in milk a diet consisted of 9.2% EF providing on average 382 g/d of C18:3n-3. Milk solids content was determined from 3 consecutive milkings every 2 weeks. Composition of FAs in milk fat was determined in 50 milk samples (24 controls and 26 EF). Milk production was 6.4% higher and fat percentage was 0.4% units lower in the EF group than in the control, with no differences in fat yields. Content and yield of C18:3n-3 in milk fat was 5.1 and 4.6 times higher in the EF group than in controls, respectively. However, the content of C18:3n-3 in milk fat reached a maximum of ≈2% and increasing the dietary supply of C18:3n-3 did not benefit to enrich milk fat. Within group test revealed that the content of C18:3n-3 in milk fat in the EF group was negatively correlated with milk fat percentage (r = –0.91) and yield (r = –0.89). However, no decrease in de novo synthesis of less than 16 carbons FAs was found in the EF group, whereas C16:0 yield were markedly decreased. Moreover, C16:0 yield in the EF cows was negatively correlated with 18:3n-3 content (r = –0.91) and yield (r = –0.65) in milk fat. It appears that the enrichment of 18:3n-3 in milk fat is limited to ≈2%, and it is negatively correlated with milk fat content and yield. It might also be speculated that C18:3n-3 itself suppresses de novo synthesis of C16:0, but not lower chain FAs, which reduced the overall milk fat content in milk.

Key Words: omega-3, milk fat

T366 Effect of grain source and milling process in ethanol production on nutrient contents and in vitro digestibility of ethanol by-product. W. Z. Yang*[1], T. A. McAllister[1], J. J. Mckinnon[2], K. A. Beauchemin[1], and D. Gibb[1], [1]*Agriculture and Agri-Food Canada, Research Centre*, *Lethbridge, AB, Canada*, [2]*Department of Animal and Poultry Science, University of Saskatchewan*, *Saskatoon, SK, Canada*.

Dried distiller grains with solubles (DDGS) can be derived from ethanol fermentation of varying with type of grains (e.g., corn, wheat, or blend of the 2) or milling process (traditional and fractional). Traditional DDGS contain the residual components (bran, protein, germ, and minerals) of the grain after the majority of the starch has been fermented, whereas, fractional DDGS contain no residual bran and germ which are removed before fermentation. The objective of this study was to compare the nutrient content and in vitro digestibility of different DDGS. Sixty DDGS samples varying grain source and milling process were collected from different ethanol plants in Canada and in US. The DDGS samples were determined for the contents of CP, NDF and fat, and were incubated in a batch culture for 0, 4, 8, 14, 24 and 48 h to measure gas production and DM digestion (DMD). The CP content (% DM) was different ($P < 0.01$) with the highest (51.8) for fractional corn DDGS, medium for wheat (37.9) and blend DDGS (35.9), and the lowest for corn DDGS (30.6). The NDF content (% DM) was lower ($P < 0.01$) for fractional DDGS (24.5), but the fat content (% DM) was higher ($P < 0.01$) for corn DDGS (10.1) than for other DDGS (mean ± SD; NDF, 32.0 ± 1.4; fat, 4.3 ± 0.4). DMD linearly ($P < 0.01$) increased with increasing time of batch culture, and no plateau was obtained after 48 h of fermentation. The DMD were lower ($P < 0.01$) for fractional corn DDGS after 24 h (33%) and 48 h (42%) of fermentation than for other DDGS (mean ± SD; 24h, 44 ± 2.1%; 48h, 54 ± 2.8%). The gas production followed the same variation pattern of the DMD. The results indicate that the nutrient contents of DDGS and extent of digestion varied with DDGS source. The information on the type of grain used and milling process before ethanol fermentation is needed to choose DDGS for accurately formulating ruminant diet.

Key Words: distillers grain, nutrient content and digestion, batch culture

T367 In vitro digestion and gas production of two varieties of barley grain sown with different seeding and N fertilization rates in seven sites across Canada. W. Z. Yang*[1], T. A. McAllister[1], M. Oba[2], and D. Gibb[1], [1]*Agriculture and Agri-Food Canada, Research Centre*, *Lethbridge, AB, Canada*, [2]*Department of Agricultural, Food and Nutritional Science, University of Alberta*, *Edmonton, AB, Canada*.

Seeding rate (SR) and N fertilizer application rate (NR) have the potential to alter the starch and protein content of the grain as well as the rate and extent of its digestion. The objective of this study was to determine

whether SR and NR change DM digestion (DMD) and gas production (GP) of barley grain in batch culture. Two malting barley varieties, Copeland and Metcalfe, were seeded at rates of 200 or 400 plants/m^2 with N fertilizer at rates of 0, 30, 60, 90 and 120 kg/ha, respectively, from 7 sites across Canada. Total 560 samples (i.e., 7 sites × 2 varieties × 2 SR × 5 NR × 4 replications) were collected and ground through a 6-mm screen. Fermentability was assessed by measuring in vitro GP and DMD at 0, 4, 8, 12, 18 and 24 h of incubation. The CP content (% DM) of malt barley linearly ($P < 0.01$) increased from 10.3 to 12.2, whereas the starch content (% DM) linearly ($P < 0.01$) decreased from 61.6 to 59.8 with increasing NR. The SR had marginal effect on the contents of CP and starch of barley grains. The DMD after 24 h of batch fermentation ranged on average from 36 to 42% for both varieties and were overall not affected by the SR or NR. There were only one of 7 sites where the SR decreased ($P < 0.01$) DMD of Copeland by 12%, but increased ($P < 0.01$) the DMD of Metcalfe by 17%. The NR linearly ($P < 0.01$) reduced DMD of Copeland from 2 sites and reduced DMD of Metcalfe from one site. There was interaction ($P < 0.01$) between SR and NR on GP: the GP was higher ($P < 0.01$) for 60NR when SR was 200, whereas GP was lower ($P < 0.01$) for 120NR when SR was 400 compared with other NR, respectively. This work demonstrates that the NR changed nutrient content of barley grains and would affect its ruminal degradation rate as shown by the variation of GP.

Key Words: malt barley grain, DM digestion, batch culture

T368 Impact of monensin on rumen microbiota and its stochastic succession. P. Kongmun*[1,2], M. Wanapat[1], and Z. Yu[2], [1]*Department of Animal Science, Khon Kaen University*, *Khon Kaen, Thailand, 40002*, [2]*Department of Animal Science, The Ohio State University*.

This study examined the long-term effects of monensin on rumen microbiota and the effect of monensin on the stochasticity of rumen microbiota using an in vitro model. Rumen fluid samples were collected from 2 Holstein Friesian cows at 6 h post-feeding and constituted into a composite sample as the inoculum. Two sets of cultures (n = 5 each) were incubated at 39°C under anaerobic condition: the monensin cultures contained 5 ppm monensin, while the control cultures contained no monensin. The cultures were transferred every 2 d for 15 d. Samples were collected over the course of the incubation and subjected to analysis for microbiota using both DGGE and sequencing analysis of 16S rRNA genes. The monensin cultures had fewer bands than the control cultures, especially in the high-denaturant area of the DGGE gel that corresponds to bacteria with low GC contact. Principal component analysis (PCA) of the DGGE profiles also showed clear differences between the monensin and the control cultures, with samples collected at d 9 exhibiting the greatest difference. Considerable temporal successions of the microbiota were also evident in both sets of cultures, especially during the initial 9 d of the incubation. Both the DGGE banding patterns and the PCA analysis of the DGGE profiles showed variations among the 5 replicates within the same set of cultures. Because all the cultures were grown in identical test tubes under identical conditions, we attributed these variations among replicates to stochastic succession. It is interesting to note that the early monensin cultures had little stochastic succession among the 5 replicates. A total of 233 random clones were sequenced from individual 16S rRNA gene libraries. At 97% sequence identity level, 46 unique phylotypes were identified that were assigned to genera of *Firmicutes*, *Bacteroidetes*, *Proteobacteria*, and uncultured bacteria. PCA analysis of these phylotypes is concordant with that of the DGGE profiles. The observations in this study may help explain, at least partially, the variations often observed among individual animals fed the same diet.

Key Words: monensin, rumen microbiota, stochasticity

T369 The effect of body condition at calving and supplementation with *Saccharomyces cerevisiae* on energy status and some reproductive parameters in early lactation dairy cows. R. M. Al Ibrahim*, M. A. Crowe, P. Duffy, L. O`Grady, M. E. Beltman, and F. J. Mulligan, *University College Dublin*, *Dublin 4, Ireland*.

The objective was to examine potential benefits of live yeast culture (YS) supplementation on postpartum (PP) energy status and fertility indices of dairy cows managed to have low or high body condition score (BCS, 1 – 5 scale) at calving. Forty Holstein dairy cows were randomly allocated to a 2 × 2 factorial arrangement. Treatments were: BCS at calving (low, L ≤3.5 or high, H ≥3.75; n = 20) and YS supplementation (2.5 g/cow/d for pre-calving and 10 g/cow/d for post-calving × 10^9 CFU of *S. cerevisiae*/g) (supplemented, Y or control, C; n = 20). Daily milk yield was recorded and weekly milk composition, BCS and BW were assessed from calving to wk 10 PP. Estimated energy balance PP was calculated on a weekly basis individually as the difference between the net energy (NE) intake and the sum of NE for maintenance and milk production. Insulin and IGF-I concentrations were determined on d 14 and 7 pre-calving and 1, 5, 15, 25 and 35 PP. Daily ovarian ultrasonography was performed from d 10 PP to monitor the size and development of the first dominant follicle, first ovulatory follicle and days to first ovulation PP. Pre-ovulatory peak of serum estradiol concentration was determined. Data were analyzed using the Mixed procedure in SAS v 9.1, 2004. Cows in H group (over-conditioned) at calving ingested less NE, produced more milk NE output, and consequently had a significantly ($P < 0.05$) exacerbated negative energy balance in comparison with L group (moderately conditioned) during early lactation. Higher ($P < 0.05$) insulin concentrations and a tendency for higher ($P = 0.06$) preovulatory peak estradiol concentrations in L group were detected in the early PP period. Feeding YS had no effect on energy status of lactating dairy cows with high or low BCS at calving, while it improved serum insulin concentration, preovulatory peak of estradiol and the size of first ovulatory follicle in the early PP period. These observed effects of YS supplementation require to be substantiated with further research.

Key Words: dairy cows, yeast culture, energy balance, reproduction

T370 Effect of supplemented diets with sucrose and/or starch on ruminal peptide-N concentration of Holstein steers. M. Danesh Mesgaran*, F. Rezaii, A. R. Heravi Moussavi, and A. Vakili, *Dept. Animal Science, Ferdowsi University of Mashhad, Mashhad, Iran*.

The objective of this study was to determine the effect of diets containing different types of non-fiber carbohydrates [sucrose (Su), starch (St) or equal mixture of Su and St (Su+St)] on ruminal peptide-N concentration of Holstein steers. Four ruminally fistulated steers (body weight = 280 ± 15 kg) were assigned to a 4 × 4 Latin square with 28 d periods. The basal diet contained alfalfa hay, barley grain, soybean meal and sugar beet pulp (400, 290, 190 and 50 g/kg respectively). The non-fiber carbohydrates were added to the basal diet at the rate of 70 g/kg DM. Diets were offered at 2.5 times of the maintenance requirements (7 kg DM/day). Animals were fed twice daily at 08:30 and 16:30. Samples of rumen contents were taken, by suction, at 0.0, 2, 4 and 6 h after the morning feed. Ruminal fluid was prepared for peptide-N analysis using sulfate-tungstate precipitation method. Tungstate acid-precipitate nitrogen was assayed by a standard macro-Kjeldahl procedure. Data were analyzed using mixed procedure of SAS (2003) for repeated measures. Results of the present experiment indicate that peptide-N concentration tended to be lower when steers were fed Su, St and Su+St than BD ($P = 0.09$). Mean Peptide-N concentrations of the sampling times were BD = 2.1, Su = 1.7, St = 1.4 and Su+St = 1.5 mg/dL. Therefore, it might be concluded that the nitrogen metabolism in the rumen is affected by the

type of non-fiber carbohydrates used in the present diets. The effect of sampling time on Peptide-N concentrations was significant ($P < 0.05$). Peptide-N concentrations showed a quadratic significant response to the sampling time ($P < 0.05$). Peptide-N concentrations increased after the morning feeding and declined at 6 h after that. The concentrations of peptide-N at 6 h after the morning feeding (BD = 1.8, Su = 1.4, St = 1.2 and Su+St = 1.3 mg/dL) was less than those of before feeding (BD = 1.9, Su = 1.6, St = 1.3 and Su+St = 1.4 mg/dL).

Key Words: rumen, peptide-N, carbohydrates

T371 Effect of diets supplemented by sucrose and/or starch on in vivo ruminal *Ruminococcus flavefaciens* populations of Holstein steers determined by real time-PCR. M. Danesh Mesgaran*, F. Rezaii, A. R. Moussavi Heravi, M. Nassiri, and A. Vakili, *Dept. Animal Science, Ferdowsi University of Mashhad, Mashhad, Iran*.

The objective of the present work was to investigate the effect of diets containing different types of non-fiber carbohydrates on *Ruminococcus flavefaciens* populations in the rumen fluid of Holstein steers determined by real-time polymerase chain reaction (RT-PCR). Four ruminally fistulated Holstein steers (body weight = 280 ± 15 kg) were assigned to a 4x4 Latin square with 28 d of each period. Basal diet (BD) was formulated to contain of alfalfa hay, barley grain, soybean meal and sugar beet pulp (400, 290, 190 and 50 g/ kg DM, respectively). Sucrose (Su), starch (St) or a 1:1 mixture of Su and St (Su+St) was added to the basal (70 g/ kg DM). Diets were offered as 2.5 times of maintenance requirements (7 kg DM/d) at 0830 and 1630 h. Rumen fluid samples were collected before and 4 h after the morning feeding at the last day of each period. Samples were analyzed for *Ruminococcus flavefaciens* quantitation using RT-PCR. The DNA extraction was performed from the samples using the QIAamp DNA stool mini kit (Qiagen Ltd, Crawley, West Sussex, UK). *Ruminococcus flavefaciens* rDNA concentrations were measured by RT-PCR relative to the total bacteria amplification (ΔΔCt). The 16s rRNA gene-targeted primer sets used in the present study were forward: CGAACGGAGATAATTTGAGTTTACTTAGG and reverse: CGGTCTCTGTATGTTATGAGGTATTACC. Cycling conditions were 95°C for 5 min, 40 cycles of 95°C for 15 s, 60°C for 15 s and 72°C for 30 s. Data were expressed relative to the quantification of the total bacterial population, and analyzed using mixed procedure of SAS (2003) and means were compared by the Tukey test at $P < 0.05$. Present results indicate that the supplementation of the basal diet with Su+St tended to decrease ($P = 0.07$) the relative population of *Ruminococcus flavefaciens* in the rumen samples taken before the morning feeding (95×10^{-5} vs. 279×10^{-5}). The adding of Su to the basal diet increased the population of *Ruminococcus flavefaciens* (8689×10^{-5}) compared with BD ($P = 0.06$; 279×10^{-5}) and Su+St ($P = 0.05$; 307×10^{-5}) in the rumen samples of 4 h after the morning feeding.

Key Words: rumen, carbohydrates, *Ruminococcus*

T372 Exogenous proteolytic enzyme increases degradation of dried distillers grains with solubles during in vitro ruminal fermentation. J. M. Vera, J.-S. Eun*, D. R. ZoBell, and A. J. Young, *Utah State University*, *Logan*.

We performed a series of in vitro batch culture experiments to assess if an exogenous proteolytic enzyme (EPE) would improve degradation of dried distillers grains with solubles (DDGS) and beef growing and finishing TMR diets containing DDGS. A commercial enzyme product (Protex 6L, Genencor Division of Danisco, Rochester, NY) having only a protease activity was investigated in this study. In all experiments, strained ruminal fluid was obtained from 2 cannulated beef cows. In experiment 1, the EPE was added to the DDGS at 0, 0.7, 1.4, and 2.1 mg/g DM in a filter bag, and they were incubated for 24 h in gas-tight culture vials (125-mL capacity) with ruminal fluid. The EPE addition resulted in quadratic responses on degradability of DM, NDF, and ADF, and its optimum dose rate was found at 1.4 mg/g DM. In experiment 2, efficacy of the EPE added at 1.4 mg/g DM to DDGS was assessed for 96 h using the Daisy II in vitro fermentation system (Ankom Corp., Macedon, NY). Degradability of NDF and ADF increased starting at 18 h of incubation. In experiment 3, efficacy of the EPE was further investigated using beef growing and finishing TMR diets containing 20% DDGS on a DM basis. Experimental procedures were the same as those used in experiment 2. Addition of the EPE tended to increase ($P = 0.07$) NDF degradability of growing and finishing diets at 12 h of incubation, but the effect of EPE on fiber degradation of beef diets was minor at the later hours of incubation. Total VFA production did not differ due to EPE addition in beef diets. Adding EPE in DDGS as a single substrate resulted in a sizable increase in DM and fiber degradability, but its effects were reduced when added in beef growing and finishing diets containing approximately 20% DDGS. It is recommended that the EPE be further evaluated in a beef steer growth study using diets containing relatively high DDGS inclusion rates.

Key Words: exogenous proteolytic enzyme, dried distillers grains with solubles, in vitro fermentation

T373 Effects of eugenol addition on milk fatty acid composition of dairy cows fed high- or low-concentrate diets. C. Benchaar*[1], W. Z. Yang[2], H. V. Petit[1], and P. Y. Chouinard[3], [1]*Agriculture and Agri-Food Canada*, *Dairy and Swine R&D Centre, Sherbrooke, QC, Canada*, [2]*Agriculture and Agri-Food Canada*, *Lethridge Research Centre, AB, Canada*, [3]*Université*, *Département des Sciences Animales, Québec, QC, Canada*.

Four primiparous lactating cows (BW = 568 kg; DIM = 67) were used in a 4 × 4 Latin square design (28-d periods) with a 2 × 2 factorial arrangement of treatments to determine the effects of eugenol (EUG) addition (0 vs. 50 mg/kg of DMI) and concentrate proportion of the diet (high-concentrate: HC vs. low-concentrate: LC; 65 vs. 35%, DM basis) on milk fatty acid (FA) composition. Diets contained 17.2% CP and were formulated to be isocaloric ($NE_L = 1.65$ Mcal/kg DM) using a commercial source of calcium salts of long-chain FA (Megalac) in LC diets. Analyses of FA were performed on pooled samples collected from 4 consecutive milkings (d 22 to 23). Data were analyzed as a 2 × 2 factorial using the MIXED procedure of SAS (SAS Inst., Inc., Cary, NC). Significance was declared at $P \leq 0.05$ and tendency at $0.05 < P \leq 0.10$. No interaction concentrate level × EUG was observed for any of the FA measured. Milk FA profile was not changed by EUG supplementation. Proportions (g/100 g of total FA) of C16:0 (28.2 vs. 24.5%) and *cis*-9 C18:1 (19.4 vs. 16.1%) were higher while the proportion of *cis*-9, *cis*-12 C18:2 (2.04 vs. 2.69%) was lower in milk fat of cows fed LC diets than in that of cows fed HC diets. Milk fat concentrations of *trans*-10 C18:1 (0.34 vs. 0.30%), *trans*-11 C18:1 (1.06 vs. 0.96%; $P = 0.08$), and *cis*-9, *trans*-11 C18:2 (CLA; 0.53 vs. 0.44%) increased in cows fed LC diets as compared with cows fed HC diets, but the ratio *trans*-11 C18:1 to *trans*-10 C18:1 was not significantly affected by concentrate proportion. These results suggest that under the experimental conditions of this study, neither the addition of EUG (50 mg/kg of DMI) nor the increase in dietary concentrate proportion of the diet modified the pathway of biohydrogenation of FA in the rumen.

Key Words: essential oil/eugenol, concentrate proportion, milk fatty acid

T374 Effects of sugar beet pulp substituted for ground corn on the performance and health of Chinese Holstein dairy cows. M. Wang, J. Y. Zhang, J. Q. Wang*, D. P. Bu, L. Y. Zhou, and P. Sun, *State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences*, *Beijing, China*.

Sixty multiparous Holstein cows (60 ± 22 DIM, 31.2 ± 6.2 kg of milk/d) were used to study the effect of sugar beet pulp (SBP) substituted for ground corn on performance, nutritional status as measured using blood metabolites and health. Cows were randomly divided into 2 pens and within each pen where 3 groups (control, 20SBP or 40SBP) and each group comprised of 10 cows (n = 10). The cows were fed a diet containing either ground corn (control) or SBP (20% or 40% of the ground corn replaced with SBP on the basis of corn DM, 20SBP and 40SBP) as the main energy source. Cows were fed 3 times daily in a tie-stall barn. Feed intake was recorded daily. Cows were milked 3 times daily. Blood samples were collected monthly via venous puncture from coccygeal vein 2 h after morning feeding. Data were analyzed statistically by using PROC MIXED of SAS. The results showed that dry matter intake (21.45, 21.58 and 21.56 kg/d), milk production (28.52, 28.45 and 27.89 kg/d), energy corrected milk (ECM, 28.50, 28.76, 28.33 kg/d) were not effected by increasing SBP substitution ($P > 0.05$). The milk protein (2.95, 2.98, 3.04%), milk fat (3.55, 3.65, 3.66%), milk lactose (4.73, 4.78, 4.79%), total solids (TS,12.18,12.33,12.43%), and solid non-fat (SNF, 8.53, 8.58, 8.66%) showed no significant differences among 3 treatments. In blood metabolite, the concentrations of blood urea nitrogen (BUN, 23.39, 19.76, 20.94 mg/dl) and glucose (52.34, 44.2, 44.66 mg/dl) decreased when cows fed SBP in the diets ($P < 0.01$). Nonesterified fatty acid (NEFA) and β-hydroxybutyrate (BHBA) concentrations were not significantly different among treatments. Manure score was lower (2.97, 2.85, 2.89, respectively) for 20SBP than for the other treatments ($P < 0.05$). However, no significant differences existed among 3 treatments on somatic cell counts (SCC), body condition score (BCS), locomotion score, and average body weight ($P > 0.05$). The results indicate that supplemented dried sugar beet pulp is equal to corn as an energy source for lactating dairy cows when fed at the replacing 20 and 40% of corn the DM.

Key Words: sugar beet pulp, ground corn, performance

T375 Garlic botanical reduces methane production in rumen fluid determined in vitro. S. Cavini[1], D. Bravo[2], S. Calsamiglia[1], G. F. Schroeder*[3], M. Rodriguez[1], and A. Ferret[1], [1]*Universitat Autonoma de Barcelona*, *Spain*, [2]*Pancosma*, *Geneva, Switzerland*, [3]*Cargill Innovation Campus*, *Elk River, MN*.

The intent of this study was to evaluate the effect of increasing doses of a particular garlic extract standardized in propyl propyl thiosulfonate (PPT) on rumen fermentation pattern and methane production in vitro. The effect of PPT on in vitro microbial fermentation using ruminal fluid from a dairy cow was determined using the gas production technique. Thirty milliliters of a 1:4 ruminal fluid-to-buffer solution were introduced into glass polypropylene tubes supplied with 0.5 g of DM of a 60:40 forage:concentrate diet and incubated for 72 h at 39°C. Gas production was measured and samples were collected for VFA, ammonia, and methane (CH_4) concentrations. Treatments were control (CON), 20, 40, 80, 120 and 160 mg/L of PPT (abbreviated PPT20 to PPT160) and 500 mg/L of Monensin (MON) as positive control. Each treatment was tested in duplicate and in 2 replicated periods. Results were analyzed with PROC MIXED and PROC REG of SAS. The PPT linearly decreased total VFA ($Y = -0.084X + 86.20$, R^2=0.76) with PPT160 producing more VFA (69.7 m*M*) than MON (57.9 m*M*). The PPT quadratically depressed the molar proportion of acetate ($Y = -0.0002X^2 + 0.012X + 77.2$, $R^2 = 0.96$). Inversely, PPT quadratically increased the molar proportion of propionate ($Y = 0.0001X^2 - 0.006X + 13.1$, $R^2 = 0.97$) with PPT160 producing still less propionate than MON (14.6 vs. 18.4 mol/100 mol). Increasing doses of PPT quadratically decreased CH_4 production ($Y=-0.0006X^2 + 0.042X + 14.61$, $R^2 = 0.97$) with PPT160 producing 6.01 μL/L (compared with CON = 14.3 and MON = 1.8 μL/L). Furthermore, in order to take into consideration the parallel reduction in CH_4 and VFA, the ratio CH_4/VFA was also analyzed, resulting in decrease by PPT dose ($Y = -7.10^{-6}X^2 = 5.10^{-4}X + 0.174$, $R^2 = 0.94$) with PPT160 being associated with a 50.3% decrease. The present results indicated that a garlic extract standardized in thiosulfonates exhibited promising effect on reduction of CH_4 production in vitro. An in vitro dose between 120 and 160 mg/L may be optimal.

Key Words: methane, garlic, in vitro

T376 In vitro methane production by ruminal microorganisms is affected by the diet of donor animals. M. L. Tejido[1,2], M. J. Ranilla*[1,2], C. Saro[1,2], and M. D. Carro[1,2], [1]*Dpto. Producción Animal, Universidad de León*, *24071, León, Spain*, [2]*Instituto de Ganadería de Montaña (CSIC-ULE), Finca Marzanas s/n*, *24346 Grulleros, León, Spain*.

Six rumen-fistulated sheep were fed 4 diets in a partially replicated 4 × 4 Latin square design to investigate the effects of forage to concentrate ratio (F:C) and type of forage (FOR) in the diet on in vitro methane production. The diets consisted on either 70:30 (HF) or 30:70 (HC) F:C ratio, and either alfalfa hay (A) or grass hay (G) as FOR. In each period, ruminal fluid from each sheep was used to inoculate batch cultures containing the same 4 diets as substrate. Cultures were incubated at 39°C for 24 h. There were no F:C x FOR interactions ($P > 0.05$) for any measured variable. Methane and total volatile fatty acids (VFA) production was 17.5 and 10.0% times greater ($P < 0.05$) with HC-inoculum compared with HF-inoculum. Changing the F:C in the diet of sheep did not affect ($P > 0.05$) propionate production for any substrate, but production of butyrate was augmented ($P < 0.01$) as F:C increased. Methane:VFA ratio and apparent dry matter digestibility were not affected ($P > 0.05$) by F:C in the diet of sheep. For all substrates, inoculum from sheep fed A diets promoted greater ($P < 0.05$) production of methane and total and individual VFA, as well as greater ($P < 0.01$) acetate:propionate ratios and apparent dry matter digestibility compared with inoculum from sheep fed G diets. Methane:VFA ratio was greater ($P < 0.05$) with A-inoculum compared with G-inoculum for HC substrates, but no effect of FOR was observed for HF substrates.
There were clear differences in methane production among inocula from different sheep, which persisted across diets and substrates. Methane emission estimated from VFA production was about 21% greater ($P < 0.001$) than that directly measured, but both values were significantly related ($r = 0.612$; $P < 0.001$; $n = 128$). The results indicate that methane production in vitro is affected by both F:C ratio and type of forage in the diet of donors, and these variables should be taken into account when conducting in vitro experiments.

Key Words: methane, forage:concentrate ratio, forage

T377 Hydrogen sulfide release by ruminal microbes maintained in batch culture. M. Ruiz-Moreno*[1], E. Seitz[1], J. Garrett[2], and M. D. Stern[1], [1]*University of Minnesota*, *St. Paul,* [2]*Quali Tech Inc., Chaska, MN.*

Hydrogen sulfide (H_2S) release in the rumen depends upon ruminal pH, sulfur availability and its interaction with other minerals. An in vitro rumen fluid incubation was conducted using 2 sources of sulfur and 2 sources of Zn, Cu and Mn in a 2 × 2 factorial arrangement of treatments during 2 consecutive 24-h periods. A synthetic diet consisting of 36% cellulose, 32% starch, 19% CP, 5% fat and 2.4% sugar provided substrate for microbial metabolism. Sulfur was added as $NaSO_4$ or sulfur-bound lignosulfonate to a final concentration of 0.75% of DM. Copper, Zn and Mn were added as $CuSO_4$, $ZnSO_4$ and $MnSO_4$ or as protected Cu, Zn and Mn (SQM protected minerals, Quali Tech Inc.) to a final concentration of 16, 56 and 71 ppm of DM, respectively. Rumen fluid was obtained from a ruminal cannulated lactating dairy cow and mixed with McDougall's artificial saliva to a 1:4 ratio. Treatments were assigned in 6 replicates to 120-mL serum bottles containing 40 mL of the inoculum mix and 0.5 g dietary DM. Serum bottles were flushed with N_2, crimp sealed and incubated during 24 h at 39.1°C. At the end of incubations, gas volume was measured, H_2S in the headspace of bottles was analyzed and final pH of incubations was recorded. Results were analyzed as a 2 × 2 factorial design. An interaction between lignosulfonate and mineral source was detected. Addition of SQM minerals and lignosulfonate resulted in lower pH ($P < 0.05$) than that without lignosulfonate (5.87 vs. 5.95, respectively), while absence of SQM minerals resulted in intermediate pH of incubations despite lignosulfonate (5.90 ± 0.04). Addition of lignosulfonate without SQM minerals decreased total gas production ($P < 0.001$) compared with the other treatments (173.1 vs. 175.9 mL/g OM). Lignosulfonate resulted in a lower ($P < 0.001$) production of H_2S (416.2 vs. 475 µg/g OM). In contrast, addition of SQM minerals increased ($P < 0.001$) production of H_2S (469.5 vs. 421.5 µg/g OM). Results indicate that source of trace mineral can influence the dynamics of rumen fermentation.

Key Words: rumen, hydrogen sulfide, in vitro

T378 Comparison of bacterial diversity in the rumen of sheep and in Rusitec fermenters as assessed by ARISA–PCR. M. J. Ranilla*[1,2], M. L. Tejido[1,2], C. Saro[1,2], and M. D. Carro[1,2], [1]*Dpto. Producción Animal, Universidad de León*, *24071, León, Spain*, [2]*Instituto de Ganadería de Montaña (CSIC-ULE), Finca Marzanas s/n*, *24346 Grulleros, León, Spain*.

This study was designed to compare the effects of 4 diets on bacterial communities in bacterial pellets (BP) isolated from the solid (SAB) and liquid phase (LAB) of the rumen of sheep with those observed in Rusitec fermenters. The 4 experimental diets had forage:concentrate ratios (F:C) of 70:30 (HF) or 30:70 (HC) and alfalfa hay or grass hay as forage (FOR). SAB and LAB were isolated from each sheep (4 per diet) and fermenter (n = 4) immediately before feeding, and bacterial diversity was analyzed by ARISA-PCR of the 16S ribosomal DNA. A total of 170 peaks were detected in the ARISA electropherograms across the full set of 64 BP. The number of peaks (NP) in BP from sheep ranged from 42 to 82 for LAB, and from 31 to 81 for SAB (168 peaks in total). In fermenters, NP ranged from 53 to 79 for LAB, and from 21 to 69 for SAB (162 peaks in total). No effect of F:C ($P > 0.05$) on NP or Shannon index (SI) was observed on LAB in any system. F:C did not affect SAB profile in fermenters, but NP and SI were greater ($P < 0.05$) in SAB from sheep fed HF diets compared with those from HC-sheep. Feeding grass hay diets promoted greater ($P < 0.01$) SAB diversity in both systems compared with alfalfa hay diets. FOR did not ($P > 0.05$) affect LAB profile in sheep, but grass hay-fed fermenters had greater ($P < 0.01$) LAB diversity compared with fermenters fed alfalfa hay diets. The results indicate that bacterial diversity was more markedly affected by FOR than by F:C. There was a positive relationship (P = 0.001) between the NP in LAB and that in SAB in Rusitec, but no relationship ($P = 0.72$) was found in sheep; this would indicate that dietary effects on bacterial diversity were similar in LAB and SAB in fermenters, but contrasting in sheep. When all samples were analyzed together by clustering analysis, 2 distinct clusters were observed for in vivo and in vitro BP, which suggests a different structure of the bacterial communities in sheep and fermenters.

Key Words: rumen, fermenters, bacterial diversity

T379 Effect of supplemented diet by sucrose or starch on fungi populations in rumen fluid as determined by real-time polymerase chain reaction in Holstein steers. A. Vakili*, M. Danesh Mesgaran, H. Jahani Aziz-abadi, F. Rezaii, and S. Ghovvati, *Dept. of Animal Science, Ferdowsi University of Mashhad*, *Mashhad, Iran*.

The objective of this work was to investigate the effect of diets containing different type of non-fiber carbohydrates (sucrose or starch) on fungi populations in rumen fluid as determined by real-time polymerase chain reaction. Four Holstein steers (BW = 280; SD = 15 kg) were assigned to a 4 × 4 Latin square with 21-d periods. A basal diet was formulated to be contained of alfalfa hay, barley grain, soybean meal and sugar beet pulp (400, 290, 190 and 50 g/ kg, respectively). Starch (St) or sucrose (Su) or a 1:1 mixture of starch and sucrose (St+Su) was added to the basal diet at the rate of 70g/kg DM. Diets were offered as 2–2.5 times of maintenance requirements (7 kg DM/d). Rumen fluid samples were collected before and 4 h after the morning feeding. DNA was extracted from the samples using the QIAamp DNA stool mini kit (Qiagen Ltd, Crawley, West Sussex, UK) following the manufacturer′s instructions. Fungi rDNA concentrations were measured by real time PCR relative to total bacteria amplification (ΔΔCt). The 16s rRNA gene-targeted primer sets used in the present study were forward: GAGGAAGTAAAAGTCGTAACAAGGTTTC and reverse: CAAATTCACAAAGGGTAGGATGATT. Cycling conditions were 95°C for 5 min, 40 cycles of 95°C for 15s, 60°C for 15s and 72°C for 30s; fluorescence readings were taken after each extension step, and a final melting analysis was obtained by heating at 0.1°C/s increment from 60 to 95°C, with fluorescence collection at 0.2°C at intervals. Data are expressed relative to quantification of the total bacterial population. Data were analyzed using mixed procedure of SAS (2003). Statistical model was: $Y_{ijk} = \mu + T_i + C_j + P_k + \varepsilon_{ijk}$, where Y_{ijk} is dependent variable, μ is the overall mean, T_i is treatment effect, C_j is cow effect, P_k is period effect, and ε_{ijk} is error. The results of this experiment showed that different type of non-fiber carbohydrates didn't have any effect on fungi populations before or 4 h after the morning feeding[St = 52 and 44,Su = 48 and 45, St+Su = 47 and 42, SEM = 5 and 3 ($10 \times ^{-7}$) fungi relative to total bacteria, respectively].

Key Words: fungi, real-time PCR, rumen

T380 Sodium acetate/acetic acid as a buffer solution to simulate an acidic in vitro rumen environment. R. C. Araujo*[1], A. V. Pires[1], and A. L. Abdalla[2], [1]*ESALQ, Universidade de São Paulo*, *Piracicaba, SP, Brazil*, [2]*CENA, Universidade de São Paulo*, *Piracicaba, SP, Brazil*.

Incubation media based on $NaHCO_3$ and NH_4HCO_3 as buffers have a pH close to 6.8. A low-pH medium would provide a more realistic in vitro rumen simulation of animals fed feedlot diets. Treatments were: CTL6.8 – Theodorou's medium with a pH of 6.8 based on $NaHCO_3$ (7.28 g/L of medium) and NH_4HCO_3 (0.83 g/L of medium) as buffers; CTL5.8 – control acidified with 72% sulfuric acid to achieve a pH of 5.8; NaAc – Theodorou′s medium with Na acetate (56.6 g/L of medium) and glacial acetic acid (2.08 mL/L of medium) as buffers to achieve a pH of 5.8. In each flask (160 mL), 0.5 g of an 80:20 concentrate:forage diet

(91.4% DM) was incubated with 50 mL of medium and 25 mL of rumen fluid at 39°C for 16h. A randomized complete block design was used with n = 8 for gas production and n = 4 for all other variables. Two inocula (3 animals each; mean pH = 5.61 ± 0.11) from lambs adapted to the above diet were used as a source of variation. Data were analyzed by PROC Mixed of SAS with differences declared when $P < 0.05$. The pH variation after 0, 4, 8, 12, and 16h of incubation was: CTL6.8 – 6.77, 6.57, 6.45, 6.39, 6.31; CTL5.8 – 5.82, 5.51, 5.38, 5.34, 5.31; NaAc – 5.68, 5.65, 5.61, 5.59, 5.57, respectively. Mean pH was lowest for CTL5.8 (5.47), followed by NaAc (5.62) and CTL6.8 (6.50). CTL6.8 showed the greatest values for gas production (151.1 mL), CH_4 production (13.3 mL), and truly degraded DM (TDDM; 70.7%). Gas production (86.9 vs. 80.2 mL), CH_4 production (4.2 vs. 2.1 mL), and TDDM (51.4 vs. 49.6%) were similar between CTL5.8 and NaAc, respectively. It was not possible to determine C_2 concentration for NaAc. Total SCFA (94.0 vs. 61.4 m*M*) and C_2 (50.5 vs. 21.4 m*M*) concentrations as well as C_2 to C_3 ratio (2.20 vs. 0.95) were greater for CTL6.8 than CTL5.8. Concentration of C_3 was the greatest for CTL6.8 (23.8 m*M*), intermediary for CTL5.8 (22.7 m*M*), and the lowest for NaAc (19.4 m*M*). In spite of less pH variation, Na acetate/acetic acid solution as buffer interfered in C_2 determination and showed similar results in comparison with an acidified $NaHCO_3/NH_4HCO_3$-based medium.

Key Words: buffer, medium, pH

T381 Milk selenium content and performance of cows supplemented with selenized yeast. L. Q. Melo[1], L. L. Bitencourt[1], S. Siécola Júnior[1], G. S. Dias Júnior[1], N. M. Lopes[1], V. A. Silveira[1], I. R. Rios[1], R. A. N. Pereira[2], and M. N. Pereira*[1], [1]*Universidade Federal de Lavras*, *Lavras, Brazil*, [2]*Empresa de Pesquisa Agropecuária de Minas Gerais*, *Lavras, Brazil*.

This study evaluated the effect of replacing sodium selenite (45.1% of Se) with selenized yeast (Selemax, Biorigin, Brazil. 2245 ppm of Se). Twenty-eight Holsteins were fed a Se supplement free diet for a 60-d standardization period (0.08 ppm of Se in the diet), before being paired blocked and assigned to a treatment for 105 d: Orally given gelatin capsules containing 2.1 g of Selemax (4.64 mg of Se) or 0.011 g of Selenite (4.88 mg of Se) daily. Milk yield and DMI were measured daily, and milk composition on days −1 and 0, 15 to 17, 36 to 38, 57 to 59, and 99 to 101. Milk Se content was determined on d 0, 4, 8, 16, 37 and 57. Total collection of feces and urine was performed on d 39 to 41 for Se balance. Blood samples were obtained on d 0, 43 and 106 to determine Se content and glutathione peroxidase activity. Data were analyzed as repeated measures over time with Mixed of SAS. The model contained the effects of covariate (measure of the same variable at the end of the standardization period), block, treatment, time, and time by treatment interaction. Cow within treatment tested the treatment effect. Daily milk yield was 26.7 kg for Selemax and 26.9 kg for Selenite ($P = 0.84$), milk SCC (× 1,000 cells) was 354 and 352, respectively ($P = 0.99$), and no difference in milk solids or DMI were detected ($P > 0.22$). Selemax increased milk Se content from 8 to 32.3 μg/kg ($P < 0.01$), observed after 4 d of supplementation and throughout data sampling. Plasma Se content was 91.4 and 77.3 μg/L ($P = 0.14$) for Selemax and Selenite, respectively. Glutathione peroxidase activity was greater for Selenite on d 43 and for Selemax on d 106 ($P = 0.05$ for the interaction). There was no difference in Se excreted in urine and feces or retained ($P > 0.46$). Selenized yeast increased milk Se content shortly after starting the supplementation.

Key Words: selenium, yeast, glutathione peroxidase

T382 Effect of direct-fed microbial (DFM) products on rumen bacterial communities in Holstein cows at 2 and 6 weeks postcalving. E. A. Galbraith*[1], A. H. Smith[1], K. J. Mertz[1], Z. Wu[2], and J. D. Ferguson[2], [1]*Danisco*, *Waukesha, WI*, [2]*University of Pennsylvania School of Veterinary Medicine*, *Kennett Square*.

Increase in performance was measured in a study to determine the efficacy of 3 DFM treatments in dairy production. Treatment with a *Propionibacterium* DFM 2 weeks prepartum followed by a *Lactobacillus* DFM through 22 weeks postpartum or *Bacillus pumilus* 8G-134 at either 5×10^9 or 1×10^{10} CFU/head/day both pre- and postpartum resulted in improved milk volume (*B. pumilus* 8G-134) and milk fat (all DFM treatments). This study investigated if these DFM treatments were also associated with changes in ruminal microbial populations at 2 and 6 weeks postcalving. At 8 h postfeeding, cows were restrained and rumen fluid collected via stomach tube. The microbial community of rumen fluid samples was monitored by terminal restriction fragment length polymorphism (T-RFLP) analysis of amplified 16S rDNA genes. Peak profiles from all samples using 3 restriction enzymes were between 70% and 93% similar. All samples tended to have several major peaks and the taxonomic identities of species responsible for these peaks were determined by searching 16S databases. Major peaks present in most samples included common rumen species of *Prevotella*, *Bacteroides*, *Butyrvibrio fibrisolvens*, *Selenomonas ruminantium*, and *Clostridium clostridioforme* and *coccoides*. Analysis of dendrograms indicated no overall clustering by treatment, sampling date, or lactation, but MANOVA analysis did pinpoint several minor TRF peaks which were significantly associated ($P < 0.1$) with treatments. On a CFU per gram basis, the level of DFM treatments fed in this trial would constitute less than 0.1% of the total rumen bacterial population, therefore below the threshold of detection of microbial ecology techniques such as T-RFLP. However, even at low concentrations, the DFM treatments affected performance and bacterial populations, suggesting an impact on bacteria that may be part of a rarer biosphere in the rumen. Examination of rumen bacterial communities may help elucidate the mode of action of these direct-fed microbials.

Key Words: dairy cows, rumen bacteria, direct-fed microbial

T383 Effects of a rumen protected B vitamin complex supplemented to multiparous Holstein cows on milk production and reproductive performance. S. O. Juchem*[1,2], P. H. Robinson[1], and E. Evans[3], [1]*University of California*, *Davis*, [2]*California State University*, *Fresno*, [3]*Technical Advisory Services*, *Bowmanville, ON, Canada*.

Increase in milk yield of dairy cows through supplementation with B vitamins was reported, but the impact on reproductive performance of dairy cows in unknown. Objectives were to evaluate the effect of supplementation with a complex of rumen protected B vitamins (RPBV) that contained biotin, pantothenic acid, folic acid, cyanocobalamin, and pyridoxine to early lactating multiparous cows on milk yield, milk composition and reproductive performance during the first 170 d of lactation. Multiparous Holstein cows (n = 1243) that calved between November of 2007 and April of 2008 were assigned to 2 treatments as cows moved from fresh to one of the 4 early lactation pens: control diet (CT); and B vitamin diet (BV), supplementation with 3.6 g/cow/d of RPBV. Early lactation diets were identical for CT and BV treatments, except for the RPBV supplement fed in the first TMR load to the 2 treatment pens. Cows were artificially inseminated upon estrous detection every morning, and pregnancy diagnosis was performed by per rectum palpation at 42 ± 3 d after breeding. Yields of milk and milk composition were measured monthly. Body condition (BC) was scored from a subgroup of 170 cows at 40 and 100 DIM. A total of 949 cows provided data for statistical analysis, 448 CT and 501 BV cows. Cows were moved to treatment pens at 22.3 DIM. Loss of BC was similar ($P = 0.11$) for CT

(−0.055) and BV (−0.034) cows during early lactation, as well as group DMI, 25.4 and 25.0 kg/d, respectively. Milk yield was similar ($P = 0.18$) for BV and CT during the first 170 d of lactation, 44.9 vs. 44.4 kg/d, respectively. Milk fat content was reduced by feeding RPBV (3.29 vs. 3.38%; $P < 0.01$), but milk fat yield was not affected (1464 vs. 1485 g/d; $P > 0.15$). Day at first service was not different ($P = 0.44$) for BV and CT cows (67.9 vs. 67.2 d), but BV cows had higher ($P < 0.05$) first service conception rate than CT cows (40.8 vs. 35.8%). In summary, supplementation with a RPBV complex improved first service conception rate, whereas milk yield was not affected.

Key Words: biotin, folic acid, cyanocobalamin

T384 Effect of feeding live yeast on performance of Holstein cows during summer. R. S. Marsola*, M. Favoreto, F. T. Silvestre, J. H. Shin, A. T. Adesogan, C. R. Staples, and J. E. P. Santos, *University of Florida*, *Gainesville*.

Objectives were to evaluate the effect of amount of dietary live yeast (LY) intake on performance of cows under heat stress. Holstein cows, 27 multiparous and 33 primiparous, were blocked by parity and milk yield in the first 20 DIM and randomly assigned to receive 0 g/d LY, 0.5 g/d LY (20 billion cells/g, *Saccharomyces cerevisiae* strain CNCM I-1077, Levucell SC20, Lallemand Animal Nutrition, Milwaukee, WI), or 1 g/d LY in the diet from 30 to 107 DIM. Cows were milked twice daily and DM intake and milk yield were measured daily. Milk components were measured once weekly. Cows were weighed weekly. Blood was sampled weekly and analyzed for concentrations of NEFA. Cows were fed chromic oxide in the last 2 wk of the study for calculation of total tract digestibility of nutrients. Ruminal fluid was collected once by rumenocentisis 6 h after feeding for measurement of pH. During the study period, the mean daily temperature was 26.8 C and humidity was 83.2%, and the temperature and humidity index ranged from 73 to 81. Data were analyzed by the GLIMMIX procedure of SAS and linear and quadratic orthogonal contracsts were used. Rectal temperature was not affected by LY and averaged 38.9 ± 0.04°C. Feeding LY did not influence DMI, yields of milk, 3.5% FCM, energy-corrected milk (ECM), and milk fat. Feeding LY caused a linear increase in feed efficiency (ECM/DMI) and milk true protein yield, and had a quadratic effect on OM digestibility, but tended to decrease calculated energy balance. Mean rumen pH increased, and proportion of cows with low pH (<5.8) decreased linearly with LY. Feeding 1 g/d of LY increased efficiency of feed conversion into ECM, yield of true protein, and rumen pH, and reduced the risk of sub-acute rumen acidosis.

Table 1.

	g/d				P	
	0	0.5	1	SEM	Linear	Quadratic
DM intake, kg/d	20.9	20.3	20.3	0.4	0.25	0.61
Milk, kg/d	37.1	36.9	38.1	0.8	0.36	0.46
3.5% FCM, kg/d	36.0	35.0	37.4	0.9	0.33	0.12
ECM, kg/d	34.8	34.1	36.4	0.9	0.23	0.12
ECM/DMI	1.66	1.69	1.78	0.04	0.03	0.52
Milk fat, kg/d	1.23	1.18	1.27	0.04	0.42	0.12
Milk protein, kg/d	0.99	0.99	1.05	0.02	0.03	0.15
Energy balance, Mcal/d	3.33	2.99	1.68	0.61	0.06	0.51
NEFA, mEq/L	84	107	118	12	0.04	0.68
BW, kg	612	608	613	4	0.91	0.35
Rumen pH	5.99	6.03	6.30	0.11	0.04	0.40
pH < 5.8, % cows	45.0	36.8	10.5	—	0.02	0.27
OM digestibility, %	70.9	72.3	69.5	0.9	0.22	0.06

Key Words: dairy cow, heat stress, live yeast

T385 Population dynamics of protozoa in dairy cows fed with Rumensin200 and tallow during dry and lactating stages. H. Castillo, A. Castillo*, D. Dominguez, G. Villalobos, M. Arana, and J. A. Ortega, *Universidad Autonoma de Chihuahua*, *Chihuahua, Chihuahua, Mexico*.

Addition of Rumensin200 and tallow in TMR for dairy cows on protozoan populations was explored in dry and early-lactating cows. Ionophores have been used in ruminants to decrease acidosis and to mitigate gaseous emissions in dairy operations, by inhibiting growth of microorganisms such as protozoa. Also, tallow as an energy alternative in TMR has shown changes in fiber digestibility and gases production, mainly due to the interaction of its unsaturated component with rumen microorganisms. For this experiment, 4 ruminally fistulated Holstein cows were fed rations based on a 90:10 (dry) and 40:60 (lactating) forage to concentrate ratios. Four treatments were randomly assigned in a 4 × 4 Latin Square experimental design as follows: TMR (T1), TMR + 2/3.3 g Rumensin 200(dry/lactating), (T2), TMR + 3,2% DM tallow (T3) and TMR + 2/3,3 g Rumensin 200+ 3,2% DM tallow (T4). Samples of ruminal content were taken at 0, 1, 2, 4, 8, 12, 18 and 24 h after feeding, filtered, preserved with an equal volume of 5% formalin and frozen. Thawed samples were treated with brilliant green and glycerol for direct protozoa count on a Neubauer chamber under a microscope at 40X. Oxidation-reduction potential (ORP) and pH were recorded *in rumen* during the same sampling times. Total number of protozoa at 24 h after feeding did not differ ($P > 0.001$) among treatments in lactating cows, whereas the addition of Rumensin200 to TMR for dry cows caused a significant decrease ($P > 0.001$) in population size (5.0^5 vs. 1.06^5, respectively). Also, protozoa were less diverse in lactating compared with dry cows; while the *Diplodiniae* species were dominant (98%) in lactating cows with any treatment, dry cows fed T3 exhibited a more diverse community formed by 68% *Diplodiniae* and 29% *Entodinium*. Monitoring of pH did not show significant differences ($P > 0.001$) among treatments in both dry and lactating stages, while ORP values suggested a more reduced environment (−241 to –310 mV) in lactating than in dry cows (−234 to –294 mV). This experiment showed changes in protozoan community composition led by modification of the rumen environment.

Key Words: Rumensin, tallow, protozoa

T386 Construction and analysis of metagenomic fosmid library from rumen microflora of Chinese Holstein dairy cow. D. Li, J. Q. Wang*, K. L. Liu, D. P. Bu, and W. Feng, *State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences*, *Beijing, China*.

The vast majority of rumen microbial diversity has been inaccessible by culture dependent methods. Recent progress in molecular microbial ecology has reveled that traditional culturing methods fail to represent the scope of microbial diversity in rumen, since only less than 11% of viable microorganisms are recovered by culturing techniques. To investigate the full extent of microbial diversity and compare genomic studies among ruminant microflora species by metagenomic method, a fosmid library was constructed with genomic DNA isolated directly from rumen content. Preparation of ruminant genomic DNA for library construction was extracted by LMP agarose gel plug. Extracted ruminant genomic DNA was digested with *Hin*dIII. Purified DNA of 36–48 kb length was recovered by pulsed field electrophoresis and ligated with pcc2FOS vector and transformed into *E. coli* EPI300. The fosmid genomic library of rumen microbe was successfully constructed with the capacity of 1050 Mb in which the insert fragment size was about 35 kb, and about 30000 clones. Excluding the 2% of empty clones, the

coverage of this library is 93% genome equivalents. This fosmid library offers a new tool for gene screening and cloning, and for comparative genomic studies among ruminant microflora species.

Key Words: metagenomics, fosmid library, rumen microflora

T387 Effects of *Saccharomyces cerevisiae* and *Aspergillus niger* (fermentation soluble meal extracted) on productivity of Holstein cows in early lactation. R. Heydari, M. Dehghan-Banadaky*, K. Rezayazdi, and A. Zali, *Department of Animal Science, Campus of Agriculture and Natural Resources, University of Tehran*, *Karaj, Tehran, Iran*.

The objective of this study was to investigate the effects of feeding *Saccharomyces cerevisiae* (SC) and *Aspergillus niger* fermentation solubles meal extracted (AN) to early lactation cows. Twenty-four Holstein lactating cows (8 primiparous and 16 multiparous; 24 ± 7 DIM) were assigned to 1 of 4 dietary treatments as follows: 1) SC (Biosaf SC47)10 g/d/cow; 2) AN (Bospro) 30 g/d/cow; 3) SC 10 g/d/cow and AN 30 g/d/cow; 4) control (no additive). Cows were fed the same total mixed ration (19.5% alfalfa hay, 19.5% corn silage, 7.1% beet pulp and 53.9% concentrate on dry matter basis) and additives were top-dressed during experimental period (75 d). Milk production and DM intake were recorded daily and milk samples were collected weekly from all cows for measurement of somatic cell count (SCC) and milk composition. Blood samples were taken from each cow on the last day of experiment, 3 h after morning meal for metabolic profiling. Data (except blood data) were statistically analyzed using the repeated measures option in Proc Mixed of SAS. DMI was similar between treatments (21.44, 20.41, 21.83 and 21.54 kg/d, respectively). Cows fed SC (treatment 1 and 3) produced more milk than other groups, but fat corrected milk (FCM4%) was not significantly affected by treatments ($P > 0.05$). Milk protein percent significantly increased in cows fed SC as well as milk protein yield. However, other milk composition percentage and SCC were similar for all treatments. Changes in body weight and body condition score (BCS) were not influenced by treatments. Blood metabolites includes: glucose, nonesterified fatty acids, urea nitrogen, triglycerides and phosphorous were unaffected by treatments. These results indicate that supplementation of SC can improve milk production and milk composition, but AN did not affect productivity.

Key Words: *Saccharomyces cerevisiae*, *Aspergillus niger*, milk production

T388 Diversity of nitrogen-fixing bacteria in Holstein dairy cow rumen. S. Zhao, J. Wang*, D. Bu, L. Zhou, and C. Zhang, *State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences*, *Beijing, China*.

The rumen has a suitable environment for N_2-fixation, because of N_2 presence and the presents of some nitrogen fixing bacteria. The gene *nif*H encodes the dinitrogenase reductase, an enzyme for N_2 fixation, is conserved and used to analyze the phylogenetic diversity of the nitrogen-fixing microorganisms. To reveal the diversity of nitrogen-fixing microorganisms in dairy cow rumen, the *nif*H clone library was constructed. Rumen total DNA was extracted based on the method of freezing/thawing and N-lauroyl sarcosine/proteinase K lysis. Polymerase chain reaction was used to amplify the *nif*H genes from rumen total DNA. PCR products were purified and ligated to pMD19-T vector. *Nif*H gene clones got by transforming ligation product into *E.coli* JM109 were sequenced. The sequences were analyzed by Blast on GenBank and phylogenetic tree was built by Mega 4.0. In results, a total of 64 *nif*H gene clones were obtained. Most of the *nif*H genes belonged to *Fermicute* with the percent of 85.93%, and some belonged to *Archaea*, *α-Proteobacteria*, *Chlorobi* with the percent of 7.81%, 4.70%, 0.56%, respectively. The *nif*H phylogenetic tree also revealed that there was a remarkable diversity of nitrogenase genes in the rumen. The study provided first evidence for the diversity of nitrogen-fixing bacteria from dairy rumen.

Key Words: nitrogen-fixing bacteria, *nif*H, rumen

T389 Dietary cation-anion difference: Effects on fluid metabolites and health status of transition cows in Karst area. W. X. Wu*, *College of Animal Science, Guizhou University*, *Guiyang, China*.

There has little information of dietary cation-anion difference (DCAD, mmol/kg DM) on the performance of dairy cows in Karst area, especially in southwest, China. This study is conducted to evaluate the effects of DCAD on the fluid metabolites, health status, and subsequent lactation performance of transition cows in Karst area. Thirty pregnant, nonlactating Holstein multiparous cows were randomly assigned to 3 blocks of 10 cows based on their age (4 yr), body weight (600 kg), and expected calving date (21 d). Animals were fed 1 of 3 DCAD diets: control (+81), treatment 1 (+20), and treatment 2 (−32), respectively. Anionic salts were included to reduce DCAD. Feeding of reduced DCAD resulted in lower urinary pH than control ($P < 0.05$). Plasma Ca and Cl levels in treatment 2 was higher over those in control ($P < 0.05$). There were no significant difference in plasma glucose and urea nitrogen; Na, K, and P concentrations for 3 dietary treatments ($P > 0.05$). Anionic salts supplementation reduced the cases of hypocalcemia (3:1:1) and retained placenta (4:2:1). Dry matter intake, milk yield and contents of protein, fat, and lactose were unaffected by DCAD modulation ($P > 0.05$). These results suggested that negative DCAD is beneficial for transition cows in Karst area. Further study is necessary to investigate the effect of DCAD on the reproductive performance.

Key Words: dietary cation-anion difference, Karst area, transition cows

T390 Effects of subacute ruminal acidosis challenges on lipopolysaccharide endotoxin (LPS) in the rumen, cecum, and feces of dairy cows. S. Li, A. Kroeker, E. Khafipour, J. C. Rodriguez, D. O. Krause, and J. C. Plaizier*, *Department of Animal Science, University of Manitoba*, *Winnipeg, MB, Canada*.

Feeding high grain diets to cows can cause subacute ruminal acidosis (SARA) and increase the amount of dietary starch that is digested in the large intestine. Grain-induced SARA can increase free lipopolysaccharide endotoxins (LPS) in the rumen, due to increased lysis of gram-negative bacteria. Increased starch in the large intestine may also reduce the pH of the digesta, and increase LPS in the large intestine and in the feces. This could explain symptoms of SARA, as it may be easier for LPS to translocate into the blood in the large intestine than in the rumen. SARA can also be induced by feeding forage pellets. This does not increase the content of starch in the diet. Hence, the effects of this form of SARA on the large intestine may differ from that of grain-induced SARA. To test this, a study was conducted with non-lactating dairy cows with cannulas in the rumen and in the cecum. A Latin square with 3 4-wk periods was used. In wk 1–3 cows received a control diet containing 70% of forage (DM basis) and 30% mixed concentrates. In wk 4 cows received either the control diet, a high grain diet for a grain pellet-induced SARA challenge (GPI_SARA, 38% wheat-barley pellets, 32% mixed concentrates, and 30% of forages), or a diet that contained alfalfa pellets for an alfalfa-pellet induced SARA challenge (API_SARA, 45% of mixed concentrates, 32% of alfalfa pellets, and 23% of other forages). During this week, rumen pH was monitored continuously in all cows.

Rumen fluid, digesta from the cecum, and feces were sampled immediately before feed delivery and at 6 h after feed delivery. All samples were analyzed for LPS. The pH of cecum samples were determined. Both SARA challenges resulted in depressions of rumen pH that were representative of SARA, and decreased the pH of digesta in the cecum, but not as much as the rumen pH. GPI_SARA greatly increased LPS in the rumen, cecum, and feces. API_SARA increased LPS in the rumen, but not in the cecum and in the feces. Results confirm our hypothesis that grain-induced SARA, but not SARA induced by feeding pelleted forages, increases LPS in the large intestine and in the feces.

Table 1. Rumen and cecum pH and LPS in the rumen, cecum and feces

	Control	API_SARA	GPI_SARA	SEM	P-value
Average rumen pH	6.30[a]	5.99[b]	5.98[b]	0.04	<0.01
Time < rumen pH 6, min/d	332[b]	770[a]	744[a]	57	<0.01
Time < rumen pH 5.6, min/d	56[b]	255[a]	299[a]	30.7	<0.01
Cecum pH	7.07[a]	6.86[b]	6.79[b]	0.06	<0.01
Rumen LPS, EU/mL	8,333[b]	18,425[b]	124,566[a]	8,738	<0.01
Cecum LPS, EU/mL	18,289[b]	15,631[b]	128,410[a]	20,379	<0.01
Feces LPS, EU/mL	13,909[b]	18,998[b]	101.555[a]	16,355	<0.01

[a, b]Means with different superscripts in a row differ (P < 0.05).

Key Words: SARA, LPS, grain

T391 Supplementing *Megasphaera elsdenii* modulates diurnal rumen fermentation profile in dairy cows. Q. Zebeli[1], S. Iqbal[1], A. Mazzolari[1], S. M. Dunn[1], W. Z. Yang[2], and B. N. Ametaj*[1], [1]*University of Alberta*, *Edmonton, AB, Canada*, [2]*Agriculture and Agri-Food Canada*, *Lethbridge, AB, Canada*.

Megasphaera elsdenii is a direct-fed microbial possessing lactate-utilizing properties. We hypothesized that its supplementation might modulate the fermentation profile in the rumen of dairy cows. This study sought to evaluate the effects of supplementing *M. elsdenii* on diurnal volatile fatty acids (VFA) concentration and profile in the rumen fluid of mid-lactation dairy cows. Eight rumen-cannulated Holstein cows were used in a paired 2 × 2 crossover design with 2 21-d periods. All cows were offered a total mixed ration containing (dry matter basis) 32% rolled barley grain, 15% alfalfa hay, 40% barley silage, and 13% protein-, and vitamin-mineral supplement. A culture of 35 mL of *M. elsdenii* ATCC 25940TM, containing 10^7 - 10^9 CFU/mL, was inoculated daily via rumen fistula to each cow pertaining to the treatment group (TRT), whereas control cows (CTR) were inoculated with 35 mL of carrier only. Rumen samples were collected on d 21, shortly before the morning feeding at 0800 and every 2 h up to 2000, and VFA were analyzed by GC. ANOVA was conducted with MIXED procedure of SAS accounting for repeated measures. Data showed that treatment did not affect the concentration of total VFA (128 vs. 125 m*M*; $P > 0.05$), but lowered the molar proportion of acetate (61.3 vs. 59.9% of total VFA; $P < 0.01$) and isobutyrate (1.9 vs. 1.7%; $P < 0.01$). On the other hand, the TRT cows had greater proportions of butyrate (12.7 vs. 14.4%; $P < 0.01$) and valerate (1.9 vs. 2.3%; $P < 0.01$) than the CTR cows. There was an hour by treatment interaction for acetate to propionate ratio ($P = 0.03$) and the proportion of propionate in the rumen fluid ($P = 0.05$). Rumen caproate and isovalerate were not affected by treatment ($P > 0.05$). In conclusion, data of this study indicated that supplementation of *M. elsdenii* modulated the fermentation in the rumen of dairy cows shifting its profile from acetate to the production of butyrate and valerate.

Key Words: dairy cow, fermentation profile, *Megasphaera elsdenii*

T392 Effects of supplementing *Megasphaera elsdenii* on preprandial rumen fermentation profile in dairy cows. Q. Zebeli[1], S. Iqbal[1], A. Mazzolari[1], S. M. Dunn[1], W. Z. Yang[2], and B. N. Ametaj*[1], [1]*University of Alberta*, *Edmonton, AB, Canada*, [2]*Agriculture and Agri-Food Canada*, *Lethbridge, AB, Canada*.

Ingestion of large amounts of cereal grains leads to rapid accumulation of volatile fatty acids (VFA) and lactate in the rumen fluid and major changes in their profile. *Megasphaera elsdenii*, a rumen obligate anaerobe, has lactate-utilizing properties and the potential to modulate rumen fermentation profile by converting lactate into VFA. This study sought to evaluate the effects of supplementing *M. elsdenii* on VFA concentration and profile in the rumen fluid in mid-lactation dairy cows. Eight rumen-cannulated Holstein cows were used in a paired 2 × 2 crossover design with 2 21-d periods (first 11 d used for adaptation). All cows were offered a total mixed ration containing (dry matter basis) 32% rolled barley grain, 15% alfalfa hay, 40% barley silage, and 13% protein-, and vitamin-mineral supplement. A culture of 35 mL of *M. elsdenii* ATCC 25940TM, containing 10^7 - 10^9 cfu/mL, was inoculated daily via rumen fistula to each cow pertaining to the treatment group (TRT), whereas control cows (CTR) were inoculated with 35 mL of carrier only. Preprandial rumen samples were collected shortly before morning feeding on d 12, 14, 16, 18, and 21, and VFA were analyzed by GC. ANOVA was conducted with MIXED procedure of SAS accounting for repeated measures. Data showed that treatment did not affect the concentration of total VFA in the rumen fluid ($P > 0.05$), but tended to increase the molar proportion of propionate (19.9 vs. 21.0% of total VFA; $P = 0.09$), and lower the acetate to propionate ratio (3.32 vs. 3.09; $P = 0.07$). The TRT cows also had lower concentration of valerate (2.4 vs. 1.8 m*M*; $P = 0.04$) and isovalerate (2.7 vs. 2.2 m*M*; $P < 0.01$) than their CTR counterparts. Other VFA such as acetate, butyrate, isobutyrate, and caproate were not affected by the treatment ($P > 0.05$). In conclusion, results of this study indicated that supplementation of *M. elsdenii* slightly modulated the preprandial fermentation profile in dairy cows.

Key Words: dairy cow, fermentation profile, *Megasphaera elsdenii*

T393 Diagnosis of subacute ruminal acidosis (SARA) using the Optium Xceed Diabetes Monitoring System. S. Li[1], A. Kroeker[1], D. O'Gorman[2], D. O. Krause[1], J. C. Rodriguez[1], and J. C. Plaizier*[1], [1]*Department of Animal Science, University of Manitoba*, *Winnipeg, MB, Canada*, [2]*Marigot Ltd.*, *Carrigaline, Co. Cork, Ireland*.

The current diagnosis of subacute ruminal acidosis (SARA) relies on measuring the pH of rumen fluid samples, which are difficult to collect and may not be representative. Studies have reported that monitoring of blood glucose may aid in the diagnosis of SARA. However, SARA caused by feeding high grain diets and SARA caused by feeding diets with insufficient physically effective fiber, e.g., a diet containing alfalfa pellets, can affect blood glucose differently. This may affect the accuracy of this measurement for the diagnosis of SARA. The Optium Xceed Diabetes Monitoring System for glucose measurement was tested for the diagnosis of SARA. The study included 6 rumen cannulated nonlactating dairy cows in a 3 × 3 Latin square with 4 wk periods. In wk 1–3 cows received a control diet (70% forage and 30% mixed concentrates (DM basis)) . In wk 4, cows received either the control diet, a high grain diet for a grain pellet-induced SARA challenge (GPI_SARA, 38% wheat-barley pellets, 32% other mixed concentrate, and 30% forages), or a diet that contained alfalfa pellets for an alfalfa-pellet induced SARA challenge (API_SARA, 45% mixed concentrate, 32% alfalfa pellets, and 23% other forages). During wk 4, rumen pH was monitored in all cows, and blood was sampled immediately before feed delivery and at 6 h after feed delivery. Glucose in whole blood was measured using

the Optium Xceed Diabetes Monitoring System, which can be used on farm. The average daily rumen pHs were 6.30, 5.99, and 5.98, for control, API_SARA, and GPI_SARA, respectively. The durations of the rumen pH below 5.6 were 56.4, 225.2 and 298.7 min/d for control, API_SARA, and GPI_SARA, respectively. This shows that both forms of SARA resulted in similar depressions of rumen pH and that SARA was induced. Blood glucose was higher during GPI_SARA than during control (4.47 vs. 4.25 mmol/L,), but blood glucose did not differ between the API_SARA and control. This shows that the Optium Xceed Diabetes Monitoring System can aid in the diagnosis of grain induced SARA, but that additional tests may be needed for the diagnosis of SARA caused by diets with insufficient physical effective fiber.

Key Words: SARA, diagnosis, blood

T394 Simplified procedure for quantifying ruminal microbe populations using real-time PCR. C. R. Mullins*, L. K. Mamedova, and B. J. Bradford, *Kansas State University*, *Manhattan*.

A variety of molecular techniques exist to quantify ruminal microbiota; however, sample processing requirements for most techniques are complex and time consuming. The objective of this work was to use real-time PCR to quantify relative abundance of 10 microbial populations while simplifying the sample preparation process. Our trial utilized ruminal contents from 8 ruminally cannulated Holstein cows used in a 4 × 4 Latin square experiment that examined the effect of varying wet corn gluten feed inclusion rate (0–36% DM). Rumen samples were collected every 9 h over a 3-d period so that 8 samples were taken from each cow each period, representing every 3 h of a 24-h period, thus accounting for diurnal variation. Digesta and rumen fluid were collected as one sample to capture the free-floating and particle adherent microbes in similar proportions as found in the rumen. Samples were collected from 5 locations throughout the rumen, mixed, and a representative subsample (200 g) was collected and frozen at −20°C. Prior to processing, samples were thawed at room temperature until they became pliant, then composited by cow period. Each composited sample was diluted with distilled, deionized water at a 1:1 ratio and homogenized. A subsample was then obtained from the homogenized mixture and used for microbial DNA isolation using a commercial kit (Zymo Research Fecal DNA kit). Quantitative real-time PCR was used to determine relative abundance of bacterial populations using previously validated primers specific for genes encoding 16S ribosomal RNA. Efficiencies were calculated to determine population abundance relative to the total bacterial population. Dietary treatments had few effects, but diets that decreased ruminal pH tended to decrease the *Butyrovibrio fibrosolvens* population ($P = 0.09$).The relative population densities for most species quantified were within the range reported previously; for example, the *Prevotella* genera and *Fibrobacter succinogenes* accounted for 39.9% and 1.0% of the ruminal bacteria, respectively. This procedure offers a simpler and quicker means to quantify relative abundance of rumen microbial populations.

Key Words: rumen, real-time PCR, DNA extraction

T395 Effects of forage-to-concentrate ratio and rumen fermentation characteristics on apparent ruminal synthesis of niacin and vitamin B6 in lactating dairy cows. M. Seck*[1,3], J. A. Voelker Linton[2], M. S. Allen[2], P. Y. Chouinard[3], and C. L. Girard[1], [1]*Agriculture and Agri-Food Canada*, *Sherbrooke, Quebec, Canada*, [2]*Department of Animal Science, Michigan State University*, *East Lansing,* [3]*Departement de sciences animales, Universite Laval*, *Quebec, Quebec, Canada*.

Effects of forage-to-concentrate ratio and rumen fermentation characteristics on apparent ruminal synthesis and post-ruminal supply of niacin (B3) and vitamin B6 were evaluated in an experiment using 14 ruminally and duodenally cannulated Holstein cows. The experiment was a crossover design with 2 15-d treatment periods and a preliminary period in which dry matter intake (pDMI) of a diet intermediate in composition between the treatments was determined. Treatments were diets containing low-forage (LF; 44.8% forage, 32.8% starch, 24.4% NDF) or high-forage (HF; 64.1% forage, 22.5% starch, 30.7% NDF) concentrations. No interactions between treatment and pDMI were observed ($P \geq 0.2$). LF decreased B3 intake (1035 vs. 1135 ± 16 mg/d; $P \leq 0.01$) but increased apparent ruminal synthesis (2831 vs. 1885 ± 250 mg/d; $P \leq 0.01$) and duodenal flow (3866 vs. 3020 ± 255 mg/d; $P \leq 0.01$) of B3 compared with HF. Although B6 intake was not influenced (91 vs. 89 ± 1; $P > 0.1$) by treatments, LF decreased apparent ruminal degradation (−3 vs. −20 ± 3 mg/d; $P \leq 0.01$) and increased B6 duodenal flow (88 vs. 68 ± 4 mg/d; $P \leq 0.01$) compared with HF. B3 flow tended to be correlated positively to B3 intake (r = 0.36, $P = 0.06$) while B6 flow was correlated positively to B6 intake (r = 0.73, $P < 0.01$). Ruminal synthesis and duodenal flow of B3 and B6 were correlated negatively to mean ruminal pH (r = −0.45, $P < 0.02$ for all) and correlated positively to true ruminally degraded starch (kg/d; r = 0.42, $P < 0.03$ for all). Ruminal synthesis and duodenal flow of B3 and duodenal flow of B6 were correlated positively to microbial N flow (g/d, r = 0.51, $P < 0.01$ for all). Niacin and vitamin B6 supply to dairy cows is increased with greater dietary starch concentration and starch digestion in the rumen.

Key Words: dairy cow, niacin, pyridoxine

T396 The effect of high inclusion of monensin on lactation performance in dairy cows. L. R. Behling*[1], K. Perfield[2], R. Martin[1], R. Greenfield[1], and S. Onetti[1], [1]*Vita Plus Corporation*, *Madison, WI*, [2]*Elanco Animal Health*, *Greenfield, IN*.

Three free-stall herds were used to conduct on-farm trials to determine if a high inclusion of monensin (MON) in the lactating cow TMR would affect milk fat production. Each herd provided 2 pens each of cows at similar DIM, parity and age. Herds were fed typical Midwestern diets, composed of alfalfa haylage and corn silage. Diets were formulated for 17.3% CP, 25.6% starch and 22.2% NDF from forage, DM basis. The trials were conducted during winter (Dec and Jan) and summer (Jul and Aug) in 2009 to evaluate potential interactions between season and MON inclusion. All cows were fed MON at an inclusion of 11.4 g/ton DM before the start of the trial. At the beginning of the trial, MON was removed from the diets in the control pens, and increased to 15.3 g/ton in the treatment pens, based on formulated DMI of 23.7 kg/d. After 2 weeks, treatment pens were increased to 19.1 g MON/ton. After 4 weeks at 19.1 g/ton, milk samples were collected from the milk line for each pen and pen milk weights were recorded. Data were analyzed using MIXED models of SAS. The model included fixed effects of treatment, season and their interaction. Herd was the specified term for the random statement. There were no season x treatment interactions on milk production and components. Inclusion of MON had no effect on milk yield, milk fat % or milk fat and protein yield. Milk protein % was significantly decreased by MON inclusion and MUN was significantly lower in the winter. In summary, inclusion of MON at 19.1 g/ton did not affect milk fat production.

Table 1. Milk production of dairy cows after 4 weeks of supplementation with 19.1 g MON/ton DM

	Winter		Summer	
	g MON/ton DM			
Variable	0	19.1	0	19.1
Milk, kg	36.3	37.1	34.5	36.1
Fat, %	3.71	3.73	3.80	3.74
Fat, kg	1.33	1.37	1.33	1.37
Protein, %[a]	3.21	3.14	3.17	3.09
Protein, kg	1.15	1.14	1.11	1.15
MUN, mg/dL[b]	11.8	11.7	15.4	15.9

[a]Significant treatment effect at $P < 0.05$.

[b]Significant seasonal effect at $P < 0.05$.

Key Words: monensin, milk fat, dairy cows

T397 Effects of a microbial fermentation product on milk production and blood metabolites on commercial dairies in eastern Canada. A. M. Gehman*[1], J. D. Johnston[2], and J. M. Tricarico[1], [1]*Alltech*, *Brookings, SD,* [2]*Ritchie Feed and Seed, Ottawa, Ontario, Canada.*

Three dairy farms located in Ontario and Quebec, Canada, were utilized to determine effects of feeding a microbial fermentation product (MFP; CP = 47% DM; soluble CP = 40% CP) on milk production, components, and blood metabolites of lactating dairy cattle. The study was conducted as a crossover design with 2 21-d periods. Experimental rations were: 1) control, 0 g/d MFP; or 2) MFP, 600 g/d MFP. Diets were isonitrogenous and isoenergetic. The MFP ration was formulated to provide 600 g/head/d MFP (2.1% ration DM) by replacing a portion of plant-based protein. Each farm was assigned to one of 2 treatment sequences: control followed by MFP or MFP followed by control. Milk production and feed intake were recorded for the last 2 d of each period, and blood samples were taken from 15 randomly selected cows on each farm during the last week of each period. Average DIM for cows that were blood sampled was 200 for control and 147 for MFP. Milk was analyzed for fat and protein, and blood was analyzed for non-esterified fatty acids (NEFA), β-hydroxybutyric acid (BHBA), and blood urea nitrogen (BUN). Energy-corrected milk tended to be greater ($P = 0.09$) for MFP than control (36.1 vs. 33.3 ± 0.8 kg/d), while dry matter intake was not different, ave: 24.0 ± 0.5 kg/d. Milk fat content was and yield tended to be higher ($P = 0.03$ and 0.09) for MFP than control (3.96 vs. 3.86 ± 0.05% and 1.34 vs. 1.22 ± 0.03 kg/d). Milk protein content was not different between treatments, ave: 3.34 ± 0.06%, but yield was greater ($P = 0.04$) for MFP than control (1.13 vs. 1.05 ± 0.02 kg/d). While BHBA and NEFA were not different between treatments, ave: 0.68 ± 0.03 and 0.17 ± 0.04 mmol/L respectively, BUN was greater ($P = 0.02$) for MFP than control (4.95 vs. 4.53 ± 0.04 mmol/L). Including MFP in a ration at 600 g/d increased energy-corrected milk by 2.8 kg/d and both milk fat and protein yield by 0.12 kg/d, while not affecting dry matter intake. Blood metabolites BHBA and NEFA were not affected by MFP, suggesting the increase in production and components was not due to mobilization of body reserves.

Key Words: dairy cow, microbial fermentation product, milk

T398 Effect of *Megasphaera elsdenii* NCIMB 41125 (Me) on production of lactating dairy cows. P. H. Henning*[1], L. J. Erasmus[2], C. H. Horn[3], and H. H. Meissner[1], [1]*MS Biotech*, *Centurion, South Africa*, [2]*University of Pretoria*, *Pretoria, South Africa*, [3]*Biotherapeutics*, *Centurion, South Africa*.

High concentrate intake in fresh cows pose an acidosis risk. *M. elsdenii* (Me) is a key ruminal lactic acid utilizer, but its numbers may be low in early lactation. Me was isolated from rumens of cattle adapted to high concentrate diets. The objective of this study was to evaluate use of Me as direct fed microbial (DFM) for dairy cows. Sixty multiparous Holstein cows were blocked according to previous milk production and BW, and randomly assigned to 4 treatments in a 2x2 factorial design. Treatments were + or - Me and low (L) or high (H) concentrate diet. The +Me cows were orally dosed with Me (10^{11} cfu once on each of d 1, 10 and 20 postpartum). The -Me cows received a placebo. Diets L and H, respectively, contained (g/kg DM) ground corn (354, 482), alfalfa hay (319, 196), *Eragrostis curvula* hay (79, 79), non-fiber carbohydrate (NFC) (448, 504) and neutral detergent fiber) NDF (282, 238). DM intake and milk yield (daily), milk composition (weekly) and BW and BCS (monthly) were measured for the first 80 d of lactation. Data were analyzed as a completely randomized block design (Genstat 5). Contrasts (+ vs. –Me for all cows, L cows and H cows, respectively) were used to determine significance of treatment effects. Since higher-producing cows may be more prone to acidosis results were also analyzed using only the 10 highest-producing cows in each treatment group. With all cows included, dosing with Me resulted in greater milk production ($P = 0.10$) (35.1 vs. 33.1 kg/d), higher mean BW ($P = 0.02$) (640 vs. 610 kg) and better BCS ($P = 0.06$) (2.63 vs. 2.38), while milk fat % was increased ($P = 0.03$) (3.14 vs. 3.07) for L cows. With only highest-producing cows included, dosing with Me increased milk production for the H group ($P = 0.06$) (39.3 vs. 35.9), without a significant increase in DM intake, and increased (both $P = 0.02$) BW (644 vs. 597) and BCS (2.71 vs. 2.26). Milk fat was again increased ($P = 0.06$) (3.56 vs. 3.21) for the L cows. Results suggest that dosing with *Megasphaera elsdenii* NCIMB 41125 may improve milk production, milk fat, body weight and body condition score, with greater benefit likely for higher-producing cows on higher concentrate diets.

Key Words: *M. elsdenii*, acidosis, dairy cows

T399 Effect of soluble yeast protein extract and dietary fermentable carbohydrate on fermentation, digestion, and N flow in rumen-simulating fermenters. G. A. Harrison*, M. D. Meyer, and K. A. Dawson, *Alltech*, *Nicholasville, KY*.

Effects of addition of soluble yeast protein extract (SYPE) to diets differing in fermentable carbohydrate (fCHO) content were investigated in single-flow rumen-simulating fermenter cultures. Twelve cultures were used in a 2 × 2 factorial design with 4 dietary treatments and 3 replications per treatment. Daily feed amounts provided to cultures were 24.1, 24.76, 24.34, and 25 g for low fCHO, low fCHO + SYPE, hi fCHO, and hi fCHO + SYPE treatments, respectively, with twice daily feeding for 6 d. SYPE was included at 2.64% of diet to raise dietary CP to 17.5 from 16.6% (DM basis). Fermentation samples were collected from cultures before morning feeding during the last 3 d of experiment. Composite effluent samples from each fermenter were used for DM and NDF disappearance and volatile fatty acid (VFA) analyses. Nitrogen flow measures were estimated by using purine to N ratios for effluent and bacteria. Data were analyzed for effects of treatment using GLM procedure of SAS and fCHO and SYPE effects determined by orthogonal contrasts. Culture pH and ammonia concentration before morning feeding were higher in cultures fed low fCHO diets ($P < 0.05$) and ammonia concentration higher in cultures fed SYPE ($P < 0.05$). Cultures fed lower fCHO diets had greater molar proportion of acetate, lower molar proportion of butyrate ($P < 0.0001$), and lower total VFA concentration ($P < 0.01$). Digestion of true DM was greater when cultures received higher fCHO diets ($P < 0.05$). Bacterial N yield was not affected by fCHO or

SYPE ($P > 0.10$) but an interaction between fCHO and SYPE was noted with an increase in bacterial N yield with SYPE addition to hi fCHO diets of 9.6% ($P < 0.05$). Efficiency of bacterial N production based on fCHO provided was greater in lower fCHO cultures ($P < 0.001$). The effects of soluble yeast protein extract addition were dependent upon dietary fermentable carbohydrate with positive responses in bacterial yield on higher fCHO diets.

Key Words: soluble yeast protein extract, fermentable carbohydrate, ruminal metabolism

T400 Effect of soluble yeast protein extract and culture feed rate on fermentation, digestion, and N flow in rumen-simulating fermenters. G. A. Harrison*, M. D. Meyer, and K. A. Dawson, *Alltech*, *Nicholasville, KY*.

Effects of soluble yeast protein extract (SYPE) and culture feed rate (FR) were investigated in single-flow rumen-simulating fermenter cultures. Twelve cultures were used in a 2 × 2 factorial design with 4 dietary treatments and 3 replications per treatment. Dietary treatments were low FR SBM, low FR SYPE, hi FR SBM, and hi FR SYPE with twice daily feeding for 6 d. Culture daily feed rates (as fed) were 20 and 30 g for low and high FR, respectively, and SYPE was included at 2.64% (DM basis) and primarily replaced soybean meal. Fermentation samples were collected from cultures before morning feeding during the last 3 d of experiment. Composite effluent samples from each fermenter were used for DM and NDF disappearance and volatile fatty acid (VFA) analyses. Nitrogen flow measures were estimated by using purine to N ratios for effluent and bacteria. Data were analyzed for effects of treatment using GLM procedure of SAS with FR and SYPE effects determined by orthogonal contrasts. Culture pH before morning feeding was lower in hi FR cultures ($P < 0.0001$). Mean ammonia concentration before morning feeding was not affected by treatment ($P > 0.10$). Volatile fatty acid pattern was altered by feed rate with molar proportions of acetate and isoacids being lower ($P < 0.05$) and molar proportion of butyrate higher with increased feed rate ($P < 0.001$). Cultures fed more feed had increased total VFA concentration ($P < 0.0001$). Digestion of true DM and NDF were not affected by treatment ($P > 0.10$). When feed rate was increased, increases were noted in measured g of RDP and bacterial N yield ($P < 0.01$). No differences were detected in fermentation, digestion, and N flow due to SYPE ($P > 0.10$). A numerical increase in bacterial N yield was observed when SYPE replaced SBM in the higher FR cultures (10.2%) but not in the lower FR cultures (interaction; $P > 0.10$). Culture feed rate influences fermentation pattern N flow in rumen-simulating fermenters.

Key Words: soluble yeast protein extract, culture feed rate, ruminal metabolism

T401 Effect of essential oils on rumen fermentation, milk production, and feeding behavior in lactating dairy cows. L. R. Tager* and K. M. Krause, *West Virginia University*, *Morgantown*.

Eight ruminally cannulated lactating Holstein dairy cows were used in a Latin rectangle design to assess the effects of 2 commercial essential oil (EO) products on rumen fermentation, milk production, and feeding behavior. Cows were fed a TMR with a 42:58 forage:concentrate ratio (DM basis). Treatments included addition of: 0.5 g/d XT 6965 (CEL; 85 mg cinnamaldehyde and 140 mg eugenol), 10 g/d XT 6965 (CEH; 1700 mg cinnamaldehyde and 2800 mg eugenol), 0.25 g/d XT 6933 (CAP; capsicum), or no oil (CON). Cows were fed ad-libitum twice daily for 21 d per period. Total VFA, individual VFA, acetate:propionate ratio, and ammonia production were not affected by EO ($P > 0.05$). Mean rumen pH as well as bouts, total h, mean bout length, total area, and mean bout area under pH 5.6 did not differ among treatments ($P > 0.05$). Total tract digestibility of OM, DM, NDF, ADF, CP, and NSC were not affected by EO ($P > 0.05$). In situ DM disappearance was not affected by EO ($P > 0.05$). However, OM disappearance tended to decrease compared with CON ($P = 0.08$; 60.3% vs. 57.6%) with CEH. Compared with CON, NDF disappearance ($P = 0.05$; 41.5% vs. 37.6%) and ADF disappearance ($P = 0.04$; 44.5% vs. 38.8%) decreased with addition of CEH. DMI, number of meals/d, h eating/d, mean meal length, rumination events/d, h ruminating/d and mean rumination length were not affected by EO ($P > 0.05$). However, length of the first meal after feeding decreased with addition of CEH (47.2 min) and CAP (49.4 min) compared with CON (65.4 min; $P = 0.01$). Milk yield and composition did not differ. CEL had no effect on rumen fermentation, milk production, or feeding behavior. CAP shortened length of the first meal without changing rumen fermentation or production, making it a possible additive for altering feeding behavior. CEH negatively affected rumen fermentation and altered feeding behavior, suggesting that a dose of 10 g/d is not beneficial to lactating dairy cows.

Key Words: essential oil, dairy nutrition, rumen fermentation

T402 Rumen-protected choline affects methionine methyl group metabolism in lactating dairy cows. S. L. A. Benoit, B. J. Bequette, and R. A. Erdman*, *University of Maryland*, *College Park*.

Methionine (Met) is a precursor for protein synthesis and the primary donor of labile methyl groups. We hypothesized that milk production responses to rumen protected choline (RPC) relate to choline sparing Met as a methyl donor. The objectives of this study were to determine the bio-availability of RPC and whether Met methyl group flux is reduced when dairy cows are fed RPC. Four multiparous Holstein cows in mid lactation were fed a nutritionally complete basal diet except for Met that was limited to 1.49% of metabolizable protein. Treatments included the basal diet or the basal diet plus 15g/d RPC as choline chloride (Reashure, Balchem Corp., New Hampton, NY) in single reversal design with 2 wk periods. Metabolic fates of Met were measured by continuous i.v. infusion of [1-^{13}C] and [methyl-^{13}C] Met, and [trimethyl-C^2H_3] choline for 12 h on d 14 of each period. Milk was collected at 3 h intervals and blood taken over the last 6 h. Supplementation with RPC did not affect total milk yield or milk fat and protein yields which averaged 39 kg/d, 1634 g/d and 1110 g/d, respectively. Based on plasma [1-^{13}C] Met and [methyl-^{13}C] Met enrichments, total Met flux, irreversible loss, and remethylation were not affected by treatment, averaging 15.2, 11.5, and 4.2 mmol/h, suggesting that 24% of Met was remethylated. In contrast, using plasma [1-^{13}C] homocysteine as the true intracellular precursor, total Met flux, irreversible loss, and remethylation rates (mmol/h) were 80.1, 67.6 ($P = 0.04$); 38.3, 33.5; and 41.8, 34.1 ($P = 0.07$), for control and RPC, respectively. Differences in plasma vs. casein [methyl-$^2H_3$] Met labeling, which arises from [trimethyl-C^2H_3] choline, suggested that ~40% of Met in the mammary gland underwent transmethylation with choline serving as the methyl donor. Finally, based on treatment differences in Met methyl flux, the bio-availability of RPC approximated to 72%. These results illustrate the central role of Met and choline in methyl metabolism and the importance of methyl group transactions in the high producing dairy cow.

Key Words: methionine, methyl metabolism, dairy cows

T403 Cloning and identification of novel hydrolase genes from a metagenomic library of dairy cow rumen microflora and characterization of the expressed cellulases. X. Gong*, M. Qi, R. J. Forster, T.

A. McAllister, and R. M. Teather, *Agriculture and Agri-Food Canada Research Centre*, *Lethbridge, AB, Canada*.

A 6,000-clone metagenomic bacterial artificial chromosome (BAC) library was constructed from microbial flora DNA extracted from the rumen contents of a grass hay-fed dairy cow and activity-based screening was employed to explore the functional hydrolase genes. Ninety-four independent clones specifying distinct hydrolytic activities (51 esterases, 18 xylanases and 25 cellulases) were identified. Subcloning and sequence analysis of a subset of these hydrolase-positive clones identified 10 endoglucanase genes. Amino acid sequences of 5 of these genes indicated less than 55% homology among them, while similarity to the cellulases in the National Center for Biotechnology Information (NCBI) databases averaged 70%. Glycoside hydrolase families 5, 8 and 9 were represented by 6, one, and 3 of the 10 endoglucanases, respectively. Subcloning and sequence analysis of a subset of the esterase-positive clones identified 10 esterase genes. These shared less than 33% homology, with an average similarity of 53% to esterases in the databases, as assessed by predicted amino acid sequence. Preliminary characterization of the encoded cellulases was carried out using crude extracts of each of the subclones. Zymogram analysis using carboxymethylcellulose as a substrate showed a single positive band for each sample, confirming that only one functional cellulase gene was present in each subclone. Optimal pH for these cellulases ranged from 6.5 to 7.0 and their optimal temperatures were 40°C to 50°C. All the endoglucanases could hydrolyze a wide range of β-1,3-, and β-1,4-linked polysaccharides with varying activities. The present work revealed an increased diversity of functional cellulases and esterases in the rumen.

Key Words: esterase, ruminal microorganisms, BAC library

T404 Development of a diet inoculate with two substrates by submerged solid fermentation. D. Díaz-Plascencia*[1], C. Rodríguez-Muela[1], F. Salvador[1], J. Jiménez[1], H. Rubio[2], S. Mena[3], and A. Elías[4], [1]*Universidad Autónoma de Chihuahua*, *Chihuahua, México*, [2]*Instituto Nacional de Investigaciones Agrícolas Forestales y Pecuarias*, *Chihuahua, México*, [3]*Universidad de Guadalajara*, *Jalisco, México*, [4]*Instituro de Ciencia Animal*, *La Habana, Cuba*.

To evaluate 2 substrates (apple byproduct (AB) and sugar cane molasses (CM)) in the preparation of an inoculate with yeasts for ruminant rations, 2 yeasts strains (YS) were used by submerged solid fermentation (YS A, commercial yeast of the *Saccharomyces cerevisiae* and YS D, *Kluyveromyces lactis*, obtained by apple pomace fermentation) under aerobic conditions in a liquid medium. Treatments used were Tr1: 200 mL of AB + 1 g of YS. Tr2: 132 mL of AB + 34 g of CM + 1 g of YS. Tr3: 66 mL of AB + 66 g of CM + 1 g of YS. Tr4: 100 g of CM + 1 g of YS. All treatments were employed for growth of both YS. Treatments were added with 1.2% of urea, 0.2% of ammonium sulfate, 0.5% of mineral supplement. Fermentation was carried out in flasks of 1,000 mL with distilled water. Five replicates by Tr and different sampling times (0, 12, 24, 48 and 96 h) were used. Variables evaluated were: pH, temperature, soluble carbohydrates, yeast count, ammonia and lactic acid. Data were analyzed as a randomized 4 × 2 factorial design in a split-plot experiment. Results showed different ($P < 0.01$) pH behavior among the substrates. Temperature had an increase ($P < 0.01$) from 0 h to 12 h in all treatments. Ammonia was different ($P < 0.01$) among treatments and among YS. Lactic acid showed effect ($P < 0.01$) among treatments and among YS. Soluble carbohydrates were different ($P < 0.01$) among treatments, YS and sampling time. Yeast count of YS D was higher ($P < 0.01$) in Tr4 with value of $2.8 \times 10^9 \pm 0.05$ cell.mL^{-1} at 48 h, versus YS A count of $9.6 \times 10^8 \pm 0.05$ cell.mL^{-1} in Tr4 at the 96 h. It can be concluded that the use of sugar cane molasses, increases the growth of yeast, especially *K. lactis*, during the preparation of a diet inoculated by submerged solid fermentation.

Key Words: yeasts, fermentation, apple byproduct

T405 Glycerol can replace corn grain in diets for transition dairy cows. E. R. Carvalho*, N. S. Schmelz, H. White, and S. S. Donkin, *Purdue University*, *West Lafayette, IN*.

Expansion of the biofuels industry has increased the availability of glycerol as an alternative feed for dairy cows. The objective of this study was to determine the effects of glycerol on feed intake, milk production, rumen VFA, and metabolic parameters in transition dairy cows. Twenty-six multiparous Holstein cows were paired by expected calving date and fed diets containing either high moisture corn or glycerol from −28 through +56 d relative to calving. Glycerol was included at 11.5 and 10.8% of the ration DM for the pre- and postpartum diets, respectively. Prepartum feed intake was not changed ($P \geq 0.05$) by glycerol feeding (14.6 vs. 14.9 kg/d, glycerol vs. control) nor did postpartum feed intake differ ($P \geq 0.05$; 20.7 vs. 19.8 kg/d, glycerol vs. control). Overall milk yield did not differ ($P \geq 0.05$; 37 vs. 35.8 kg/d, glycerol vs. control), but there was a tendency ($P \leq 0.15$) for a treatment × week of lactation effect that was greater for glycerol. There were no effects of glycerol on milk composition, milk urea nitrogen, somatic cells, and energy balance ($P \geq 0.05$). During the prepartum period, blood glucose was reduced ($P \leq 0.05$; 53.4 vs. 59.1 mg/dL, glycerol vs. control) and β-hydroxybutyrate was increased ($P \leq 0.05$; 0.82 vs. 0.58 mmol/L, glycerol vs. control) in cows fed glycerol. Concentrations of blood nonesterified fatty acids did not differ between the treatment groups ($P \geq 0.05$), and there was no response ($P \geq 0.05$) to glycerol for blood metabolites during the postpartum period. Total rumen VFA (mmol/L) did not differ ($P \geq 0.05$; 85.9 vs. 82.3, glycerol vs. control), but percentage of rumen propionate (28.6 vs. 22.7%, glycerol vs. control) and butyrate (15.3 vs. 11.5%, glycerol vs. control) were greater ($P \leq 0.05$) for cows fed glycerol at the expense of acetate (51.5 vs. 61.4%, glycerol vs. control). These data indicate that glycerol is a suitable replacement for corn grain in diets for transition dairy cows and suggest that glycerin, a biofuels coproduct, is compatible with transition cow health and productivity.

Key Words: biofuels, glycerol, transition cows

T406 Evaluation of performance of lactating dairy cows supplemented with branched chain volatile fatty acids (Nutricattle). E. R. Val Neto*[1], R. P. Lana[1,2], H. N. Val[3], M. I. Leão[1], and A. B. Mâncio[1], [1]*Universidade Federal de Viçosa*, *Viçosa, MG, Brazil*, [2]*CNPq*, *Brasília, DF, Brazil*, [3]*Faculdades Associadas de Uberaba (FAZU)*, *Uberaba, MG, Brazil*.

Tropical pasture is the main source of cattle feed, but in the dry season it is deficient in protein, which is essential for microbial growth. The search for technology to increase animal performance may be a feasible alternative to reduce costs with dairy cattle nutrition. This work aimed to compare the performance and the efficiency of lactating cows on pasture, supplemented with concentrate containing 16% crude protein (CP) on dry matter basis using cottonseed meal with 38% CP as protein source, with or without a feed additive containing branched chain volatile fatty acids (Nutricattle). Twenty-four lactating Holstein × Gir crossbred cows were evaluated (average body weight = 436.5 kg, days in milk = 119, body condition score = 2.75, and average milk yield = 7.55 L/day). Animals were offered 1.0 kg/animal/day of concentrate in 2 milking times. In the first week, cows were fed the same diet. After the adaptation period, each lot was randomly assigned to feed the concentrate with or without 24 g of additive/cow/day. Data were analyzed in a randomized blocks design, including milk production and body condition score as covariates, using F test. Although there was a reduction in supplement intake in the fourth week, average milk yield of the additive treatment (8.3 L) was higher ($P = 0.01$) than the average milk yield of the control (7.3 L). There was no difference in the final body condition score between treatments ($P = 0.48$), but the additive increased 0.5 units during the experimental period. In relation to milk quality, no difference was observed in milk fat ($P = 0.21$) and cryoscopy ($P = 0.71$) between treatments. Therefore, although pastures usually have good quality during the rainy season, according to this result, the inclusion of Nutricattle additive was nutritionally efficient, increasing milk production by 12%.

Key Words: cattle, nutrition, volatile fatty acids

T407 Intake and apparent nutrient digestibility in dairy cows fed with different levels of sunflower cake in the ration. E. S. Pereira*[1], P. G. Pimentel[1], M. R. G. F. Costa[1], J. G. L. Regadas Filho[2], and J. E. L. Sousa[1], [1]*Universidade Federal do Ceará*, *Fortaleza, Ceará, Brasil*, [2]*Universidade Federal de Viçosa*, *Viçosa, Minas Gerais, Brasil*.

The aim of this study was to evaluate the intake and apparent nutrient digestibility of dairy cows fed rations containing increasing levels of sunflower cake (SC). The SC has an average 164.29 g/kgDM of crude protein (CP) and 116.28 g/kgDM of ether extract (EE). Eight multiparous Holstein × Zebu cows, between 50 and 74 d in milk and 20 ± 2 kg milk/day were allocated in a 4 × 4 double Latin square design. Sunflower cake was fed in the concentrate at the levels of 0; 7; 14 and 21% and Tifton hay was used as main forage in a 60:40 forage to concentrate ratio. The PROC GLM of SAS was used for the statistical analysis. Periods were 16 d long; the first 10 d of each period were for dietary adaptation, with weight and samples of diets, refusals and feces taken during d 11 to 16 of each period to determine the consumption and apparent digestibility of dry matter (DM) and nutrients. Meals were offered to allow 10% refusals according to the calculated ration consumed on the previous day. The internal marker indigestible acid detergent fiber was used to estimate the fecal DM excretion. The ether extract content of the experimental rations was, respectively, 27.14; 29.79; 31.15 and 35.41g/kgDM, to the levels 0; 7; 14 and 21% of SC inclusion. Dry matter intake of the rations was not affected by the treatments (14.06 kg/day, 2.75% of live weight and 130.89 g/kg of unit metabolic body weight). The intake of the rations without SC and at the level of 21% varied of 0.39 to 1.09 and 9.18 to 10.88 g/day, respectively, for EE and total digestive nutrients, showing linear increase ($P = 0.001$). The apparent digestibility of DM and neutral detergent fiber increased linearly with the addition of the byproduct (69.96 to 72.43 and 59.85 to 64.13%, respectively), while the digestibility of CP and EE showed quadratic behavior ($P < 0.05$). Sunflower cake can be recommended as a potential alternative for feeding dairy cows at the maximum level of inclusion of 21% in the concentrate.

Key Words: byproducts, lipids, ruminants

T408 Milk production and composition from cows with different levels of sunflower cake in the ration. E. S. Pereira*[1], P. G. Pimentel[1], M. R. G. F. Costa[1], J. G. L. Regadas Filho[2], and J. E. L. Sousa[1], [1]*Universidade Federal do Ceará*, *Fortaleza, Ceará, Brasil*, [2]*Universidade Federal de Viçosa*, *Viçosa, Minas Gerais, Brasil*.

The objective of this research was to evaluate the milk production and composition of dairy cows fed diets containing increasing levels of sunflower cake. The sunflower cake has an average 164.29 g/kgDM of crude protein and 116.28 g/kgDM of ether extract. Eight multiparous Holstein x Zebu cows, between 50 and 74 d in milk and 20 ± 2 kg milk/day were allocated in a 4 × 4 double Latin Square Design. Sunflower cake was fed in the concentrate at the levels of 0; 7; 14 and 21% and Tifton hay was used as main forage in a 60:40 forage to concentrate ratio. The PROC GLM of SAS was used for the statistical analysis. The milk production increased linearly with the addition of the byproduct (18.88 to 19.29 kg/day), while 4% fat-corrected milk yield showed linear decrease (18.28 to 17.05 kg/day, $P < 0.05$). The milk fat and protein content decreased linearly with greater proportions of sunflower cake in the ration (3.79 to 3.23 and 3.28 to 3.17%, respectively). The lactose content was not affected by increasing levels of sunflower cake in the ration, but the N-ureic in milk decreased linearly. The palmitic acid (C16:0) decreased linearly with the addition levels of the byproduct, although for the other saturated fatty acids, as well as to the monounsaturated and polyunsaturated fatty acids were not observed significant differences ($P > 0.05$). Sunflower cake can be recommended as a potential alternative for feeding dairy cows at the maximum level of inclusion of 21% in the concentrate.

Key Words: byproducts, lipids, ruminants

T409 Supplemental metabolizable lysine delivered with Megamine-L improves productive performance of lactating cows. E. Block*[1], E. Evans[2], and N. Clark[3], [1]*Church and Dwight Co., Inc.*, *Princeton, NJ,* [2]*Evans Technical Consulting Services, Bowmanville, ON, Canada,* [3]*Atlantic Dairy and Forage Institute, Fredericton Junction, NB, Canada.*

Sixteen cows were fed one of 4 diets in a 4 × 4 Latin square treatment arrangement designed to evaluate the delivery of intestinally available lysine in a new product, Megamine-L (MEG-L; 16% lysine). The control diet was formulated using CPM Dairy v3.0 for 35 kg of milk with 3.8% fat and 3.1% protein and contained methionine at 2.4% of the metabolizable protein (MP) and lysine at 6.1% of the MP using corn

and clover silages, corn and barley grain, soybean meal, urea, Megalac, and Smartamine-M. Excess metabolizable protein and energy were at zero in the final formulation. MEG-L was substituted for Megalac in the 3 treatment diets at 50, 100 and 150 g/cow/day. Results are shown in the table. Supplementing MEG-L in all diets resulted significant ($P < 0.05$) increases in production performance with the 100g/d feeding rate being closest to ideal lysine supplied. Using actual productive performance data and DMI for each cow in CPM Dairy resulted in an average metabolizable lysine estimate for MEG-L of 46%.

Table 1. Production responses of dairy cows fed 3 levels of Megamine-L (MEG-L)

	g/d MEG-L				
	Control (0)	50	100	150	P≥F
Milk, kg/d	31.1[a]	34.1[b]	35.4[c]	34.8[b]	0.047
3.5 FCM, kg/d	34.2[a]	37.5[b]	40.3[c]	39.1[c]	0.035
ECM, kg/d	31.2[a]	34.1[b]	35.4[c]	34.8[c]	0.041
DMI,kg/d	22.2	21.8	21.6	22.4	0.786
Fat Yield, kg/d	1.28[a]	1.40[b]	1.54[c]	1.48[bc]	0.040
Protein Yield, kg/d	973[a]	1.15[b]	1.18[b]	1.16[b]	0.038
Milk/DMI	1.40[a]	1.56[b]	1.64[c]	1.55[b]	0.028
Estimated metabolizable Lys from MEG-L, % of lysine	0	47.2	50.0	43.6	

[abc]Values with different superscripts differ ($P \leq 0.05$).

Key Words: metabolizable lysine, lactating cow, milk production

T410 A model to compare effects of supplemental fat sources on performance and dry matter intake in dairy cows: Effects of fat inclusion level. E. Block*[1] and E. Evans[2], [1]*Church and Dwight Co., Inc.*, *Princeton, NJ,* [2]*Evans Technical Consulting Services, Bowmanville, ON, Canada.*

Experiments conducted to evaluate the addition of fat to diets for dairy cows have involved a range in the amounts supplied. This study was conducted to assess production and dry matter intake responses to different sources of fat (calcium salts, prilled fatty acids, tallow, and vegetable oil) compared with control diets (no added fat) as influenced by level of dietary fat inclusion (normal levels, defined as lower dietary fat than milk fat output vs. excessive levels, defined as higher dietary fat than milk fat output). Data obtained from full peer reviewed manuscripts published since 1990 were used for model development if diets were considered typical (protein from 15 to 22%; NDF from 27 to 44%). Data were analyzed using a GLM procedure accounting for experiment and fat source. Treatment values were compared as differences from control. A Tukey's test was conducted to determine pairwise differences between treatments and control. Milk yield (MY), fat yield (FY), energy corrected milk (ECM), and ECM/DMI were improved ($P < 0.05$), protein yield (PY) was unchanged and DMI was reduced when fat was included in the normal range in diets. The model showed that the improvements in MY, FY and ECM caused by fat inclusion in the normal range were associated with studies involving calcium salts primarily with little effects of prills, tallow, and vegetable oils while tallow was primarily responsible for the decline in DMI when comparing fat additions to control diets. When dietary fat was excessive, there were no changes in MY, FY, PY or ECM compared with control diets. In diets containing excessive fat, NE intake increased, but DMI decreased relative to the controls.

Key Words: dietary fat, dairy cow, production performance

T411 A model to compare the effects of fat sources upon performance and dry matter intake in dairy cows: Effects of trial duration. E. Block*[1] and E. Evans[2], [1]*Church & Dwight Co., Inc.*, *Princeton, NJ,* [2]*Evans Technical Consulting Services, Bowmanville, ON, Canada.*

Fat contributes to energy balance as well as milk output, and there can be carryover effects in shorter term (ST, <28 d) changeover trials and Latin square trials that would lead to erroneous conclusions relative to long-term (LT) blocked feeding trials. This study was conducted to model responses to supplemental fat sources (calcium salts, prilled fatty acids, tallow, and vegetable oil) as determined from ST and LT trials. Data obtained from full manuscripts published since 1990 were used for model development if diets were typical (protein from 15 to 22%; NDF from 27 to 44%). Data were analyzed using a GLM procedure accounting for experiment and fat source. Treatment values were compared as differences from control. A Tukey's test was conducted to determine pairwise differences between treatments and control. In the ST model, milk yield (MY), fat yield (FY), energy corrected milk (ECM) and ECM/DMI increased ($P < 0.05$) with fat supplements relative to control. The increases in MY and ECM/DMI were associated with studies involving calcium salts only. Protein yield (PY) was not affected ($P > 0.05$). DMI and calculated NEI declined ($P < 0.05$) in ST with added fat and this was primarily associated with the feeding of tallow. In the LT model there were no trials using prilled fatty acids that fit the criteria for inclusion. In this LT model MY, ECM, NE balance, and ECM/DMI were improved with fat, with no effects of fat on FY or PY. The increase in NE balance was associated with vegetable oil while the improvement in ECM/DMI was associated with calcium salts. DMI did not change with added fat in the LT trials ($P > 0.05$). The magnitude of effects of feeding fat was much greater in LT than in ST trials.

Key Words: dietary fat, dairy cow, production performance

T412 Hourly effective rumen degradation ratio in wheat DDGS, Corn DDGS and Blend DDGS from bio-ethanol plants: Effect of bio-ethanol plant and DDGS type. W. G. Nuez-Ortín* and P. Yu, *Department of Animal and Poultry Science, College of Agriculture and Bioresources, University of Saskatchewan*, *Saskatoon, SK, Canada*.

The objectives of this study were to compare different types of DDGS and different bio-ethanol plants on hourly effective rumen degradation ratio (ED), determined based on the model published by Sinclair et al. in 1993. The corn DDGS, wheat DDGS and blend DDGS (70% wheat: 30% corn), and wheat and corn samples with 3 to 5 different batches were obtained. The data was analyzed using a mixed procedure of SAS with a CRD model. In dairy cows, the optimum ratio between the effective extent of degradability of N and OM to achieve maximum microbial synthesis and minimize N loss is 25 g N per kg OM truly digested in rumen. The results showed that (1) wheat exhibited higher than optimal ED ratio at all incubation times except at 2 h, ranging from 23 to 991 g N/kg OM, while corn showed less than optimal ratio during the entire incubation, ranging from 0 to 24 g N/kg OM. (2) Comparing with DDGS, the hourly ED ratios of N/OM for wheat were higher ($P < 0.05$) than those for DDGS samples at 0, 12 and 24 h, however, the ratios for corn were lower ($P < 0.05$) at all incubation times. (3) Comparing among the 3 types of DDGS, wheat DDGS had the highest ($P < 0.05$) ratios (26–103 g N/kg OM), while ratios for blend DDGS (29–89 g N/kg OM) were numerically higher ($P > 0.05$) than those for corn DDGS (14–56 g N/kg OM). The hourly ED ratios of N/OM tended to rise with increasing incubation time for wheat DDGS and blend DDGS; however, they remained constant for corn DDGS. This reflects a higher difference in the hourly effective degradation of N at later stages for blend DDGS

and wheat DDGS than for corn DDGS rather than differences in the hourly effective degradability of OM. (4) The bio-ethanol plant effect was significant at the beginning and end of incubations. The hourly ED ratios of N/OM for wheat DDGS from SK-Plant 1 was greater at 0 h (42 vs. 16 g N/kg OM) but lesser at 12 h (80 vs. 88 g N/ kg OM) and 24 h (85 vs. 114 g N/kg OM). The results shown here indicate that DDGS samples exhibited more than optimal rumen degradation ratio.

Key Words: hourly effective rumen degradation ratio, bioethanol co-products, dried distillers grains with solubles

T413 Production response of Holstein lactating cows to roasted or electron beam irradiated whole soybean. A. Akbarian[1], G. Ghorbani[1], M. Khorvash[1], P. Showrang[3], M. Dehghan-Banadaky*[2], and M. Jafari[1], [1]*Isfahan University of Technology*, *Isfahan, Iran*, [2]*University of Tehran*, *Karaj, Tehran, Iran*, [3]*Nuclear Science and Technology Research Institute, Atomic Energy Organization of Iran*, *Tehran, Iran*.

Nine lactating Holstein cows (130 ± 15 DIM, 39 ± 2 kg/d milk yield) were used in a duplicated 3 × 3 Latin square design experiment with 3 21 d periods. Cows were fed with rations with 60% concentrate and 40% forage. Treatments consisted of untreated, roasted and electron beam irradiation (63 kGy) formulated to meet energy and protein requirements recommended by the NRC (2001). The amount of feed and orts offered were measured daily for individual cows to calculate dry matter and crude protein intake. Cows were milked 3 times daily. The data were analyzed with Proc Mixed of SAS. The statistical model included fixed effects of treatment, square and their interaction. The effects of period and cow within the square were random. Dry matter and crude protein intake were not significantly different among treatments ($P > 0.05$, Table 1). Milk production and energy corrected milk of cows fed ration containing roasted whole soybean tended to increase ($P > 0.05$). Fat, protein and lactose contents of milk were not differ ($P > 0.05$) among treatments. There was a significant effect on milk efficiency of cows fed different diets ($P < 0.05$). Results showed that feeding roasted whole soybean improved milk production efficiency of cows.

Table 1. Production performance for Holstein cows fed diets contained untreated, roasted or irradiated whole soybean

	Diets			
Items	Untreated	Roasted soybeans	Irradiated whole soybean	SEM
DMI (kg/day)	26.7	24.9	27.1	0.63
CP Intake (kg/day)	4.5	4.4	4.5	0.2
Milk yield (kg/day)	38.1	39.4	38.6	0.99
ECM (kg/day)	41.5	41.9	42.5	1.01
Milk efficiency (milk yield/DMI)	1.4[b]	1.6[a]	1.4[b]	0.04
Fat %	4.1	4.1	4.2	0.07
Protein %	3.3	3.2	3.2	0.03
Lactose %	4.6	4.6	4.6	0.05

[a,b] Means with different letters differ ($P < 0.05$).

Key Words: whole soybean, roasted, electron beam irradiated

T414 The relationship between nitrogen use efficiency and N isotopic fractionation in dairy cows using milk samples collected in the morning or afternoon. L. Cheng*[1], R. Dewhurst[2], J. Larkin[2], F. Buckley[3], C. Thackaberry[3], and G. Edwards[1], [1]*Lincoln University*, *Christchurch, Canterbury, New Zealand*, [2]*Teagasc*, *Dunsany, Co. Meath, Ireland*, [3]*Teagasc*, *Fermoy, Co. Cork, Ireland*.

This study investigated the potential to use fractionation of N isotopes among milk fractions to assess NUE. Nine Holstein-Friesian cows grazing on ryegrass and white clover mixture pasture only were used in this study. All cows were milked twice daily, one morning and afternoon milk samples from each cow were collected for analysis. Milk samples were defatted by centrifugation and protein was precipitated using acetone (4 acetone: 1 milk (vol/vol)). Whole milk, protein pellet (PP) and the supernatant (NPN) were freeze-dried and analyzed for ^{15}N (delta-^{15}N units; per ml). The ^{15}N in milk fractions, between am and pm samples, and the relationship between N isotope fractionation and milk urea N (MUN; mg/dL) were compared using one-way ANOVA (ANOVA) with cow as experimental block and linear regression. The mean ^{15}N in PP (7.05; SD = 0.248) was significantly ($P < 0.001$) higher than in whole milk (6.81; SD = 0.265), while ^{15}N in NPN was significantly ($P < 0.001$) lower (1.61; SD = 0.448). The correlation between am and pm values was weaker for MUN ($P < 0.05$) than for ^{15}N in milk fractions ($P < 0.001$). ^{15}N in NPN was lower for am samples (1.41 vs. 1.91; SED = 0.172; $P < 0.05$), while MUN tended to be higher (17.5 vs. 16.1; SED = 0.77; $P = 0.07$). There was a positive linear relationship ($y = 2.58x + 12.51$; $r^2 = 0.35$; $P = 0.05$) between MUN (y) and ^{15}N in average NPN (x), but this differed between am and pm samples. This may be related to differences in N isotopic discrimination between urea derived from excess N in the rumen or tissues, or differences in the other components of milk NPN. In conclusion, there were consistent differences between cows in the ^{15}N content of milk and milk fractions, though further work is needed to elucidate the effects of different pathways on N isotopic discrimination.

Key Words: stable nitrogen isotopes, milk urea nitrogen, discrimination

T415 Effect of replacing blood meal with rumen-protected amino acids on milk production and composition in lactating dairy cows. G. E. Aines*[1], G. F. Schroeder[2], M. Messman[2], and M. J. de Veth[1], [1]*Balchem Corporation*, *New Hampton, NY*, [2]*Cargill Animal Nutrition, Innovation Campus*, *Elk River, MN*.

A study was conducted to determine the effects on milk production and composition when lysine (Lys) and histidine (His) supplied by porcine blood meal were replaced by lipid-encapsulated rumen-protected forms (Balchem Corporation) of these 2 amino acids. Forty-four Holstein cows (mean 102 DIM) were used in a randomized block design. Treatments were: 1) Positive Control (PC) = diet which contained blood meal (0.4% of DM) and was balanced to meet metabolizable Lys and His, 2) Negative Control (NC) = similar to PC but removing blood meal, meeting a minimum of 80% of the metabolizable Lys and His requirements, 3) NC+His = NC diet supplemented with rumen-protected His to provide the same total level of His supply as the PC, and 4) NC+His+Lys = similar to NC+His but supplemented with rumen-protected Lys to provide the same levels of the 2 amino acids as the PC. NC and PC diets contained 17.0 and 17.8% CP, respectively. His and Lys were top dressed twice daily. DMI and milk yield were recorded daily and averaged by week. Milk composition was analyzed on the last day of each week. Data was analyzed using the PROC Mixed procedure of SAS with repeated measures and pretreatment milk yield was used as a covariate. Cows on NC treatment produced less milk (40.4 kg) compared with PC (42.5 kg, $P < 0.05$). NC+His had similar milk yield (39.9 kg) compared with NC, however, NC+His+Lys increased milk yield (42.6 kg) compared with NC and NC+His indicating that Lys was first limiting or co-limiting with His. PC and NC+His+Lys milk production were not different.

Milk components, DMI and feed efficiency were not different among treatments. MUN (mg/dl) was significantly ($P < 0.01$) lower for NC, NC+His and NC+His+Lys (11.8, 12.2 and 11.5, respectively) compared with PC (16.7), indicating that protein was used more efficiently in the lower protein diets. The results suggest that replacing the essential amino acids Lys and His that are supplied from porcine blood meal with equal levels from rumen-protected sources can maintain milk yield despite lower CP levels.

Key Words: blood meal, histidine, lysine

T416 Fatty acid composition of milk from Holstein cows fed diet supplemented with fish oil and canola oil from transition period to early lactation. T. S. Vafa, A. Heravi Moussavi*, A. A. Naserian, M. Danesh Mesgaran, and R. Valizadeh, *Ferdowsi University of Mashhad, Excellence Center for Animal Science, Faculty of Agriculture, Mashhad, Khorasan Razavi, Iran*.

The objective of this study was to examine the effects of feeding fish oil and canola oil from transition period to early lactation on milk fatty acid composition. Experimental diets were supplemented with either 0% oil (Control, n = 9), or 2% oil (supplemented, 1% canola oil-1%fish oil, n = 9), and fed 2 times a day from day −21 to 50 related to calving. Cows were blocked by parity, previous 305–2x milk production and expected calving time. Milk samples of first, third and sixth week of lactation were collected for fatty acids analysis using gas chromatography. All milk fatty acid results were expressed as g/100g of total fatty acids. The data repeated in time were analyzed by using a mixed model for a completely randomized design with repeated measures. Significance was declared at $P < 0.05$. As revealed in table1, total short (SCFA; C4:0- C8:0) and medium (MCFA; C10:0- C16:0) fatty acids decreased and total poly unsaturated fatty acids (PUFA) increased in supplemented diet. The proportion of C16:0, C16:1 and C18:0 decreased in supplemented diet. The proportion of trans (t) 10, cis (c) 12–18:2, c9, t11–18:2, c9, c12–18:2, t9, t11–18:2, t-18:1, eicosapentanoic acid (EPA) and docosahexaenoic acid (DHA) increased in supplemented diets, but the proportion of c11–18:1 and c9–18:1 were similar between diets. The results of this study demonstrate that feeding a combination of fish oil and canola oil had significant effect on milk fatty acids composition.

Table 1. Effects of pre- and post calving feeding of fish oil and canola oil on milk fatty acids composition (g/ 100 g FA)

Fatty acids	Control	Supplemented	SE	P-value
16:0	22.72	20.53	1.33	**
16:1	0.71	0.60	0.01	**
18:0	12.9	11.59	0.32	*
t 18:1	0.15	0.18	0.07	*
c9 18:1	23.81	26.13	1.9	ns
t9,t12-18:2	0.16	0.23	0.01	**
t9,t11-18:2	0.02	0.05	0.002	***
t10,c12-18:2	0.03	0.05	0.007	**
c9,t11-18:2	0.38	0.65	0.02	***
EPA	0.05	0.11	0.01	**
DHA	0.08	0.14	0.005	**
SCFA	7.88	6.92	0.12	**
MCFA	14.59	11.61	0.63	**
PUFA	3.59	4.76	0.06	***

ns = not significant; *$P < 0.05$, **$P < 0.01$, ***$P < 0.0001$.

Key Words: fish oil, canola oil, milk fatty acids

T417 Partial replacement of soybean meal by encapsulated urea in commercial dairy herds. V. A. Silveira[1], N. M. Lopes[1], R. C. Oliveira[1], B. Gonzales[1], A. V. Siqueira[1], L. P. P. Bier[2], M. S. Zoni[3], W. Giardini[4], R. Almeida*[2], and M. N. Pereira[1], [1]*Universidade Federal de Lavras, Lavras, MG, Brazil*, [2]*Universidade Federal do Paraná, Curitiba, PR, Brazil*, [3]*Milkonsult, Castro, PR, Brazil*, [4]*Alltech do Brasil, Brazil*.

Two on-farm trials were conducted to evaluate the partial replacement of soybean meal by encapsulated urea (OptigenII, Alltech do Brasil, Brazil). From a control treatment, 1 kg of soybean meal was replaced by 160 g of Optigen plus 2.5 kg of corn silage in trial 1 or 150 g of Optigen plus 0.85 kg of ground corn in trial 2. Researchers were responsible for manually mixing the treatments in proportion to the offered TMR and performing data collection in each farm. Trial 1 started with 68 Holsteins (243 DIM) paired blocked based on parity and yield and allocated to a treatment for 21 d, after a 5-d standardization period. Trial 2 started with 120 cows (291 DIM), also paired blocked and allocated to a sequence of 2 treatments in a crossover design with 21-d periods. Seven cows were lost in trial 1 and 23 were lost in trial 2. Response variables were measured on d 17 to 21 of treatment allocation, during which feed offered and orts were sampled daily. Data for trial 1 was analyzed with the GLM of SAS with a model containing the effects of covariate (measure of the same variable at the end of the standardization period), block and treatment. Data from trial 2 used a model containing the effects of cow, period, and treatment. Orts as a percentage of the offered diet fresh matter was 4.7 and 5.3% for trial 1 and 2.7 and 2.3% for trial 2, for Control and Optigen treatments, respectively. The DM, CP and NDF content of the offered diets and orts were similar across treatments, as well as cow′s body weight and body condition score. Milk yield was 38.4 kg for Control and 38.9 kg for Optigen in trial 1 ($P = 0.62$), and 27.0 kg and 27.2 kg in trial 2 ($P = 0.64$), respectively. No difference in milk solids secretion was detected ($P > 0.44$). Optigen increased MUN from 16.3 to 17.3 mg/dL in trial 1 ($P < 0.01$), but did elicit such a response in trial 2 ($P = 0.14$). Optigen tended to increase the group ratio of milk to feed in trial 2 ($P = 0.08$). Replacing soybean meal by Optigen did not induce lower performance, although increased MUN was observed when Optigen combined with corn silage replaced soybean meal.

Key Words: non-protein nitrogen, slow-release urea, Optigen

T418 The effect of feeding a prototype of ruminally protected lysine (RPL) on production performance and plasma amino acid profile of early lactation dairy cattle. J. E. Nocek[1], M. Miura[2], and I. Shinzato*[2], [1]*Spruce Haven Farm and Research Center, Auburn, NY*, [2]*Ajinomoto Co., Inc., Tokyo, Japan*.

Thirty-six lactating Holstein cows were used to examine the effects of ruminally protected lysine (RPL) supplementation and dosage on production performance and plasma amino acid profile of high-producing dairy cows. Multiparous cows were balanced across treatments based on their 4 week of lactation average milk production as follows: Control, 75, 150, 225 g/d of RPL. These treatments were designed to deliver 0, 4.5, 9.0 and 13.5 g/cow/d of supplemental intestinally available lysine, respectively. Cows started the experimental period on the fifth week post-calving and remained on treatment for 4 weeks. Prior to treatment administration, all cows received the control diet, which contained 75% of forage from corn silage, for one week. Control diet was fed to all cows throughout the experimental period, however, in addition, cows received 500 g/d of corn meal premix top dressed once daily to deliver 0, 75, 150 or 225 g/d of RPL. Dry matter intake was the highest for cows receiving 225g RPL compared with Control or 150g RPL. As a percentage of body weight, DMI remained higher for cows receiving 225g RPL

compared with 75g RPL. Mean milk yield was higher ($P < 0.05$) for cows receiving 75g RPL than Control (43.4 vs. 40.2 kg), with 150g and 225g RPL not being different than either. Fat percentage was higher ($P < 0.05$) for 150g and 225g RPL compared with 75g (3.83 vs. 3.35%, respectively), with control not being different. However, fat percentage for 75g RPL increased with time on treatment. Fat yield reflected this same numeric tendency ($P = 0.08$). Protein percentage was higher for control compared with 75g RPL with 150g and 225g not being different from either. Protein yield, lactose, MUN and SCC were not affected by RPL treatment. There were no significant ($P > 0.10$) or notable effects of RPL level on plasma AA concentration. These results demonstrated lysine is limiting in high corn silage diets for milk production.

Key Words: ruminally protected lysine, milk production, plasma amino acids

T419 Effect of HMBi supplementation on splanchnic methionine metabolism in postpartum transition cows. M. Larsen*, K. F. Dalbach, B. M. L. Raun, and N. B. Kristensen, *Faculty of Agricultural Sciences, Aarhus University*, *Tjele, Denmark*.

Eight second lactation Holstein cows implanted with permanent indwelling catheters in major splanchnic blood vessels were used to study the effect of dietary supplementation with the methionine hydroxyl analog (2-hydroxy-4-methylthio butanoic acid isopropyl ester; HMBi; Adisseo, France) on splanchnic methionine (Met) metabolism. At calving, cows were assigned to 1 of 4 diets in a 2 × 2 factorial design with one factor being HMBi supplement (2.6 g/kg dry matter) compared with no supplement (CTRL). The second factor was source of alcohol (ethanol vs. propanol). Diets were fed ad libitum in equally sized meals at 8 h intervals. Eight hourly sets of arterial, portal vein, and hepatic vein samples were obtained at −15 ± 5 d prepartum as well as 4, 15, and 29 d in milk (DIM). Met was analyzed in pooled plasma by GC-MS. The statistical model included both factors, DIM and possible interactions, where DIM was considered as a repeated measure. No interactions were observed between factors studied. Postpartum, milk yield and dry matter intake were unaffected by HMBi supplementation ($P \geq 0.32$) and averaged 34 ± 1 and 18 ± 1 kg/d, respectively. Casein content in milk tended to decrease at a lower rate with HMBi compared with CTRL as lactation progressed (interaction, $P = 0.06$). Milk fat content tended ($P = 0.07$) to be greater with HMBi. The change in arterial Met concentration from prepartum to 4 DIM differed ($P < 0.01$) between HMBi (from 20 to 23 μM) and CTRL (from 21 to 17 μM). Postpartum, arterial Met concentrations tended ($P = 0.09$) to remain greater with HMBi. The net portal and net splanchnic releases of Met were unaffected ($P \geq 0.50$) by HMBi and averaged 7.7 ± 0.3 and 5.3 ± 0.3 mmol/h, respectively. The net hepatic removal of Met tended ($P = 0.08$) to be greater with HMBi as compared with CTRL (2.7 and 2.0 ± 0.3 mmol/h, respectively). In conclusion, dietary HMBi supplementation to postpartum transition cows prevented a decrease in plasma Met in the first week postpartum without requiring time for adaptation to HMBi feeding. The greater hepatic removal of Met with HMBi indicates that Met was supplied in excess relative to other amino acids.

Key Words: transition, methionine, metabolism

T420 The effect of abomasal infusion of histidine and proline on milk composition and amino acid utilization in high producing lactating dairy cows. M. W. Hofherr*, D. A. Ross, and M. E. Van Amburgh, *Cornell University*, *Ithaca, NY*.

Histidine has been shown to be a limiting amino acid in grass fed lactating dairy cows and to alter fat secretion under certain conditions. A significant increase in milk protein output and a reduction in arginine uptake by the mammary gland were observed when proline was infused into the duodenum of 2 cows. The objective of this experiment was to determine the effects of abomasal infusion of histidine and proline on lactation performance in cows fed more conventional diets and to measure amino acid utilization by the mammary gland. Four rumen-fistulated Holstein cows (52 ± 19 DIM) with indwelling intercostal arterial catheters were used in a 4 × 4 Latin square experiment. Experimental treatments were continuous abomasal infusion of water (control), His (10g/d), Pro (20 g/d), and His (10 g/d) + Pro (20 g/d), with 7-d treatment periods. Cows were fed a TMR (14.4% CP, 2.3 Mcal/kg ME) once per day for ad libitum intake and refusals were measured and analyzed. The CNCPS v6.1 was used to formulate a diet to exceed the metabolizable energy requirement, provide 95% of the predicted metabolizable protein requirement, and supply adequate amounts of all essential amino acids, except Arg. Fat corrected milk yields were not affected by treatment (51.8 kg/d, TRT C; 50.6 kg/d, TRT H; 49.0 kg/d TRT H^+P; 52.4 kg/d TRT P), however abomasal infusion of Pro decreased feed intake and improved feed efficiency by 0.17 kg 3.5% FCM per kg dry matter ($P < 0.05$). Pro infusion increased lactose percentage ($P < 0.05$) but not yield. The lactose response suggests that longer infusions might have resulted in increased milk yield. A similar effect for lactose and feed efficiency was observed for the H^+P treatment. In this experiment abomasal infusion of His resulted in no performance difference or change in efficiency. Our results indicate that postruminal supplementation of Pro might increase milk fat production and feed efficiency in high producing dairy cows.

Key Words: amino acids, feed efficiency, infusion

T421 Response of dairy cows to the supplementation of fatty acids from calcium salts of soybean oil or heated soybeans. G. S. Dias Júnior[1], N. M. Lopes[1], L. L. Bitencourt[1], V. A. Silveira[1], G. G. S. Salvati[1], N. N. Morais Júnior[4], E. O. S. Saliba[3], R. A. N. Pereira[2], and M. N. Pereira*[1], [1]*Universidade Federal de Lavras*, *Lavras, Brazil*, [2]*Empresa de Pesquisa Agropecuária de Minas Gerais*, *Lavras, Brazil*, [3]*Universidade Federal de Minas Gerais*, *Belo Horizonte, Brazil*, [4]*Instituto Federal de Educação Ciência e Tecnologia do Espirito Santo*, *Colatina, Brazil*.

This study evaluated the effect of supplementing corn silage based diets with fatty acids from calcium salts of soybean oil (Megalac E, Química Geral do Nordeste SA, Nova Ponte, Brazil) or from cracked whole roasted soybeans (Alfa Nutrisoja, Cooperalfa, Chapecó, Brazil). The content of Megalac was 1.4% of diet DM and the content of heated soybeans was 5.4. The dietary EE content was 4.3% of DM for Control and 6.0 for the fat supplemented diets. Diets contained 42.3% of DM from corn silage, 14.2% from high moisture corn, and 0.9% from bicarbonate. The dietary content of soybean meal and citrus pulp were 22.1 and 18.6 for Control, 18.4 and 16.9 for Soybean, and 22.5 and 16.8 for Megalac; diets CP content were 16.3, 16.7, and 16.6, respectively. Twenty-four Holsteins (638 kg, 216 DIM) received a sequence of the treatments in 8 concurrently run 3 × 3 Latin Squares, with 28-d periods, and 21 d of adaptation. Daily milk yield was 31.7 kg for Control, 32.7 for Soybean, and 31.8 for Megalac ($P = 0.43$). Megalac reduced daily DMI from 21.4 to 20.5 kg compared with Control ($P = 0.05$). There was a trend for decreased time of the first daily meal with Megalac ($P = 0.07$). Milk to feed ratio was 1.56 for Megalac and 1.48 for Control ($P = 0.07$). Megalac decreased milk fat content from 3.11 to 2.64% and daily fat yield from 0.986 to 0.828 kg ($P < 0.01$), resulting in lowered daily milk energy secretion ($P = 0.04$). Soybean had no effect on milk solids ($P > 0.33$). Rumen protozoa count was decreased by both fat supplements ($P < 0.01$), no difference was detected in MUN ($P = 0.92$)

or the daily excretion of allatoin in urine ($P = 0.54$). Supplementation of corn silage based diets with fatty acids from calcium salts of soybean oil decreased milk fat secretion and diet intake, and tended to increase feed efficiency, while the same fat content from whole roasted soybeans did not induce a similar response.

Key Words: calcium soap, fat, soybean oil

T422 Variability of estimated protected proteins of feather meals. J. A. Davidson*, K. B. Cunningham, H. C. Puch, and B. L. Miller, *LongView Animal Nutrition Center, Land O'Lakes Purina Feed, Gray Summit, MO*.

The objective was to evaluate the quality of sources of feather meal in regard to ruminal undegraded protein and available protein. Nine feather meal samples along with control samples of SurePro (non-enzymatically browned soybean meal) and SBM were evaluated utilizing in sacco techniques. Samples prepared in 51-μm polyester bags were exposed for 12 h within a ruminally-cannulated steer fed a forage:concentrate diet of 60:40 at DMI of 3.5% of BW. Additional subsets of bags were utilized to determine a 0-h protein disappearance and protein disappearance after digestion with pepsin (0.1 *N* HCl) for an additional 12 h. The RUP value was calculated as percent remaining after 12-h exposure in rumen and available protein (AP) was the difference between % protein disappearance at 12-h exposure in rumen and 12-h pepsin digestion. The mean ± SE estimated RUP for the feather meals, SurePro, and SBM were 78 ± 1.9%, 81 ± 0.6%, and 40%, respectively. The mean ± SE AP for the feather meals, SurePro, and SBM were 25 ± 3.9%, 70 ± 0.9%, and 38%, respectively. In comparison, the NRC 2001 estimates of RUP as % CP for feather meals were 62 to 65% with a RUP digestibility of 65 to 70%; 69 to 79% RUP with 93% digestibility for SurePro; and 31 to 43% RUP with 93% digestibility for SBM. Thus, the NRC 2001 described the AP of feather meal, SurePro, and SBM as 40 to 46%, 64 to 73%, and 29 to 40%, respectively. Based on our measurements, the AP of feather meal is 15% lower than those of NRC 2001, whereas SurePro and SBM were within the reported range. In conclusion, this data set demonstrates the need to continually monitor and evaluate protected protein sources. In sacco methods along with pepsin digestion are tools to characterize the consistency and quality of RUP and AP from multiple sources. Feather meal as a source of RUP for lactating cow diets does not consistently have high digestibility and is a poor alternative to other feed ingredients.

Key Words: protected protein, feather meal, in sacco methods

T423 Milk fat responses to dietary short and medium chain fatty acids in lactating dairy cows. D. Vyas*, B. B. Teter, and R. A. Erdman, *University of Maryland, College Park*.

During diet induced milk fat depression, the short- and medium-chain fatty acids (SMCFA), synthesized de novo in the mammary gland, are reduced to a much greater extent than the long-chain fatty acids (LCFA) originating from the diet. Our hypothesis was that SMCFA limit milk fat synthesis even under conditions when milk fat is not depressed. Our objective was to test the potential limitation of SMCFA on milk fat synthesis via dietary supplementation. Sixteen lactating Holstein cows (86 ± 41 DIM) randomly assigned in groups of 4 per pen and fed corn silage based TMR were supplemented with 1 of 4 dietary fat supplements (600g/d) in a 4 × 4 Latin square design with 21-d experimental periods. Treatments consisted of fat supplements containing mixtures of calcium salts of LCFA (Megalac; M) and a SMCFA mixture (S) (C8:0- 3.3%, C10:0- 7.6%, C12:0- 9.85%, C14:0- 32.12% and C16:0- 47.11%) that contained 0, 200, 400, and 600 g/d S substituted for M (S0, S200, S400, and S600, respectively). No significant changes were observed with dry matter intake, milk yield, and fat corrected milk (FCM), whereas milk fat concentration was increased ($P = 0.008$) by 0.17, 0.25, and 0.33 percentage units for the respective S treatments. Fat yield peaked with S200 and milk protein content and yield were reduced at the higher S levels due to a trend toward reduced milk yield in the S600 treatment. In conclusion, SMCFA supplementation increased milk fat content in a linear fashion but the trend toward reduced feed intake and milk production at the highest level of supplementation might have masked the effects of SMCFA on total milk fat synthesis.

Table 1. Production responses to increasing SMCFA

SMCFA, g/d	0	200	400	600	SEM	P-value
DMI, kg/d	26.5	26.4	26.5	25.5	0.53	0.24
Milk, kg/d	43.6	43.9	42.7	41.1	1.1	0.08
3.5%FCM, kg/d	45.04	46.75	45.98	44.75	1.8	0.36
Milk fat, %	3.75^{b}	3.92^{ab}	4.0^{a}	4.08^{a}	0.16	0.008
Milk fat, g/d	1614	1709	1694	1663	89.9	0.28
Milk protein,%	3.10^{ab}	3.12^{a}	3.09^{ab}	3.06^{b}	0.05	0.03
Milk protein, g/d	1351	1373	1318	1257	41.5	0.05

[a–b]Least squares means within a row with different superscripts differ.

Key Words: milk fat, short-chain fatty acids

T424 Effect of feeding varied levels of crude protein and absorbable methionine on milk yield in lactating dairy cows. G. A. Broderick*[1], R. A. Patton[2], W. Heimbeck[3], and C. Parys[3], [1]*U.S. Dairy Forage Research Center, Madison, WI*, [2]*Nittany Dairy Nutrition, Inc., Mifflinburg, PA*, [3]*Evonik Degussa GmbH, Hanau, Germany*.

Supplementing with limiting AA should allow less CP to be fed; reducing dietary CP will decrease urinary N and ameliorate the environmental impact of dairying. Rumen-protected Met (RPM) fed as Mepron to provide 9 g/d of absorbable Met allowed similar milk yield at 15.8% CP as at 17.1% CP without RPM (Broderick et al., J. Dairy Sci. 92:2719, 2009). A lactation trial was conducted to assess response to RPM at different CP levels. TMR were prepared from alfalfa and corn silages, dry and high moisture corn, and solvent and expeller soybean meals. Diets were formulated to 28% NDF and 12, 14, 16 or 18% CP (DM basis); at each level of CP, RPM provided 0, 4.5, 9.0 and 13.5 g/d of absorbable Met, assuming 25 kg/d of DMI and 0.6 g absorbed Met/g of Mepron (total = 16 diets). Sixty-four cows were blocked by DIM into 16 squares and randomly assigned to balanced 4 × 4 Latin squares. The 4 levels of RPM were fed at each CP level for 4, 4-wk periods. Data from the last 2-wk of each period were analyzed for linearity of response to dietary CP and RPM using the Mixed model of SAS; LS means are reported. Analysis of TMR extracts with the Met-nitroprusside reaction confirmed that RPM was fed in desired amounts but CP was higher than formulated. Dietary CP increased DMI, BW gain and yield of milk, 3.5% FCM, fat and protein but did not affect milk/DMI. Production was not increased when diets contained 15.8% or more CP. Although the NRC model indicated that diets had Lys/Met ratios ranging from 3.3 to 3.7, and observed milk yield was more than MP-allowable milk on 12.9 and 15.8% CP, more absorbable Met had no effect on production in this trial.

Table 1. Production data

	Dietary CP, %				
Item	12.9	15.8	18.2	20.2	P > F
DMI, kg/d	24.2[b]	26.6[a]	27.1[a]	27.0[a]	0.04
Milk, kg/d	38.6[b]	44.8[a]	45.9[a]	45.8[a]	0.04
FCM, kg/d	40.5[b]	47.5[a]	50.1[a]	49.0[a]	0.03
Fat, kg/d	1.47[b]	1.73[a]	1.86[a]	1.78[a]	0.06
Protein, kg/d	1.13[b]	1.38[a]	1.39[a]	1.38[a]	< 0.01
MUN, mg/dL	7.3[d]	12.9[c]	16.9[b]	19.3[a]	< 0.01
	Absorbable Met, g/d				
	0	4.5	9.0	13.5	P > F
DMI, kg/d	26.5	26.3	26.0	26.2	0.31
Milk, kg/d	44.0	44.1	43.5	43.4	0.27
FCM, kg/d	46.8	47.3	46.0	46.9	0.45
Fat, kg/d	1.70	1.73	1.68	1.73	0.51
Protein, kg/d	1.32	1.33	1.30	1.32	0.51
MUN, mg/dL	14.2	14.0	14.3	14.0	0.78

[a–d] ($P < 0.05$).

Key Words: methionine, rumen-protection, milk yield

T425 Methionine supplementation to diets varying in rumen undegradable soy protein. N. N. Morais Júnior[3], V. A. Silveira[1], N. M. Lopes[1], G. S. Dias Júnior[1], G. Pessoa Júnior[1], G. G. S. Salvati[1], C. O. Faria[5], R. A. N. Pereira[2], N. D. Luchini[4], and M. N. Pereira*[1], [1]*Universidade Federal de Lavras*, *Lavras, Brazil*, [2]*Empresa de Pesquisa Agropecuária de Minas Gerais*, *Lavras, Brazil*, [3]*Instituto Federal de Educação Ciência e Tecnologia do Espirito Santo*, *Colatina, Brazil*, [4]*Adisseo*, *Alpharetta, GA*, [5]*Better Nature Research*, *Ijaci, Brazil*.

Methionine (Met) is one of the 2 amino acids (AA) that limits milk production. The objective of this study was to evaluate the effect of supplementing a source of Met to 2 diets with different rumen undegradable protein content. Twenty Holsteins were allocated to 5 4x4 Latin Squares in a 2 × 2 factorial arrangement of treatments. Each period lasted 21 d of which the last 7 were for data collection. Treatments consisted of feeding a diet composed of 38.5% corn silage, 7.8% tifton hay, 24.2% corn, 5.0% soybean meal, 8.3% citrus pulp, and 13% of raw or roasted soybeans (Alfa Nutrisoja, Cooperalfa). The Met supplement (isopropyl ester of 2-hydroxy-4-(methylthio) butanoic acid. MetaSmart, Adisseo) was orally given twice a day to the allocated cows. Diet CP content was 15.8% and EE was 6%. No significant results were observed for the interaction of amino acid and soybean main effects ($P > 0.15$). Roasted soybeans increased milk yield from 34.7 to 37.7 kg, protein yield from 1.003 to 1.078 kg, and fat yield from 1.060 to 1.162 ($P < 0.01$). The milk to feed ratio was 1.49 for raw and 1.59 for roasted soybeans ($P < 0.01$). MetaSmart induced non-statistically detectable increases in milk yield from 36.0 to 36.4 kg ($P = 0.46$), protein from 1.032 to 1.049 kg ($P = 0.29$), and fat from 1.101 to 1.120 kg ($P = 0.45$). Daily DMI was 24.0 kg for cows on MetaSmart and 23.4 for controls ($P = 0.13$). The milk urea nitrogen was 13.1 mg/dL for raw and 12.5 for roasted soybeans ($P = 0.04$). There were no detectable treatment effects on total tract digestibility ($P > 0.62$) and plasma glucose ($P > 0.76$). MetaSmart decreased the daily excretion of urinary allatoin and the ratio of allantoin to digestible OM intake ($P = 0.02$). Plasma urea nitrogen (PUN) content of 10 samples obtained over a 24-h period was analyzed as repeated measures over time with Mixed of SAS. Raw soybeans increased PUN from 14.3 to 15.4 mg/dL ($P < 0.01$), while MetaSmart decreased it from 15.1 to 14.6 ($P = 0.05$). For these soybean based diets, the response to increased flow of dietary AA in the metabolizable protein was larger than the response to Met, suggesting than other amino acids may have been more limiting to milk production.

Key Words: amino acid, methionine, protein

T426 Effects of level of rumen degradable protein and corn distillers grains in corn silage-based diets on milk production and ruminal fermentation in lactating dairy cows. G. I. Zanton* and A. J. Heinrichs, *The Pennsylvania State University*, *University Park*.

Two of the potential obstacles precluding inclusion of higher levels of dry distillers grains with solubles (DDGS) in corn-based, dairy cow diets are the low levels of rumen degradable protein (RDP) and the fatty acid content and composition of DDGS. Therefore, the objective of this experiment was to evaluate the production and rumen responses to dietary alterations in the level of RDP and DDGS for dairy cows fed a high corn silage diet. The experimental design was a replicated, 4 × 4 Latin square with 21 d periods: 14 d of adaptation and 7 d of sampling; 16 uncannulated cows and 4 rumen cannulated cows were blocked and assigned randomly to treatment sequences. Rations (basal ingredients: 47% corn silage, 3% long grass hay, 12% finely ground corn, 4% extruded soybean meal, 7.5% canola meal; mean composition: 17.4% CP, 36% NDF, 36% NFC, 1.69 Mcal NE_L/kg) were provided as total mixed rations and were formulated to be high or low RDP, with or without DDGS replacing soybean-based concentrates: high RDP, no DDGS (HDRP0); low RDP, no DDGS (LRDP0); low RDP, 10% DDGS; and low RDP, 20% DDGS. Contrasts of interest were HRDP0 vs. LRDP0 and linear and quadratic effects of level of DDGS; differences were declared at $P < 0.05$. Body weight (696 kg) and dry matter intake (26.6 kg/d) were not affected by treatment ($P > 0.50$). Rumen ammonia concentration was greater for HRDP0 than LRDP0 ($P < 0.01$), but was unaffected by level of DDGS inclusion. Mean and minimum rumen pH and time < pH 5.5 was not different between diets ($P > 0.25$). Milk production tended to be lower for cows fed HRDP0 than LRDP0 ($P < 0.06$) and tended to be linearly reduced as DDGS inclusion increased ($P < 0.07$). Milk protein yield tended to be greater for cows fed LRDP0 than HRDP0 ($P < 0.07$), but was unaffected by DDGS level. Milk fat production, concentration, and fat corrected milk were linearly reduced by increasing levels of DDGS ($P < 0.01$).

Key Words: dry distillers grains with solubles, rumen degradable protein, corn silage

T427 Effect of quebracho-chestnut tannin extracts at two dietary crude protein levels on performance and rumen fermentation of dairy cows. M. J. Aguerre*[1], M. A. Wattiaux[1], M. C. Capozzolo[1], P. Lencioni[2], and C. Cabral[2], [1]*University of Wisconsin-Madison*, *Madison*, [2]*Silvateam, Indunor S. A*, *Argentina*.

The objective of this study was to determine the effects of a dietary tannin mix on lactating cow performance and rumen fermentation, and whether any responses were affected by dietary CP. Eight ruminally cannulated and 16 noncannulated multiparous Holstein cows (669 ± 55 kg BW; 89 ± 36 DIM) were randomly assigned to a diet of 15.5 or 16.8% CP (%DM) and to 1 of 4 levels of tannins in three 4 × 4 Latin squares within each level of dietary CP. Rice hull was removed from 50:50 forage to concentrate ratio (%DM) total mixed rations as a tannin extract mixture from Quebracho and Chestnut trees was included at 0 (control), 0.45, 0.90 and 1.8% of dietary DM. There was no interaction between dietary CP and tannin supplementation. Reducing dietary CP had no effect on measurements, except for reducing milk urea N (MUN; 18.8 vs. 15.6mg/dL, $P < 0.05$) and ruminal NH_3-N (11.0 vs. 9.3 mg/dL, $P < 0.05$). Overall, milk yield (40.4 kg/d), 3.5%FCM (40.3 kg/d), milk

fat and lactose content and yield, and ruminal pH were not affected by tannin. The *P*-values for a linear increase in BW gain (0.46 kg/d), a linear increase in feed efficiency (1.68 kg milk/kg of DMI) and a linear decrease in DMI (24.4 kg/d) with incremental levels of tannin extracts in the diet were 0.11, 0.15 and 0.07, respectively. Relative to control (2.87%), milk true protein content increased to 2.91% ($P < 0.05$), did not change (2.86%) and decreased to 2.83% ($P < 0.05$) when tannin was 0.45, 0.90 and 1.8% of dietary DM respectively. Also, relative to control (1.14 kg/d), milk protein yield did not change with inclusion of tannin, but it was higher ($P < 0.05$) at the 0.45 than the 0.9 or 1.8% inclusion level (1.16, 1.12 and 1.11 kg/d, respectively). Relative to other treatments, the 1.8% tannin in the diet lowered MUN (13.8 vs. 12.9 mg/dL, $P < 0.05$) and rumen NH_3-N (10.6 vs. 8.1 mg/dL, $P < 0.05$). Results indicate that regardless of dietary CP, 0.45% tannin extract in the diet had a small positive effect on milk protein content independently of a reduction in ruminal protein degradation, which was observed along with a reduction in MUN, only at the 1.8% level of inclusion.

Key Words: tannin, performance, protein

T428 Effect of quebracho-chestnut tannin extracts at two dietary crude protein levels on nitrogen partitioning in lactating dairy cows. M. J. Aguerre*[1], M. A. Wattiaux[1], M. C. Capozzolo[1], P. Lencioni[2], and C. Cabral[2], [1]*University of Wisconsin-Madison, Madison*, [2]*Silvateam, Indunor S. A.*, *Argentina*.

Our objective was to determine the effects of a dietary tannin mix on nitrogen (N) partitioning and whether responses were affected by the level of dietary CP. Eight multiparous Holstein cows (708 ± 41 kg of BW; 125 ± 41 DIM) were randomly assigned to a diet of 15.5 or 16.8% CP (%DM) and to one of 4 levels of tannin in a 4 × 4 Latin squares within each level of dietary CP. Rice hull was removed from 50:50 forage to concentrate ratio (%DM) total mixed rations as a tannin extract mixture from Quebracho and Chestnut trees was included at 0 (control), 0.45, 0.90, and 1.8% of dietary DM. Nitrogen mass balance was conducted by a 3-d total fecal and urine collection. There was no CP by tannin interaction for any of the measured variables. Reducing dietary CP had no effect on DMI (24 kg/d), N intake (613 g/d), milk N (172 g/d) and N efficiency (milk protein N/N intake; 0.28) but increased fecal N (214 vs. 257 g/d, $P = 0.07$) and decreased (all Ps < 0.05) urinary N (232 vs. 167 g/d), urinary urea N (164 vs. 99 g/d) and apparent N digestibility (65.4 vs. 57.2%). Although manure N (fecal N + urinary N; 435 g/d) remained unaltered, lowering dietary CP from 16.8 to 15.5% resulted in a 40% reduction in urinary to fecal N ratio (1.10 vs. 0.66; $P < 0.05$). Tannin did not affect N intake, milk N, or N efficiency, however, it increased fecal N relative to control (214 vs. 243 g/d; $P < 0.05$) with no differences among inclusion levels. In addition, urine N was lower when tannin inclusion rate was 1.8% of dietary DM compared with 0, 0.45 and 0.9% inclusion rates (211 vs. 177 g/d; $P < 0.05$). Inclusion of tannin in the diet did not alter manure N, but it lowered the urinary N to fecal N ratio. Relative to control, urinary N to fecal N ratio was decreased by 18% in the 2 intermediate tannin inclusion rates (1.05 vs. 0.87, respectively; $P < 0.05$), the latter value being further reduced ($P < 0.05$) to 0.72 at the 1.8% inclusion rate (a 31% reduction compared with control). Results indicated that reducing dietary CP and inclusion of tannin extract in the diet had additive effects on altering urinary to fecal N ratio.

Key Words: tannin, nitrogen, manure

T429 Digestibility of amino acids in rumen undegraded corn silage determined by the modified three-step procedure. S. M. Fredin*[1], S. E. Boucher[2], D. Sapienza[3], N. L. Whitehouse[1], and C. G. Schwab[1], [1]*University of New Hampshire, Durham*, [2]*William H. Miner Agricultural Research Institute, Chazy, NY*, [3]*Sapienza Analytica, LLC, Slater, IA*.

Five corn silage (CS) hybrids were utilized in an evaluation of the modified 3-step procedure (mTSP) to estimate intestinal (ID) and total tract digestibility (TTD) of crude protein (CP) and AA. Samples were ground to 2-mm and ruminally incubated in situ for 16 and 24 h in 2 lactating cows averaging (mean ± SD) 43 ± 8 d in milk fed a 58% forage, 42% concentrate ration. Two time points were chosen to evaluate differences in ID due to ruminal incubation time using the MIXED procedure of SAS. After ruminal incubation, rumen undegraded CS was incubated for 1 h in a pepsin-HCl solution and for 24 h in a pancreatin solution. Estimates of ruminal degradability, ID, and TTD of CP and AA were calculated. In vivo estimates of ruminal degradability, ID, and TTD of CP and AA were previously determined for the same CS samples using the mobile bag technique (MBT). Coefficients of determination between in vivo and mTSP data were calculated using the REG procedure of SAS. With the mTSP, average ruminal degradability of CP and total AA for all CS samples (incubated for either 16 or 24 h; n = 10) was 74.0 ± 5.85 and 78.9 ± 3.91%, respectively. Estimates of ruminal degradability of CP and total AA were 13.3 and 9.5% greater for the mTSP compared with ruminal degradability estimates from the MBT evaluation. No difference was observed ($P > 0.05$) for in vitro estimates of ID of CP and AA ruminally incubated for 16 or 24 h. Intestinal digestibility of CP and total AA measured with the mTSP for all rumen undegraded CS samples were 10.6 ± 5.15 and 36.9 ± 8.13%, respectively. Estimates of ID obtained using the mTSP and the MBT were not correlated (R2 = 0.07 for CP and R2 = 0.23 for total AA). The mTSP tended to under-predict intestinal digestibility of CP and total AA by 16 and 13%, respectively. Correlations between the 2 methods were improved for TTD of CP (R2 = 0.92), total AA (R2 = 0.82), and essential AA (averaged R2 = 0.72). The mTSP may not be an acceptable in vitro method to determine ID of AA in rumen undegraded CS, but, it may be suitable to determine TTD of AA.

Key Words: corn silage, amino acid digestibility, modified three-step procedure

T430 Evaluation of sampling protocols to estimate ruminal microbial protein production using urinary excretion of purine derivatives. S. E. Boucher*, H. M. Dann, P. K. Krawczel, H. M. Gauthier, J. D. Darrah, and R. J. Grant, *William H. Miner Agricultural Research Institute, Chazy, NY*.

Urinary excretion of purine derivatives (PD) is a technique commonly used to estimate ruminal microbial protein production. However, urine sampling protocols for this technique reported in the literature vary. The objective of this experiment was to evaluate 2 urine sampling protocols to estimate ruminal microbial protein production in lactating cows. Sampling protocols (SP) were employed on cows concurrently enrolled in a 4 × 4 Latin square trial with 21-d periods designed to evaluate the effects of a feed additive and dietary rumen undegraded protein content on ruminal microbial protein production. Urine samples were collected: 1) 4 h post-feeding (1630) on d 18 and 19 of each period and analyzed separately (SP1) or 2) at 0200 and 1630 on d 18, 19, and 20 of each period and composited by cow by period for analysis (SP2). At each time point a minimum of 40 mL of urine was collected. Aliquots of samples were analyzed for allantoin, uric acid, and creatinine concentrations. In cattle, allantoin and uric acid are the primary PD excreted in urine, and creatinine is used as a marker for urine volume. Daily excretion of urinary PD and microbial N production calculated by each protocol were analyzed using the MIXED procedure of SAS to determine least

squares means (LSM), standard errors, and the variance components associated with each sampling method. The LSM of microbial N for the 4 dietary treatments estimated from SP1 and SP2 were 544, 558, 508, and 553 (SE = 19), and 476, 465, 445, and 476 g/d (SE = 18), respectively. The residual variance as a proportion of total variance for SP1 and SP2 was 28 and 37%, respectively. The residual variance is the proportion of the variance associated with day-to-day variation and measurement errors within cows. Based on differences in LSM and variance components with the 2 sampling protocols, standardization of urine sampling protocols when utilizing urinary excretion of PD to estimate microbial protein production in ruminants is needed.

Key Words: microbial protein production, urinary purine derivatives, sampling protocols

T431 Determining the difference in the supply of metabolizable methionine to dairy cows fed four methionine supplements using concentrations of selenium in milk. J. E. Plank*, W. P. Weiss, and N. R. St-Pierre, *The Ohio State University*, *Columbus*.

Accurately quantifying the amount of metabolizable methionine (Met) supplied by Met supplements can be economically beneficial to dairy producers. A previously developed method to estimate the supply of metabolizable Met, based on changes in the concentration of Se in milk when Met sources are fed, was used to compare metabolizable Met supplied from 4 Met supplements: DL-Met, Smartamine, 2-hydroxy-4-(methylthio)-butanoic acid (HMB) and the isopropyl ester of HMB (HMBi). Twenty Holstein cows were fed a diet containing 32% corn silage, 17% corn, 14% legume hay, 13% distillers grains and 13% wheat middlings as a percent of dietary dry matter (DM), as well as 0.3 mg of Se from Se-yeast/kg of dietary DM. Then, in a truncated Latin square experiment (2 blocks, 2 14 d periods), a methionine or control supplement was added to their diet. Methionine supplements were mixed with soyhulls and were fed twice daily as a 500g/day topdressing to provide 18g of Met/day, while control cows were fed 500g/day of soyhulls. Cows were allowed 11 d for adjustment followed by milk sampling on d 12–14 of each period. The specific activity (SA) of milk (the ratio of Se concentration to milk N concentration) was calculated for each treatment. Supplementing Met reduced the SA of milk for cows treated with HMBi (11.0 μg Se/mg N) and Smartamine (11.1 μg Se/mg N) relative to control (12.1 μg Se/mg N, $P < 0.05$), but SA of milk from other treatments did not differ from control. The SA in milk from treatment cows was divided by SA in milk from control cows to determine the change in supply of metabolizable Met. The digestible met flow for control cows, calculated using the Dairy NRC model, was 44 g/day. The calculated flow of metabolizable Met for cows supplemented with DL-Met, Smartamine, HMB and HMBi was 44.4, 48.3, 45.7 and 45.2 g/day respectively. DM intake was different only for cows supplemented with HMBi (21.1 kg/day vs. 19.7 kg/day for control, $P < 0.01$) and the data were adjusted accordingly. The average milk production was 30.3 kg/day and was not affected by the treatments.

Key Words: methionine, milk protein, selenium

T432 The relationship between milk urea nitrogen concentrations, diet, and milk production on Northeast dairy farms. K. M. Kouri*, *Poulin Grain*, *Newport, VT*.

Previous research has shown that concentrations of milk urea nitrogen (MUN) can be measured to monitor the efficiency of dietary protein utilization, and to decrease costs associated with feeding excess protein. The objective of this study was to determine the relationship between MUN concentrations, time of year, milk production, and diet on Northeast dairy farms. Data from 18 dairy farms (approximately 9300 cows) in Vermont and New York were collected and analyzed to identify associations with and possible predictors of MUN concentrations. Monthly milk production and composition for each farm was collected by local milk cooperatives. A subset of 8 farms was used to determine the relationship between MUN concentrations and nutritional measures. Across all farms, MUN levels averaged 11.3 ± 1.2 mg/dl and milk production was 33.8 ± 2.6 kg/d. Concentrations of MUN were affected by time of year ($P < 0.01$), being highest in the summer and lowest in the late winter. There was a positive relationship between MUN and milk yield ($r = 0.70$; $P < 0.08$), and a negative relationship between MUN and both fat ($r = -0.50$; $P < 0.03$) and protein ($r = -0.70$; $P < 0.002$) percentages. In contrast, there was a positive relationship between MUN and percent other solids ($r = 0.80$; $P < 0.04$). There was a modest negative relationship between MUN and forage:concentrate ratio ($r = -0.50$; $P < 0.17$). Somatic cell count, crude protein, rumen degradable protein, rumen undegradable protein, and soluble protein were not correlated with MUN levels in milk ($P > 0.05$). In conclusion, MUN concentrations changed throughout the year and this should be considered when making nutritional management decisions based on MUN. In addition, the positive relationship between MUN and milk production performance of farms in the current study indicates that dietary protein was not being fed in excess.

Key Words: milk urea nitrogen, Northeast dairy farm, production

T433 A critique of dose-response plots that relate changes in content and yield of milk protein to predicted concentrations of lysine in metabolizable protein by the NRC (2001), CPM-Dairy (v.3.0.10), and AMTS.Cattle (v.2.1.31) models. N. Whitehouse*[1], C. Schwab[1], D. Luchini[2], and B. Sloan[2], [1]*University of New Hampshire*, *Durham,* [2]*Adisseo, Atlanta, GA.*

The objective of this study was to critique the Lys dose-response plots for the NRC, CPM and AMTS models (Whitehouse et al., 2009) with an expanded database. To help ensure that Met was not limiting production responses to supplemental Lys, regression analysis for NRC was limited to data where Met was greater than 2.16% of MP; the Met constraint used previously was 2.07%. The resulting data set for NRC contained 59 observations; the data sets for CPM and AMTS contained 48 and 37 observations, respectively. Observations were less for CPM and AMTS because the models, particularly AMTS, predicted lower concentrations of Lys in MP for the high corn-based basal diets without Lys supplementation than NRC. This created ranges of Lys in MP for more studies than with NRC where the highest predicted concentration of Lys in MP did not overlap with the ranges of Lys in MP for the rest of the studies. This precluded being able to identify a fixed reference concentration of Lys in MP that was intermediate to the lowest and highest values in as many of the Lys studies; a fixed reference concentration is needed to calculate the production responses (plus and minus values) for the y-axis of the dose-response plots. The resulting breakpoint estimates for the required concentrations of Lys in MP for maximal content and yield of milk protein were 6.89 and 6.95% for NRC, 7.23 and 7.36% for CPM, and 6.84 and 6.74% for AMTS. Using this expanded database pinpointed that diets rich in corn protein have very low predicted concentrations of Lys in MP when evaluated through AMTS and CPM, due primarily to the low Lys concentrations in RUP as estimated by the insoluble protein method. This not only precluded the use of certain data, but had consequences on the slopes (0.141 vs. 0.128 vs. 0.105) for NRC, CPM and AMTS and the breakpoints determined. It is suggested that an assessment be undertaken of what database is used for AA profiles of ingredients before updating present formulation guidelines.

Key Words: lactating cows, lysine, methionine

T434 Fatty acid supplementation to periparturient dairy cows fed diets containing low basal concentrations of fatty acids. L. F. Greco*, M. Garcia, M. G. Favoretto, R. S. Marsola, L. T. Martins, R. S. Bisinotto, E. S. Ribeiro, F. S. Lima, W. W. Thatcher, C. R. Staples, and J. E. P. Santos, *University of Florida*, *Gainesville*.

Objectives were to evaluate the impacts of supplementing diets containing low amounts of long chain fatty acids (FA, < 1.8%) with either mostly saturated free FA (SFA) or with Ca salts enriched with polyunsaturated FA (PUFA, 27% C18:2n6 and 3.5% C18:3n3 of the total FA) on performance of Holstein cows. Prepartum cows were allocated randomly to 1 of 3 dietary treatments from 60 d before expected calving date until 90 d postpartum. Supplementation with FA (% dietary DM) consisted of 0% (CTL, n = 26), 1.7% SFA (n = 25), and 1.7% as Ca salts of PUFA (EFA, n = 25). The DMI was recorded daily from 30 d pre- to 90 d postpartum. Body weight and BCS were measured at 60 and 30 d prepartum, at calving and then weekly postpartum. Milk production was measured daily and composition was evaluated weekly. Blood samples were collected weekly before calving and then thrice weekly postpartum for 40 d. Prepartum DMI was lower for cows fed EFA (11.3, 11.4 and 10.2 kg/d, respectively for CTL, SFA and EFA). Feeding EFA reduced postpartum DMI in multiparous but not in primiparous cows. Milk and protein yields were greater for primiparous cows fed EFA, however, fat yield did not differ. Postpartum BW, BW change, and BCS were not different among treatments. Feed efficiency was better and mean concentrations of plasma BHBA were greater for multiparous cows receiving supplemental EFA. Mean concentrations of plasma NEFA were lower for primiparous cows not fed supplemental fat. Cows supplemented with EFA had improved efficiency of converting feed into milk, and increased concentrations of BHBA despite similar BW and BW changes.

Table 1.

	CTL		SFA		EFA		P[1]		
	P[2]	M[3]	P	M	P	M	TRT* Parity	Fat	FA
DMI, kg/d	15.1	21.0	16.5	22.1	17.5	18.6	0.01	0.42	0.12
BW, kg	495	641	502	671	515	629	0.37	0.55	0.45
Milk, kg/d	28.1	35.3	25.8	37.8	30.7	37.5	0.07	0.27	0.06
Milk fat, kg/d	1.0	1.3	0.8	1.3	1.0	1.3	0.17	0.10	0.24
Milk protein, kg/d	0.8	1.0	0.7	1.0	0.9	1.0	0.08	0.40	0.05
Milk/DMI, kg/kg	1.9	1.7	1.6	1.8	1.8	2.1	0.03	0.94	0.01
BHBA, mg/100 mL	6.4	8.4	5.6	7.6	5.8	12.3	0.01	0.45	0.01
NEFA, mEq/L	432	468	317	464	341	522	0.04	0.13	0.11

[1]TRT = treatment; Fat = CTL vs. EFA+SFA; FA = EFA vs.SFA.

[2]Primiparous.

[3]Multiparous.

Key Words: dairy cow, fatty acids, linoleic acid

T435 Intake, digestibility and productive performance of dairy cows fed with sunflower meal. A. S. de Oliveira*[1], J. M. S. Campos[2], E. P. Viana[2], D. S. Caixeta[2], S. C. Valadares Filho[2], A. M. F. Santiago[2], J. P. do Carmo[2], A. C. S. Souza[2], G. H. Soares[2], J. P. Giordani[2], and L. F. do Lago[2], [1]*Universidade Federal de Mato Grosso*, *Sinop, MT, Brazil*, [2]*Universidade Federal de Viçosa*, *Viçosa, MG, Brazil*.

Twelve multiparous Holstein cows (128 ± 38 DIM and 627 ± 48 kg BW) were distributed in three 4 × 4 Latin squares by DIM, with 4 periods of 21 d (7 d of mensurations) to evaluate the effect of sunflower meal (SFM; 37.5% of CP) in diet (0, 7, 14 and 21% of DM) on intake, total tract apparent digestibility and productive performance. Diets TMR were isonitrogen (16.2% of CP), containing 55% of corn silage (DM basis). The SFM replaced mixture (37.5% of CP) containing 53.57% of soybean meal and 47.37% of wheat middlings. Fecal samples were directly collected once daily at 1600, 1400, 1200, 1000 e 800 h, of 15 to 19 d of each period. Indigestible ADF (after 264 h of ruminal incubation) was used to estimate fecal output. Milk samples were collected on 18 and 19 d of each period at am and pm milking. Data were analyzed using model mixed (PROC MIXED, SAS Inst. Inc., Cary, NC). Was applied Williams test to comparison of means for quantitative data. The SFM inclusion increased RDP (10.6, 10.7, 10.9 and 11.1% of DM), NDF (39.9, 40.8, 4. and 42.6), lignin sulfuric acid (2.3, 2.5, 2.8 and 3.1% of DM) and indigestible ADF (8.6, 9.6, 10.6 and 11.6 of DM) of diets. DM (21.6 kg/d), CP (3.75 kg/d) and NFC (7.8 kg/d) intakes were not affected by SFM ($P > 0.05$), but NDF intake (7.9, 7.9, 8.0 and 8.6 kg/d) was greater ($P < 0.05$) to 21% of SFM. DM digestibility (65.1, 64.1, 64.3 amd 62.1%), total carbohydrate digestibility (60.9, 59.2, 59.2 and 57.2%) and TDN (63.8, 62.7, 62.7 and 60.5%) of diets were not affected ($P > 0.05$) until 14% of SFM, but were reduced ($P < 0.05$) with 21% of SFM. Milk yield (29.8, 28.8, 28.7 and 27.4 kg/d) and milk lactose yield (1.32, 1.28, 1.30 and 1.23 kg/d) were not reduced ($P > 0.05$) until 14% of SFM, but were reduced ($P < 0.05$) with 21% of SFM. Milk crude protein (3.22, 3.18, 3.09 and 3.11%) was reduced ($P < 0.05$) from 7% of SFM. Milk efficiency (1.33 kg of milk/ kg of DM intake), milk fat (3.61%), milk lactose (4.47%) and milk solids non-fat (8.63%) were not affected ($P > 0.05$) by SFM. The SFM can be included in up to 14% in DM diets for dairy cows with production of 30 kg/d without affecting intake, digestibility and productive performance.

Key Words: milk

T436 Metabolism of nitrogen compounds in dairy cows fed with sunflower meal. A. S. Oliveira*[1], J. M. S. Campos[2], D. S. Caixeta[2], E. P. Viana[2], S. C. Valadares Filho[2], L. F. do Lago[2], A. M. F. Santiago[2], J. P. Giordani[2], G. H. Soares[2], J. P. do Carmo[2], and A. C. S. Souza[2], [1]*Universidade Federal de Mato Grosso*, *Sinop, MT, Brazil*, [2]*Universidade Federal de Viçosa*, *Viçosa, MG, Brazil*.

Twelve multiparous Holstein cows (28.7 ± 4 kg/day of yield milk, 128 ± 38 DIM and 627 ± 48 kg BW) were distributed in three 4 × 4 Latin squares by DIM, with 4 periods of 21 d to evaluate the effect of sunflower meal (SFM; 37.5% of CP) in diet (0, 7, 14 and 21% of DM) on metabolism of nitrogen compounds (N) and efficiency of N utilization for milk production. Diets TMR were isonitrogen (16.2% of CP), containing 55% of corn silage (DM basis). The SFM replaced mixture (37.5% of CP) containing 53.57% of soybean meal and 47.37% of wheat middlings. Milk samples were collected on 18 and 19 d of each period at am and pm milking. Spot urine samples were obtained approximately 0, 3 and 6 h postfeeding on 17 d of each period. Urine volume was estimated using creatinine concentration as a marker and assuming creatinine excretion of 24.05 mg/kg of BW/d. Data were analyzed using model mixed (PROC MIXED, SAS Inst. Inc., Cary, NC). Was applied Williams test to comparison of means for quantitative data. The SFM inclusion increased RDP (10.6, 10.7, 10.9 and 11.1% of DM). Rumen microbial crude protein synthesis (MPS, estimated by the derivatives in purine urinary excretion and secretion of milk; 2.10, 2.01, 2.03 and 1.77 kg/d) was not affected ($P > 0.05$) until 14% of SFM, but was reduced ($P < 0.05$) with 21% of SFM. The g of MPS/kg TDN intake (152.6) was not affected ($P > 0.05$) by SFM, but the efficiency of RDP intake used for MPS (0.90, 0.88, 0.88, 0.73 kg de MPS/kg of RDP intake) was reduced ($P < 0.05$) with 21% of SFM. Milk urea-N (17.60 mg/dL), blood urea-N (17.80 mg/dL), urinary N-urea (195.7 g/d), urinary N (240 g/d; 40% of N intake), feces N (185.2 g/d; 30.9% of N intake) and balance N (32.6

g/d; 5.5% of N intake) were not affected ($P > 0.05$) by SFM. However, because of lower efficiency RDP intake for MPS, the milk N/intake N (24.9, 24.2, 23.5 and 22.0%) was reduced ($P < 0.05$) from 14% of SBM. The SFM can be included in up to 7% in DM diets of dairy cows without affecting metabolism of nitrogen compounds (N) and efficiency of N utilization for milk production.

Key Words: blood urea-N, microbial crude protein synthesis, n efficiency

T437 A critique of dose-response plots that relate changes in content and yield of milk protein to predicted concentrations of methionine in metabolizable protein by the NRC (2001), CPM-Dairy (v.3.0.10), and AMTS.Cattle (v.2.1.31) Models. N. Whitehouse*[1], C. Schwab[1], D. Luchini[2], and B. Sloan[2], [1]*University of New Hampshire*, *Durham,* [2]*Adisseo, Atlanta, GA.*

The objective of this study was to critique the Met dose-response plots for the NRC, CPM and AMTS models (Whitehouse et al., 2009) with an expanded database. To help ensure that Lys was not limiting production responses to supplemental Met, regression analysis for NRC was limited to data where Lys was greater than 6.45% of metabolizable protein (MP); the Lys constraint used previously was 6.16%. The resulting data set for NRC and CPM contained 91 observations; the data set for AMTS contained 82 observations. Observations were less for AMTS because the model predicted lower concentrations of Met in MP than CPM for several of the basal diets without Met supplementation. This created ranges of Met in MP where the highest predicted concentrations of Met in MP in some studies did not overlap with the lowest concentrations of Met in MP for the rest of the studies. This precluded being able to identify a fixed reference concentration of Met in MP that was intermediate to the lowest and highest values in all studies; a requisite for calculating the production responses (plus and minus values) for the y-axis of the dose-response plots. The resulting breakpoint estimates for the required concentrations of Met in MP for maximal content and yield of milk protein were 2.23 and 2.38% for NRC and 2.40 and 2.44% for CPM. These compare favorably to the respective breakpoint estimates of 2.23 and 2.38 for NRC and 2.40 and 2.44 for CPM by Whitehouse et al. (2009). For AMTS, the relationship between changes in content and yield of milk protein to predicted concentrations of Met in MP was linear, a result of the more restricted database and differences between AMTS and CPM in predicted concentrations of Met in MP. It is suggested that an assessment be undertaken of what database is used for AA profiles of ingredients before updating present formulation guidelines for Met in MP for the models evaluated

Key Words: lactating cows, methionine, lysine

T438 In situ ruminal degradability of crambe, sunflower and soybean grains, and its by-products. R. H. de Tonissi e Buschinelli de Goes*, K. A. de Souza, R. A. Patussi, K. A. G. Nogueira, D. de Faria Pereira, T. da Cunha Cornélio, K. C. da Silva Brabes, and E. R. de Oliveira, *Universidade Federal da Grande Dourados*, *Dourados, MS, Brasil*.

The ruminal degradation of dry matter (DM) and crude protein (CP) of crambe (*C. abyssinica*), sunflower, soybean grains and its by-products (crushed seeds), were evaluated by the in situ technique, using 3 rumen fistulated sheeps. The feeds were grounded though a 2mm screen and incubated directly in rumen for 72, 48, 24, 12, 6, 3, and 0 h. Potential degradation, were adjusted by a no linear regression by Gauss-Newton's method, PD = A+B*(1-exp-ct), being A = soluble fraction, B = potentially degradable fraction, c = degradation rate of the fraction B, and t = time of incubation. Effective degradability (ED = a+(b*c)/(c+k)), where k = passage rate of 5%/h. DM and CP for crambe, sunflower and soybean was 93.5, 93.6, 89.4% and 27, 22.3, 50.3%; for its by-products was 70, 87.4, 90.5%, and 52.8, 30.3, 46.8%. The Crambe soluble fraction (23.5%) and potentially degradable fraction (74.1%), provided more ED (75.4%) for DM. Crambe crushed, showed lower degradability (60.4%) and soluble fraction (20.1%) and higher rate of degradation (14.7%). The soybean and sunflower had the lowest effective degradability (47.6 and 39.7%), possibly related to low soluble fraction (4.8 and 11.7%), while its by-products had the highest ED (75.6 and 84.5%), with soluble fraction of 23.2 and 22.9%, and potentially degradable fractions of 70.3 and 73.7%. For the CP, the crushed soybean presented a higher effective degradability and potentially degradable fraction (70.9 and 89,1%), while the grain presented 38.7 and 55.6%. The sunflower, crambe and its by-products presents ED and potentially degradable fraction of 30.7, 44.0, 45.0, and 35.5% and 41.3, 38.1, 34.6, 22.0%. The soluble fractions were 8.7, 9.8, 18.3, 7.7, 13.7, and 19.3, for soybean, sunflower, crambe and its by-products. The low degradation presented by crambe and sunflower by-products can be associated with the processing of grain for oil extraction, and undegradable fraction (58.7 and 51.7%). The grains of crambe, sunflower and soybean and its by-products had a medium degradability for the dry matter and low degradability for crude protein, except soybean by-product, that showed high degradability.

Key Words: nylon bags, chemical composition, oil seeds

T439 Effects of supplemented high linoleic or linolenic oil in the diet on lipid metabolism by rumen microbes in sheep. S. H. Choi*[1], G. W. Jin[2], H. G. Lee[3], C. W. Choi[4], S. S. Chang[4], S. B. Smith[1], and M. K. Song[2], [1]*Department of Animal Science, Texas A&M University*, *College Station,* [2]*Department of Animal Science, ChungBuk National University, Cheong Ju, Chungbuk, Korea,* [3]*Department of Animal Science, Pusan National University, Miryang, Gyongnam, Korea,* [4]*National Institute of Animal Science, RDA, Suwon, Gyunggi, Korea.*

A metabolic trial with 3 ruminally cannulated sheep (60 ± 6 kg) was conducted in a 3 × 3 Latin square design to investigate the effects of high linoleic (18:2 *n*-6; soybean oil) or α-linolenic oil (18:3 *n*-3, perilla oil) on the ruminal fermentation, formation of conjugated linoleic acid (CLA) in the rumen and apparent digestibilities of nutrients. Sheep were fed 1.3 kg of diet (DM basis) consisting of 60% concentrate and 40% chopped alfalfa hay. Oils were supplemented to concentrate at 5% level of the total diet (DM basis). Rumen pH was not influenced by the oil supplementation. But ammonia-N concentration significantly decrease ($P = 0.05$) by the feeding the oil supplemented diets. Molar proportion of each VFA in rumen fluid and whole tract digestibilities of DM, CP, EE, NDF and OM were not affected by oil supplementation. The compositions of *trans*-10, *cis*-12 CLA (from 0.56% to 1.43%) in the rumen fluid were slightly higher than that of *cis*-9, *trans*-11 CLA (from 0.27% to 1.47%). Oil supplementation resulted in decreased plasma oleic acid (18:1 *n*-9) proportion ($P < 0.03$) but increased linoleic acid proportion ($P < 0.04$) at 1 h before feeding. At 1 h post-feeding, oil supplementation resulted in a decreased stearic acid (18:0) proportion ($P < 0.02$) but increased palmitoleic acid (16:1*n*-7) proportion ($P < 0.01$) in plasma. The proportions of *cis*-9, *trans*-11 CLA in plasma was slightly (from 0.18% to 0.62% ; $P = 0.37$) increased with oil supplementation at 1 h post-feeding.

Key Words: conjugated linoleic acid, plant oil, sheep

T440 Effects of increasing amounts of high-linolenic perilla fatty acid infused into the duodenum on blood lipids metabolism and

their susceptibility to peroxidation in dairy cows. Q. S. Liu[1,2], J. Q. Wang*[1], D. P. Bu[1], E. Khas[1], G. Yang[1], L. Y. Zhou[1], P. Sun[1], and K. L. Liu[1], [1]*State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences*, *Beijing, China*, [2]*College of Animal Science and Technology, Yangzhou University*, *Yangzhou, China*.

Our objective was to determine the effects of increasing amounts of high-linolenic perilla fatty acid (HLPFA) emulsion (82.4% *cis-9*, *cis-12*, *cis-15* 18:3; 14.7% *cis-9*, *cis-12* 18:2; 2.8% *cis-9* 18:1 and 0.1% other fatty acids) infused into the duodenum of dairy cows on blood lipids metabolism and the susceptibility of blood to oxidation. Four primiparous Chinese Holstein cows (BW = 476 ± 6 kg, DIM = 100 ± 2 d) fitted with duodenal cannulas were administered 2 treatments in a crossover design. Treatments were homogenized aqueous mixtures of HLPFA emulsion (0, 100, 200, 300, 400 g/d) or control containing only the emulsifying ingredients. The control infusate consisted of 15 g/d of xanthan gum, 5 g/d sodium alginate, and 25 g/d of Tween 80 in 10 L of purified water. Each period lasted 5 wk, during period 1, 2 cows received each amount of HLPFA for 1 wk each, and the other 2 cows received only the carrier infusate. In period 2, the procedures were repeated, so that the other 2 cows received the HLPFA doses in sequentially increasing amounts and the cows that previously received HLPFA received the control infusate. Blood collection was made during the last day of each infusion amount. Data were analyzed statistically by using PROC MIXED of SAS. The concentration of high density lipoprotein cholesterol and total cholesterol were increased quadratically ($P = 0.0036$, 0.0013 respectively). The concentration of α-linolenic acid in blood increased linearly as infusion increased ($P = 0.0001$). The activity of total superoxide dismutase tended to decrease linearly ($P = 0.18$), and the total antioxidant capacity also tended to decrease quadratically ($P = 0.23$), but the thiobarbituric acid reactive substances tended to increase linearly ($P = 0.066$), and the content of vitamin E in serum tended to increase quadratically ($P = 0.096$) as the infusion increased. Infusion with increasing amounts of HLPFA into the duodenum altered the composition and distribution of blood lipids, but decreased the oxidative stability of the blood in dairy cows.

Key Words: high-linolenic perilla fatty acid, blood lipid, oxidation stability

T441 Effects of feeding ruminally protected lysine, with or without isoleucine, valine and histidine, to lactating dairy cows on productive performance and plasma amino acid profiles. P. H. Robinson[1], S. Juchem[1], N. Swanepoel*[2], and E. Evans[3], [1]*UC Davis*, *Davis, CA,* [2]*Meadow Feeds, Roodepoort, South Africa,* [3]*Essi Evans Technical Advisory Services, Bowmanville, ON, Canada.*

The literature on post-ruminal Lys supplementation to diets of lactating dairy cows shows small negative responses to supplemental intestinally absorbable Lys (IAL), and our recent survey of California dairy rations identified other amino acids (AA) that could become co-limiting if supplies of IAL were met. Objectives were to estimate the rumen escape of a ruminally protected (RP) Lys (RPL) product, and an RPL also containing Ile, Val and His (RPAA), to determine effects of their feeding on performance and plasma AA profiles of lactating dairy cows. Three pens of ~310 multiparous early lactation cows were used in a 3 × 3 Latin square design with 28-d experimental periods in which the basal total mixed ration (TMR) was the same for all groups except for the RP products that were added to the treatment pens at a level designed to deliver an equal amount of IAL to both groups. However rumen stability was slightly higher for the RPL vs. the RPAA, and RPL was calculated to deliver ~13.2 g/cow/d of IAL and the RPAA calculated to deliver ~10.6, 5.4, 2.2 and 1.6 g/cow/d of IAL, Ile, His and Val respectively. Only milk protein % was increased with RPL. Replacement of RPL with RPAA increased milk and milk lactose yields, while milk protein and energy outputs tended to increase. Plasma levels of both non-essential and essential AA, including Lys, were not impacted by feeding RPL or RPAA. Overall, feeding RPL alone caused generally reduced productive performance, which could be interpreted to suggest that Lys was not supplied in sufficient quantity or that it was not required. Addition of Ile, His and Val to the RPL increased performance overall, which supports an overall hypothesis that Lys alone resulted in an imbalance and/or deficiency of Ile, His and/or Val which was alleviated by their supplementation. Overall treatment differences, regardless of statistical significance, were small and of limited practical importance. Nevertheless, feeding a complex of RPAA was beneficial beyond supplementation of RP Lys alone.

Key Words: amino acids, imbalance, body condition

T442 Effect of extruded cotton seed and canola seed on the composition of unsaturated fatty acids in plasma, erythrocytes and liver of Mehraban male lambs. A. Akbarian[1], A. Golian*[1], A. Tahmasbi[1], M. H. Ghafari[1], and M. Mirzaee[2], [1]*Ferdowsi University of Mashhad*, *Mashhad, Khorasan Razavi, Iran*, [2]*Isfahan University of Technology*, *Isfahan, Iran*.

An experiment was conducted to study the effects of supplementary extruded cotton seed (ECOS) or canola seed (ECAS) on the composition of unsaturated fatty acids in plasma, erythrocytes and liver of Mehraban male lambs. The treatments included: (1) control (C); (2) diet C+6% ECAS, (3) diet C+6% ECOS, (4) diet C+12% ECAS, (5) diet C+12% ECOS, (6) diet C+6% ECAS+6% ECOS, (7) diet C+12% ECAS +6% ECOS, (8) diet C+6% ECAS +12% ECOS, (9) diet C+12% ECAS+12% ECOS, (10) diet C+18% ECAS+18% ECOS. A completely randomized design experiment was applied to feed the 10 dietary treatments to 60 individually pen housed lambs, to have 6 lambs per diet. The average weight of 5–6 mo lambs at the commence of study was 34.3 ± 2.12 kg. The experiment lasted for 90 d. The amount of oleic acid, linoleic acid and linolenic acid in plasma and oleic acid, and linolenic acid in erythrocytes lipids were higher in lambs fed diet contained either or a combination of supplemental extruded oil seeds compared with those fed control diet. The supplementation of 6% or 12% ECAS significantly increased linoleic acid in liver lipids compared with those fed diet containing ECOS. There was a linear ($P < 0.001$) correlation between the levels of dietary ECAS or ECOS with linoleic and linolenic acids content of liver.

Key Words: lamb, extruded cotton and canola seeds, fatty acids

T443 Effects of roasted and electron beam irradiation on ruminal and intestinal disappearance of whole soybean. A. Akbarian[1], M. Khorvash[1], G. Ghorbani[1], M. Dehghan-Banadaky*[2], P. Shawrang[3], and E. Ghasemi[1], [1]*Isfahan University of technology, Department of Animal Sci.*, *Isfahan, Iran*, [2]*University of Tehran, Department of Animal Sci.*, *Karaj, Tehran, Iran*, [3]*Nuclear Science and Technology Research Institute, Atomic Energy Organization of Iran*, *Tehran, Iran*.

The aim of this study was to evaluate the effects of roasting and electron bean irradiation on in situ ruminal and intestinal dry matter and crude protein degradability of whole soybean. Whole soybeans were roasted in a commercial roaster in 145°C for approximately 30 min. The TT200 Rhodotron accelerator was used for irradiation of whole soybean at dose of 63 kGy. Three rumen and duodenum fistulated non-lactating Holstein cows (620 ± 25 kg) were used for in situ study. Rumen degradability of

dry matter and crude protein were determined using the nylon bag technique and mobile nylon bag technique used for intestinal disappearance. Bags were incubated in the rumen for 2, 4, 8, 12, 24 and 48 h and bags washed without incubation in the rumen for 0 h. Rumen degradation (p) was estimated by the curves were fitted using the nonlinear procedure (PROC NLIN) of SAS, which yielded the equation parameters a, b, and c, each of which is defined as: $P = a + b\ (1\text{-}e^{-ct})$. The soluble fraction (a) and effective degradation (ED, K = 0.05 h-1) decreased and insoluble potentially degradable fraction (b) increased in roasted soybeans (Table 1) but irradiation increased fraction of a and ED and decreased the b fraction of DM and CP ($P < 0.05$). Roasting increased but e-beam irradiation decreased intestinal digestibility of DM and CP. Base on present results, roasting could improve ED and intestinal disappearance of soybean seed but e-beam in 63 kGy could not improve aggregation of soybean protein to increase by pass protein.

Table 1. Rumen degradability and intestinal digestibility of untreated, roasted and irradiated whole soybean

Parameters	Treatments			SEM
	Untreated	Roasted soybeans	Irradiated soybeans	
DM				
a	28.6[b]	20.9[c]	33.9[a]	2.05
b	71.3[b]	79[a]	64.9[c]	3.01
c(h-1)	8.1[b]	4.9[b]	12.9[a]	0.02
Effective degradability	69.5[b]	64.1[b]	80.04[a]	2.3
CP				
a	22.5[b]	13.7[c]	36.8[a]	2.09
b	77.4[b]	86.2[a]	62.8[c]	2.2
c(h-1)	8.4[b]	6.1[b]	14.3[a]	0.02
Effective degradability	70.7[b]	60.7[c]	83.1[a]	3.6
Intestinal crude protein digestibility	73.07[b]	81.9[a]	63.1[c]	0.06

[a,b,c] Means in the same row with different letters differ ($P < 0.05$).

Key Words: whole soybean, electron beam irradiation, roasted

T444 Meta-analysis for the prediction of net portal absorption (NPA) of amino acid-N (AAN) and ammonia (NH_3) in ruminants. C. Côrtes*[1], R. Martineau[1], D. Sauvant[2], D. R. Ouellet[1], J. Vernet[3], I. Ortigues-Marty[3], and H. Lapierre[1], [1]*Agriculture and Agri-Food Canada*, *Sherbrooke, Quebec, Canada*, [2]*AgroParisTech*, *Paris, France*, [3]*URH INRA*, *Theix, France*.

To improve the efficiency of N utilization in ruminants, the objective of this meta-analysis was to predict NPA of AAN and NH_3 from feed intake and composition. Composition of feed ingredients was estimated from INRA (1988) tables, except for N and NDF when reported. Selection of publications (FLORA, Vernet and Ortigues-Marty, 2006) was done on availability of NPA-AAN or NH_3, N intake (NI), BW, and feeding treatments. The final database included 68 publications, 90 experiments (sheep n = 44, cattle: beef and dairy breeds n = 29, dairy: lactating cows n = 17) for a total of 216 treatments: NI, NPA of AA-N and NH_3 averaged (SD): 0.48 (0.20), 0.21 (0.13) and 0.19 (0.12) g N/d per kg BW. In addition to NI, dietary interfering factors (IF) were tested on sub-groups with a sufficient variation of the IF: NDF, CP, ruminally (R) digestible starch (RdS), R-degradable protein (RDP), R-undegradable protein (RUP), R-fermented organic matter (RfOM), and RfOM minus RDP (RfOM-RDP) as %DM; RUP and RDP, as %CP; RdSi (g/d per kg BW), RDP:RfOM, RDP:RfOM-RDP and RdS:RfOM. Seven and 5 IF had a significant slope with the within-experiment residues of the model $Y = \alpha + \alpha i + \beta Ni + \varepsilon$, on NPA of AAN and NH_3, respectively. Each of the IF with an effect on the residues was included to generate a model: $Y = \alpha + \alpha i + \beta Ni + \gamma X + \zeta X^2 + \varepsilon$. Looking for a common IF, RDP:RfOM was selected as the best IF: NPA-AAN = -0.001^{NS} (0.02) + 0.59***(0.05) × NI - 0.60***(0.16) × RDP:RfOM, RMSE = 0.0373, R^2adj = 88.4%, with a species effect** on the intercept: Δ = 0.05, 0, −0.05 for sheep, cattle and dairy cows; NPA-NH_3 = −0.09*(0.04) + 0.15**(0.06) × NI + 2.05***(0.48) × RDP:RfOM - 3.77***(1.08) × RDP:$RfOM^2$, RMSE = 0.0309, R^2adj = 92.3%, species × NI interaction*: Δ = −0.13, 0.09, 0.04 for sheep, cattle and dairy cows. The ratio RDP:RfOM combining the availability of N and energy in the rumen and estimated from dietary characteristics is, in addition to NI, a useful predictor of NPA of AAN and NH_3.

Key Words: amino acid, ammonia, ruminants

T445 Effect of tannins in pistachio by-product and urea infusion into the rumen on rumen fermentation and blood metabolites in Iranian Balochi sheep. H. Gholizadeh, A. A. Naserian*, R. Valizadeh, and A. M. Tahmasebi, *Ferdowsi University of Mashhad*, *Mashhad, Iran*.

The objective of this study was to determine the effects of tannins in pistachio by-product (PB) on ammonia concentrations in rumen, abomasum and blood metabolites in Iranian Balochi sheep. Three rams with ruminal cannulas and T cannulas in the abomasums were used in a 3 × 3 change over design experiment. Rams were maintained in individual metabolism crates (1.3 m × 0.5 m) which access to water at all times. Treatments were including 3 levels of PB (T1 = 0, T2 = 20 and T3 = 40% of DM). Urea was continuously infused into the rumen via peristaltic pump (1 mL/ min). Daily intake was determined. Abomasum samples were taken simultaneously from all rams twice daily during a period of 4 successive days as follows: d 1, 0900 and 1500 h; d 2, 1000 and 1600 h; d 3, 1100 and 1700 h and d 4, 1200 and 2000 h. Ruminal samples were obtained from each ram on d 3 of the 5-d collection period before the morning meal and 1, 2, 3, 4, 6 and 8 h after feeding. Blood samples were collected from each rams at the end of experiment via jugular vein 2 h after morning feeding. Dry matter intake (DMI) decreased for sheep fed PB (0.75, 0.74 and 0.64 kg, respectively). This reduction was significant for T3 and no differences were observed between T1 and T2. The addition of PB in the diet reduced ammonia concentration in the rumen. In contrast, ammonia concentration in the abomasum increased (25.01, 26.09 and 31.90 mg/dL, respectively). Treatment effects on blood urea nitrogen (BUN) did not differ ($P > 0.05$), but tended to be greater for sheep fed the PB (14.66, 16.33 and 17.66 mg/dl, respectively). Blood glucose, triglyceride and cholesterol decreased for sheep fed T3 compared with control (57 vs. 64; 8 vs. 13 and 26 vs. 40 mg/dL, respectively) It was concluded that feeding PB at high levels (40% of DM) led to decreased DMI, glucose, cholesterol and triglyceride compared with control, but the addition of 20% had no affect.

Key Words: pistachio by-product, urea, Balochi sheep

T446 The protection of nano-encapsulated conjugated linoleic acid (CLA) from biohydrogenation by rumen bacteria. S. D. Cho*[1], H. G. Park[1], H. G. Ji[2], E. G. Kweon[3], and Y. J. Kim[1], [1]*Department of Food and Biotechnology, Korea University*, *Chungnam, Korea*, [2]*Pharmachem*, *Samjung-dong, Ohjung-gu, Bucheon-city, Kyounggi-do, Korea*, [3]*Hanwoo Experimental Station, National Livestock Research Institute*, *Gangwon, Korea*.

Conjugated linoleic acid (CLA) occurs mainly in dairy products because it is produced as an intermediate in the ruminal biohydrogenation process of linoleic acid, a characteristic biochemical process carried out by some rumen bacteria. Thus, dietary sources of CLA are not well protected from

biohydrogenation. In this study, nano-encapsulated CLA; nanosome complex with lecithin was tested as one of the ways to protect CLA from ruminal biohydrogenation. CLA was emulsified with saturated lecithin, capric-capric triglyceride, glycerin, and cholesterol ester using microfludizer. Free form of CLA (CLA-FFA), and triglyceride form of CLA (CLA-TG) were coated with nanosome about the size 100 nm in diameter. To test the protection effect, rumen bacteria were cultured in rumen fluid media in 500 mL continuous culture fermenter. Fresh media was supplied at 25 mL/h with 2% fat substrates with 4 different forms (CLA-FA, CLA-TG, CLA-FFA nanosome, and CLA-TG nanosome). The change in fatty acid profiles by rumen bacteria was monitored during the 48 h incubation. Gas chromatography was used to analyze fatty acid profiles in each group. In all tested groups, the biohydrogenations of CLA were observed during incubation. In CLA-TG and CLA-FFA nanosome groups, the protection effects were not significant compared with CLA-FFA group. In CLA-FFA group, most of CLA was hydrogenated to vaccenic acid (C18:1) or stearic acid. However, in CLA-TG nanosome group, the degree of conversion to vaccenic acid from CLA was the lowest in all tested groups ($P < 0.05$). These results showed that nanoemulsification is one of the ways to protect natural form of unsaturated fatty acids from the ruminal biohydrogenation and to increase the accumulation level of CLA in the tissue of ruminants.

Key Words: conjugated linoleic acid, rumen bacteria, biohydrogenation

T447 Study on the effect of flaxseed and vitamin E supplementation on rumen biohydrogenation by Rumen Simulation Technique (RUSITEC). H. Sultana*[1], M. L. He[1], M. E. R. Dugan[2], and T. A. McAllister[1], [1]*Agriculture and Agri-Food Research Centre*, *Lethbridge, AB, Canada*, [2]*Agriculture and Agri-Food Research Centre*, *Lacombe, AB, Canada*.

Supplementation with omega-3 fatty acid (FA)-rich flaxseed, is used to increase poly-unsaturated fatty acids (PUFA) in meat and milk. High levels of vitamin E (VE) are often included in such diets to reduce oxidation of PUFA in ruminant products. In this study, the RUSITEC was used to assess the effects of flaxseed and/or VE on rumen fermentation, DM disappearance, methane emission and FA profile. Inoculum was obtained from 3 ruminally cannulated non-lactating Holstein cows fed a 75:20:5 diet of barley grain:barley silage:mineral supplement. Fermenters were fed a barley silage (2 g DM) / barley- grain concentrate (8 g DM) diet daily. The experiment was a 2 × 2 factorial with ground flaxseed replacing concentrate at 0 or 15% of DM, along with VE at 0 or 100 IU/kg DM. Volume of effluent, pH and total gas were determined daily at feeding. After 8 d of adaptation, 48-h DM disappearance from silage and concentrate were determined on d 9, 10, 11, 15, 16, and 17. Methane in gas samples and FA accumulations in 24-h effluent were analyzed on d 12, 13, 14, 18, 19, and 20. Disappearance of DM from concentrate was unaffected ($P = 0.93$) by VE, but tended to be lower ($P = 0.07$) with flaxseed. There was no significant difference in total gas or methane production among treatments. As a percent of total FA, inclusion of flaxseed increased levels of saturated ($P = 0.03$), including C18:0 ($P = 0.001$) and decreased ($P = 0.03$) levels of PUFA. Inclusion of flaxseed tended to increase percentage of C18:1 t11 ($P = 0.08$) and the ratio of C18:1 t11/t10 FA ($P = 0.08$). Inclusion of VE did not appear to influence biohydrogenation or the fatty acid profile in effluent. In conclusion, this study indicates that alteration in FA profile arises from the inclusion of flaxseed in the diet with VE having no measurable influence.

Key Words: rumen fermentation, flaxseed, fatty acid

T448 Partial replacement of common bean by-products (*Phaseolus vulgaris*) with soybean meal impacts on feed intake and apparent digestibility in growing lambs. H. P. Mejia[1], A. Z. M. Salem*[1,2], E. J. D. Coronado[1], J. L. Tinoco[1], and F. Avilés[1], [1]*Universidad Autónoma del Estado de México*, *Centro Universitario UAEM-Temascaltepec, Estado de México, C.P. 51300, México*, [2]*University of Alexandria*, *Department of Animal Production, Faculty of Agriculture (El-Shatby), Egypt*.

Four total mixed rations (TMRs) were prepared with supplementary protein supplied by soybean meal (TMR1) being replaced by protein from either 50 (TMR2), 75 (TMR3) or 100% (TMR4) of the common bean by-products (*Phaseolus vulgaris*) as the only sources of protein. Six Pelibuey male lambs (29 ± 10kg BW) were allocated into each of the dietary treatments in a random complete design of 4 TMRs × 6 repetitions (animals) and were fed ad libitum. Nutrients and energy composition as well as daily DM intake (DMI) and in vivo apparent digestibility of the treatments were determined. The CP, and energy contents (i.e., NEm, NEg) content of the all TMRs were approximately 13.5%, 1.72 and 1.1 Mcal/kg DM, respectively, while CF was 21% in TMR1 and TMR2 and was approximately 18% in TMR3 and TMR4. No significant differences were observed among the 4 treatments in DMI with a tendency to increase in TMR1 (1.15 kg DM, $P = 0.590$) than others treatments. Digestibility of DM (DMD, $P = 0.838$) and CP (CPD, $P = 0.872$) also had tendency to improve from TMR1 to TMR4 (73, 74, 74 and 76% for the DMD, and 76, 76, 77 and 78% for the CPD, and for the 4 treatments, respectively. Digestibility of CF was not affected by the replacement of *P. vulgaris* with soybean meal in TMR and all TMRs were approximately the same (72%, $P = 0.872$). In conclusion, *P. vulgaris* could be used in a partial substitution of the soybean meal and it could be used as an alternative source of protein in Pelibuey lambs diets.

Key Words: *Phaseolus vulgaris*, digestibility, lambs

T449 The effect of partial replacement of soybean meal by *Phaseolus vulgaris* byproducts on growth performance in Pelibuey growing lambs fed finishing diets. H. P. Mejia[1], A. Z. M. Salem*1,2, J. L. Tinoco[1], R. S. Robollar[1], E. J. D. Coronado[1], and F. Avilés[1], [1]*Universidad Autónoma del Estado de México*, *Centro Universitario UAEM-Temascaltepec, Estado de México, C.P. 51300, México*, [2]*University of Alexandria*, *Department of Animal Production, Faculty of Agriculture (El-Shatby), Egypt*.

Twenty-four Pelibuey male lambs ((29 ± 10 kg BW) were used to evaluate the effect of replacing soybean meal with common bean by-products (PV- *Phaseolus vulgaris*) as the only sources of protein, on average daily gain (ADG), feed conversion (FC) and economic efficiency (EE). Lambs were fed finishing diets and assigned randomly to one of 4 dietary treatments. Treatment diets were prepared with supplementary protein supplied by soybean meal (CON, n = 6), being replaced by protein from either 50 (PV50, n = 6), 75 (PV75, n = 6) or 100% (PV100, n = 6) of the common bean by-products (*P. vulgaris*). Crud protein and energy contents (i.e., NEm, NEg) were approximately similar, while crude fiber was higher in CON and PV50 compared with PV75 or PV100. No differences ($P = 0.590$) were noticed in feed intake, final weight, total gain, and ADG among all treatment diets. FC ratio was numerically ($P = 0.940$) increased in PV50 lambs, than the CON or PV75 and PV100 diets. Cost of one kg gain (i.e., EE) was also numerically decreased in PV75 and PV100 lambs when compared with CON or PV50 groups. These data indicate that feeding fattening Pelibuey growing lambs diets containing 100% of CP diet from the *P. vulgaris* did not affect feed intake or growth performance parameters that could also supported to reduce the production costs in fattening sheep.

Key Words: Pelibuey lambs, *Phaseolus vulgaris*, growth performance

T450 Effect of supplemental grower / finisher ration protein level on growth rate, chevon production and cost of gain of crossbred meat goats grazing Joy Chicory pasture. M. Lema*, S. Murray, and B. Barlow, *Tennessee State University*, *Nashville*.

Chicory (*Chicorum intybus*) is becoming popular as a warm-season forage for ruminant livestock in the United States. A study was conducted with weaned crossbred meat goats to elucidate how growing / finishing meat goats grazing Joy chicory pasture respond to supplementation with varying levels of dietary protein. Thirty 6 weaned crossbred kids (26 ± 3 kg) were blocked by body weight and genotype and divided into 3 treatment groups. Each treatment group was replicated in 2 0.4 ha Joy chicory and native grass paddocks with 6 kids per paddock and supplemented with isocaloric grower / finisher ration containing 11, 16 or 21% crude protein for 56 d. The data generated from the study was subjected to Analysis of Variance for randomized complete block design. Grower / finisher ration intake (1.13, 1.31 and 1.31 kg / day) and cost (0.41, 0.51 and 0.51 dollars / day) for the 11, 16 and 21% protein supplemented groups, respectively) were not affected by protein content of the diet. Total live weight gain (7.7 kg) and average daily gain (145.0 g) for the16% protein level were significantly higher ($P < 0.05$) than for the 11% (2.7 kg and 52.0 g, respectively) and 21% (6.0 kg and 113.0 g, respectively) protein levels. Feed cost per kg gain was significantly lower ($P < 0.05$) for the 16% protein level than for the 11 and 21% protein levels (3.5 versus 7.8 and 4.5 dollars / day, respectively). Boneless retail cut from the leg, loin, shoulder and rack followed similar trend as weight gain, being significantly higher ($P < 0.05$)for the 16% protein level than for the 11 and 21% while the 21% level was higher than the 11%. Back fat thickness and fat cover over the carcass tended to increase ($P < 0.05$) with protein level in the diet. It is concluded that optimum performance and return from meat goats grazing Joy Chicory is obtained when they are supplemented with 16% protein in the diet as compared with lower (11%) and higher (21%) levels.

Key Words: meat goat, chicory, protein level

T451 Effects of breed and slaughter endpoint on feed intake, growth performance, and carcass traits of purebred Boer and Kiko goat kids. S. Solaiman*[1], B. R. Min[1], N. Gurung[1], J. Behrends[2], E. Taha[1], and C. Hill[1], [1]*Tuskegee University*, *Tuskegee, AL,* [2]*Mississippi State University, Mississippi State.*

The objectives of this experiment were to determine the effects of 2 different breeds (Boer vs. Kiko) and 4 slaughter endpoints (SEP; d 0, 35, 63 and 88) on DMI, ADG and carcass traits of male goat kids (n = 6). Forty-eight purebred (BW = 23.9 ± 1.50 kg) kids were used in a completely randomized design experiment with a 2 × 4 factorial arrangement of treatments. Goats were stratified by BW within breed and randomly assign to 4 SEP. Kids were born between March 15 and April 7, and were represented by at least 3 sires within each breed. They were housed indoors in individual pens, had ad libitum access to water and mineral blocks, and were fed concentrate: hay (80:20%, respectively) diet once a day. At designated time, goats were transported to the Meat Science Lab., MSU, MS and were slaughtered. Performance and carcass data were analyzed using PROC MIXED of SAS. There were no interactions between breeds and SEP. Both breeds had similar DMI; however, the Kiko goats consumed more hay ($P < 0.01$) and Boer goats consumed more concentrate ($P < 0.01$). There was no different in initial BW for 2 breeds, but final BW ($P < 0.03$), ADG ($P < 0.001$), and G:F ($P < 0.001$) were higher for Boer breed. Boer goats tended to have higher HCW ($P = 0.08$) and cold carcass weights (CCW; $P = 0.08$) only on d 88. No differences were observed in transportation shrink, carcass shrink, dressing percentage, 12th rib fat thickness, and LM area between 2 breeds. Muscle and fat weights were higher for Boer breed ($P < 0.01$) at d 0, but only fat was higher ($P < 0.01$) on d 88. Although bone, muscle, and fat as a % of CCW remained relatively the same ($P > 0.10$) for both breeds up to the 3rd SEP, ratio of fat increased in Boers ($P < 0.002$) and muscle ratio increased ($P < 0.01$) in Kikos by d 88. Breed or SEP did not affect the muscle/bone and muscle/fat ratios. Breed type and SEP had no effect on meat color. We concluded that Boer goats had higher ADG and attained higher BW at earlier age, with higher grain input. However, Kiko goats had more muscle and less fat at the later SEP (d 88) with less grain input.

Key Words: breed, goats, slaughter endpoint

T452 Effects of feeding varying levels of peanut skins on fatty acid profile of growing Kiko crossbred intact male goats. N. K. Gurung*[1], A. R. Stone[1], S. G. Solaiman[1], D. L. Rankins Jr.[2], K. R. Willian[1], and W. H. McElhenney[1], [1]*Tuskegee University*, *Tuskegee, AL*, [2]*Auburn University*, *Auburn, AL*.

The objectives of this experiment were to evaluate the effects of feeding different levels of peanut skins (PS) containing diets on fatty acid profile in the longissimus muscle (LM), the mesenteric adipose (MA) depot, and the s.c. adipose (SA) depot of meat goats. Twenty 4 Kiko crossbred intact male goats (18.2 ± 1.41 kg initial BW and 3 to 4 mo of age) were randomly assigned to one of the 4 experimental diets containing 47.3% bermudagrass hay plus 52.7% concentrate mix. Diets contained 0, 10, 20, and 30% of PS on as fed basis. Feed offered and refusals were collected daily. After 92 d, goats were harvested and carcass characteristics were measured. Samples of LM, MA and SA tissues were analyzed for fatty acid profile. Data on carcass quality and fatty acid composition of LM, MA and SA were analyzed as a completely randomized design. Dressing percent, chilled carcass weight and LM area decreased linearly ($P < 0.05$) with increasing level of PS. We were able to detect 18 fatty acids in LM and MS, and 13 in SA. No changes ($P > 0.10$) were detected in the fatty acid composition (on percentage basis) across treatments with the exception of C18:0, stearic acid, which increased linearly in LM ($P = 0.05$), MS ($P = 0.06$) and SC ($P = 0.06$) with increasing level of PS. Total saturated fatty acid percentage increased linearly ($P = 0.05$) in LM fat only. Total C18:1, oleic acid, decreased linearly ($P < 0.05$) in LM fat but a quadratic trend ($P < 0.05$) was observed for MA and SA. Monounsaturated fatty acids decreased linearly ($P < 0.05$) as the level of PS increased in LM fat but was not different among MS and SA fat samples. Polyunsaturated fatty acids were not different ($P > 0.05$) among treatments for all fat samples. It was concluded that the fatty acid composition of carcass can be altered with the addition of PS in the diets.

Key Words: goats, fatty acid profile, peanut skins

T453 Effect of cull-chickpeas on carcass characteristics and commercial cuts of feedlot hair sheep. F. G. Rios*[1,4], H. Bernal-Barragán[2,4], M. A. Cerrillo-Soto[3,4], A. Estrada-Angulo[1,4], E. Gutiérrez-Ornelas[2,4], A. S. Juárez-Reyes[3,4], J. F. Obregon[1,4], and J. J. Portillo-Loera[1,4], [1]*FMVZ-Universidad Autónoma de Sinaloa*, *Culiacán, Sinaloa, México*, [2]*FA-Universidad Autónoma de Nuevo León*, *Monterrey, Nuevo León, Mexico*, [3]*FMVZ-Universidad Juárez del Estado de Durango*, *Dur-*

ango, Durango, México, [4]*Red Internacional de Nutrición y Alimentación en Rumiantes*, *Culiacán, Sinaloa, México*.

A study was carried out to determine the effect of cull-chickpeas (CCH) on carcass characteristics and their commercial cuts from Katahdin × Pelibuey lambs. Forty animals (36.1 ± 2.9 kg initial BW) were fed 5 dietary treatments based on substitution of diet cracked corn grain and soybean meal for 0, 15, 30, 45, or 60% of CCH. Animals were allotted in pens (2/pen) and randomly grouped to 4 blocks of 10 animals. At the end of a feeding trial of 84 d, the lambs were humanly slaughtered at a weight of 50.3 ± 4.2 kg. The left half of the carcass was used for carcass evaluation and dissection according to commercial standards. The fat depth was measured at the level the 12th rib. Single cuts such as neck, rack, breast, shoulder, foreshank, loin, leg, and flank were also classified. Data were analyzed according to a completely randomized block design using the GLM procedure; means comparisons were performed using Duncan's test. Orthogonal polynomial contrasts were used to determine lineal effect of treatments. Hot carcass weight (29.1 ± 2.36 kg), dressing carcass (57.8 ± 2.58%), rib eye area (15.9 ± 2.21 cm^2), and backfat thickness (3.0 ± 1.15 mm) were similar ($P > 0.05$) among treatments. Empty body weight was higher ($P < 0.05$) in lambs receiving 30% of CCH (48.5 kg), and lowest in those fed 0% (46.4 kg). Kidney, pelvic and heart fat was modified by the effect of the treatments where a lineal pattern ($P < 0.01$) was observed. Yields of loin (8.5 ± 0.84%), shoulder (19.4 ± 1.94%), rack (11.4 ± 0.85%), and foreshank (11.4 ± 1.28%), were similar ($P > 0.05$) among treatments. Breast (7.9%) was similar between lambs receiving 15 and 45% CCH, and higher ($P < 0.05$) than the other treatments (7.3%). Leg (28.6%) was lower ($P < 0.05$) in lambs receiving 60% CCH. Flank (8.2%) was higher ($P < 0.05$) in lambs fed 45% CCH. It is concluded that CCH can be included up to 45% in the diet of hair lambs. Nonetheless, as the inclusion level of CCH is favored, enhanced fat deposition results, while leg yield is reduced.

Key Words: hair sheep, cull-chickpeas, carcass characteristics

T454 Effects of intraduodenally infused soybean small peptides and amino acids on absorption of peptides in the small intestine of dairy goats. L. Wang[1,2], S. Li*[1], Z. Cao[1], and H. Liu[1], [1]*China Agricultural University*, *Beijing, China*, [2]*Ningxia University*, *Yinchuan, China*.

The object of the study was to investigate the effects of intraduodenally infused soybean small peptides (SSP) and AA on absorption of peptides in the small intestine and the net fluxes of mesentetic-drained viscera (MDV) and portal-drained viscera (PDV). Four dairy goats (BW = 38.38 ± 3.09kg), fitted with permanent cannulas at the proximal duodenum and fitted with indwelling catheters in carotid artery, proximal and distal mesenteric vein and portal vein were used in a crossover treatment design. The treatments were intraduodenal infusion of 60 g/d SSP (SSP group) or AA (AA group) providing the same daily quantities of individual free AA as SSP group . The results showed that the mesenteric, portal venous and arterial plasma concentration of PAA in SSP group were higher than in the AA group, but only the concentration of peptide serine, valine, isoleucine and arginine were significant higher than in the AA group ($P < 0.05$). The MDV net fluxes of PAA in SSP group were significant higher than in the AA group ($P < 0.05$). The PDV net fluxes of PAA in the SSP group were higher than in the AA group, but there was no significant difference between the SSP group and the AA group ($P < 0.05$). The mesenteric, portal venous and arterial plasma concentrations and the MDV and PDV net fluxes of total FAA in AA group were significant higher than in the SSP group ($P < 0.05$). The concentration of plasma glucose, insulin, glucagon and growth hormone were higher in SSP group than in the AA group, the concentration of PUN and IGF-1 in SSP group were lower than in the AA group, however, there was no significant difference between SSP group and AA group ($P > 0.05$).

Key Words: small peptide, amino acid, dairy goat

T455 Effects of graded intraduodenal soybean small peptide infusion on absorption of small peptides in the small intestine of dairy goats. L. Wang[1,2], S. Li*[1], Z. Cao[1], and H. Liu[1], [1]*China Agricultural University*, *Beijing, China*, [2]*Ningxia University*, *Yinchuan, China*.

The objective of the study was to investigate the effects of graded intraduodenal soybean small peptide (SSP) infusion on absorption of small peptides in the small intestine and the net fluxes of mesentetic-drained viscera (MDV) and portal-drained viscera (PDV). Seven dairy goats (body weight 37.88 ± 3.03kg) were used to a 4 × 4 Latin square design, fitted with permanent cannulas at the proximal duodenum and implanted with indwelling catheters in carotid artery, proximal and distal mesenteric vein and portal vein. Four infused SSP levels, i.e., 0 g/d (0.9% normal saline, 700 mL/d), 60 g/d, 120 g/d and180 g/d, were used. Infusions were conducted continuously using a peristaltic pump. Each infusion period lasted for 12 d. On the last day, Para-aminohippuric acid (PAH) was infused into the mammary vein catheter. After 1 h of infusing PAH, blood samples were collected from the carotid artery and mammary vein at 1 h intervals into centrifuge tubes containing heparin-saline. The results showed that with the increase of SSP infusion level, the mesenteric, portal venous and arterial plasma concentration and the net fluxes of MDV, PDV of peptide amino acids (PAA) were all raised significantly. The total PAA net flux of MDV in group infused with 180 g/d was higher than that group infused with 60 g/d. The absorption rate of total PAA in small intestine was decreased with the increase of quantities of SSP infusion into duodenum, the values were 28.43%, 22.23% and 17.43% respectively. The PDV net fluxes of total FAA were all lower than the MDV net fluxes of total FAA in 4 groups. The concentrations of plasma urea nitrogen were significantly increased with increasing the quantities of SSP infusion, but the concentrations of plasma glucose, insulin, growth hormone, glucagon and IGF-1 had not been affected by infusing SSP.

Key Words: dairy goats, soybean small peptide

T456 Effects of shearing on energy use by growing Angora goats. R. Puchala*[1], A. Helal[1,2], A. L. Goetsch[1], and T. Sahlu[1], [1]*American Institute for Goat Research, Langston University*, *Langston, OK,* [2]*Animal and Poultry Nutrition Department, Desert Research Center, El Matareya, Cairo, Egypt.*

Eight Angora wethers (initial BW 19.0 ± 1.14 kg) and 8 doelings (initial BW 16.3 ± 1.15 kg), approximately 17 mo of age, were used to assess effects of shearing on energy expenditure (EE) and heart rate (HR). Animals were fed a pelleted diet at 1100 h to achieve 12.5 g/d tissue gain and 7.5 g/d mohair fiber growth. Animals were placed in an indirect, open-circuit respiration calorimetry system in 4-animal sets (2 wethers and 2 doelings) for gas exchange measurement 1 d before (d 0) and for 3 d after shearing (d 1, 2, 3). Temperature and relative humidity were controlled at 20°C and 50%, respectively. Shearing was at 0900 h. To avoid effects of feeding on HR and EE, data collected during the daytime (0800 to 1900 h) were omitted. Energy expenditure was greater ($P < 0.05$) after than before shearing (3.48, 4.30, 4.01, and 3.82 MJ/d on d 0, 1, 2, and 3, respectively; SEM = 0.142). Similarly, HR (92.6, 104.8 97.5, and 100.0 beats/min; SEM = 3.02) and EE relative to metabolic size (405, 503, 468, and 448 kJ/kg $BW^{0.75}$ on d 0, 1, 2, and 3, respectively; SEM = 10.8) were affected ($P < 0.05$) by shearing. The ratio of EE to HR was similar among days after shearing (4.45,

4.87, 4.87, and 4.52 kJ/kg body weight$^{0.75}$ per heart beat on d 0, 1, 2, and 3, respectively; SEM = 0.151). A decline ($P < 0.05$) in respiratory quotient after shearing (1.049, 1.034, 1.016, and 1.015 on d 0, 1, 2, and 3, respectively; SEM = 0.0079) suggests increased body fat catabolism. Regression analysis indicated that more than 4 d would be required for EE and HR to return to pre-shearing levels. In conclusion, even with non-stressful environmental conditions, shearing Angora goats increases energy consumption.

Key Words: goats, shearing, energy

T457 Optimum duration of performance testing growing Boer bucks for growth rate, feed intake, and feed efficiency. W. Hu*[1], T. A. Gipson[1], S. P. Hart[1], L. J. Dawson[1,2], A. L. Goetsch[1], and T. Sahlu[1], [1]*American Institute for Goat Research, Langston University*, *Langston, OK,* [2]*College of Veterinary Medicine, Oklahoma State University, Stillwater.*

Central performance testing of meat goats has increased in popularity recently, but minimum test length has not been ascertained. This study was conducted to determine the minimum length of time required for accurate evaluation of growing Boer bucks for ADG, DMI, and feed efficiency as assessed by ADG:DMI and residual feed intake. Data were collected from 425 bucks in Langston University tests from 2000 to 2009. Bucks averaged 111 ± 25 d of age and 27 ± 8 kg BW at the beginning of the test, consumed a pelletized 50% concentrate diet ad libitum, and were weighed weekly. Daily feed intake was determined with Calan feeding gates (American Calan, Inc., Northwood, NH) and automated feeding units (MK3 FIRE, Osborne Industries Inc., Osborne, KS). Weekly data of 4 performance traits were analyzed using the MIXED procedure of SAS with a repeated-measures model. The first-order ante dependence [ANTE(1)] structure type was selected as the appropriate covariance structure based on goodness-of-fit criteria. Residual variance relative to that at 84 d (%) was 338, 272, 223, 188, 153, 129, 119, and 108% for ADG, 167, 159, 149, 141, 130, 119, 112, and 106% for DMI, 427, 305, 223, 164, 135, 123, 112, and 105% for ADG:DMI, and 156, 138, 131, 118, 107, 103, 102, and 102% for residual feed intake at 28, 35, 42, 49, 56, 63, 70, and 77 d, respectively. Grafted polynomial break-points determined by nonlinear regression indicated that residual variance had stabilized at 63, 63, and 57 d for ADG, ADG:feed intake, and residual feed intake, respectively. A break-point for DMI was not estimable, although the correlation between DMI at 63 and 84 d was 0.99 ($P < 0.01$) compared with r of 0.95, 0.96, and 0.97 ($P < 0.01$) for ADG, ADG:DMI, and residual feed intake, respectively. In conclusion, under these conditions the duration of Boer buck performance tests could be decreased from 84 to 63 d with little loss in accuracy.

Key Words: goats, performance testing

T458 Feeding behavior of intact yearling hair sheep and meat goat males pen-fed in single- and mixed-species groups. S. Wildeus* and R. A. Stein, *Virginia State University*, *Petersburg*.

Group size and social hierarchy influence animal performance, and here we evaluated interactions of yearling rams and bucks housed indoors in 3 × 2.5 m pens with a single feeding station. Animals were fed chopped grass hay mixed with corn and soybean (~14% CP). In Exp. 1, 2 males were allocated to 15 pens either as single- or mixed-species groups (5 replications/grouping; 15 rams and 15 bucks total). In Exp. 2, 2 or 4 males were assigned to 16 pens, either as sheep-only, or an equal number of rams and bucks (4 replications/grouping; 36 rams and 12 bucks total). In both experiments animals were fed for 17 d. Immediately after feed was placed into each pen, behavior was recorded for 10 min (position changes at feeder, duration of first meal, and incidence of fighting). Observations were made for 3 consecutive days at the beginning, middle and end of each experiment. Data were analyzed for the effect of pen composition and time of trial in Exp. 1, and pen composition, stocking rate and time of trial in Exp. 2. In Exp. 1 initial time at the feeding station was shorter ($P < 0.01$), and number of fights and position changes at feeder more frequent ($P < 0.01$) in sheep-only pens (142 ± 32 s, 6.0 ± 0.8 and 14.3 ± 2.4, respectively) than goat-only (381 ± 41 s, 0.3 ± 0.09 and 1.8 ± 0.1, respectively) and mixed pens (380 ± 41 s, 0.1 ± 0.04 and 2.0 ± 0.2, respectively). Number of fights and position changes increased ($P < 0.01$) from the start to the end of the trial in sheep-only pens (6.6 to 23.1 and 3.6 to 6.1, respectively), but not in goat-only and mixed pens. In mixed pens, goats initiated feeding more frequently than sheep (81.8 vs. 18.2%, $P < 0.01$). In Exp. 2 observations on feeding time, fighting and position changes for sheep-only and mixed pens were similar to Exp. 1. However, fighting and position changes increased in sheep-only, but not mixed pens as stocking rate increased from 2 to 4 animals (stocking rate by pen composition interaction: $P < 0.05$). Data suggest that bucks were more dominant than rams, activity levels were lower in pens with bucks, and that increasing stocking rate differentially affected behavior in the 2 species.

Key Words: behavior, goats, sheep

T459 Feeding glucogenic precursors to dairy goats carrying twins around kidding. S. Cavini[1], M. Rodriguez-Prado[1], S. Calsamiglia*[1], A. Foskolos[1], and M. A. Gomez[2], [1]*Universitat Autonoma de Barcelona*, *Bellaterra, Spain*, [2]*NUTEGA*, *Madrid, Spain*.

Ketosis is the result of an unbalance between energy supply and requirements. Dairy goats carrying twins are highly susceptible to gestational ketosis. Monopropylene glycol is a glucogenic precursor that has been successfully used to prevent ketosis. The objective of this study was to compare monopropylene glycol with other glucose precursors to prevent ketosis. Twenty-two pregnant Murciano-Granadina goats carrying twins were assigned to 4 different treatments in a randomized complete block design, where group was the experimental unit: monopropylene glycol (MG: 36.9 g/goat/d, 65% purity) considered as positive control; glycerol (GLY: 60.0 g/goat/d, 40% purity); monopropylene glycol plus B vitamins (MGB: 44.3 g/goat/d, 54% purity); glycerol plus monopropylene glycol plus B vitamins plus oligoelements (GMGB: 56.4 g/goat/d, 33 and 9.5% purity, respectively). Goats were controlled from 25 before 30 d after kidding. Goats were group fed, were received an ad libitum forage diet and were individually supplemented with 400 and 800 g of concentrate before and after kidding, respectively. Intake was recorded daily, milk production and composition determined weekly, body weight and condition score were recorded −15, 0, 15 and 30 d around kidding, and blood samples were taken on days −15, −7, −3, −1, 0, 1, 3, 5, 7, 15 and 30 around kidding to measure insulin, glucose, non-esterified fatty acids, triglycerides and β-hydroxybutyrate. Results were analyzed using the PROC MIXED procedure of SAS and differences declared at $P < 0.05$. No differences were found in body weigh and condition score. Intake of DM increased ($P < 0.04$) in GLY compared with MG (1.36 vs. 1.43 ± 0.02 kg/d) with no effects on milk production (1.93 ± 0.18 L/d). Milk fat and protein tended ($P < 0.10$) to be higher in GLY (5.69 vs. 4.83 ± 0.24% and 4.15 vs. 3.55 ± 0.16%, respectively) compared with MG. There were no differences in blood metabolites among treatments. Glycerol may be a good alternative to propylene glycol in dairy goats around kidding.

Key Words: glycerol, glycol, goats

T460 Evaluation of milk serum amyloid A 3 (M–SAA3) protein as a potential mammary health indicator in goats. A. Domènech*[1], A. Gómez–Martín[2], C. De la Fe[2], J. C. Corrales[2], and A. Serrano[1], [1]*Ruminant Production, IRTA*, *Barcelona, Spain*, [2]*Department of Animal Health, University of Murcia*, *Murcia, Spain*.

The objective of this study was to investigate the potential of M–SAA3 protein as a mammary health indicator in caprine milk. For this purpose, a preliminary study of quantification of SAA3 in half milk samples from healthy (n = 26) and clinical mastitic (n = 28) Murciano-Granadina goats was conducted. Clinical mastitis milk samples were characterized in accordance with bacterial isolation in blood and McConkey agar, Gram staining and catalase and oxidase tests. Gram + and catalase + samples were further characterized with a *Staphylococcus aureus* agglutination test. Milk samples from healthy goats were verified by negative bacterial culture and somatic cell count. Results from bacterial identification in mastitic milk samples reported 75% of Gram + infections (90.5% *Staphylococcus* spp. and 9.5% *Streptococcus* spp.). 71.5% of the Gram – milk infected samples were oxidase + (no enterobacteriae) and *Escherichia coli* was identified in the rest of them (28.5%). Milk levels of SAA3 were measured using a commercial ELISA kit (Mast ID SAA3 kit, Tridelta, Ireland). Milk levels of SAA3 from healthy and mastitic goats were log-transformed and compared using an ANOVA. Results indicated no significant differences ($P = 0.22$) in milk SAA3 levels in samples obtained from mastitic (35.05 ± 0.30μg/mL) or healthy goats (20.36 ± 0.32μg/mL). However, the CV of SAA3 milk contents was numerically greater in mastitic milk (59%) than in milk from healthy goats (26%). Results indicate that M–SAA3 might not be an accurate indicator of clinical mastitis in goat milk but do not exclude the potential of exploring M-SAA3 levels in samples of caprine subclinical mastitis. Further studies with a greater number of samples are being conducted.

Key Words: SAA3, caprine, mastitis

T461 Milk fat synthesis is progressively reduced in dairy goats fed increasing levels of an unprotected conjugated linoleic acid (U-CLA) supplement. D. Fernandes[1], J. Souza[1], M. Baldin[1], R. Dresch[1], E. C. Sandri[1], J. H. Bruschi[2], F. C. F. Lopes[2], M. A. S. Gama[2], and D. E. Oliveira*[1], [1]*Santa Catarina State University*, *Chapecó, Brazil*, [2]*National Dairy Cattle Research Center*, *Juiz de Fora, Minas Gerais, Brazil*.

This objective was to evaluate the dose-response effect of dietary U-CLA on milk fat synthesis in dairy goats. Eight Toggenburg goats (4 primiparous and 4 multiparous; 120 to 150 DIM) received 4 levels of U-CLA in a 4 × 4 Latin square (LS) design. The treatments were: 1) Control: 45 g/d of calcium salts of soybean oil (CSSO); 2) CLA15: 30 g/d of CSSO plus 15 g/d of U-CLA; 3) CLA30: 15 g/d of CSSO plus 30 g/d of U-CLA and 4) CLA45: 45 g/d of U-CLA. Each experimental period lasted 12 d, separated by 6 d washout intervals. The U-CLA contained 29% of trans-10 cis-12 CLA; therefore, it was delivered about 0, 4.5, 9.0 and 13.5 g/d of trans-10 cis-12 CLA for control, CLA15, CLA30 and CLA45, respectively. Lipid supplements were mixed into the concentrate (1.0 kg/goat/d) and fed twice a day after milking. Corn silage was fed ad libitum and orts were recorded daily to calculate forage intake. Milk production was recorded daily and milk samples were collected in the last 3 d of each period (d 10, 11 and 12). Body condition score was recorded on the 1st and 12th day of each period. Data were subjected to ANOVA and the statistical model included animal, period, LS, animal within LS, treatment and interaction LS x treatment as sources of variation. There was no interaction LS x treatment for any variable, showing that responses to U-CLA doses did not differ between primiparous and multiparous. Milk fat content and yield were linearly reduced ($P < 0.0001$) in response to increased U-CLA dose (2.90, 2.40, 1.94 and 1.72%; SE = 0.08 and 67.8, 57.7, 46.9 and 40.3 g/d; SE = 2.72, respectively). However, the increase in U-CLA dose had no effect on milk yield (2.32, 2.37, 2.41 and 2.35 kg/d; SE = 0.08), milk protein content (2.76, 2.78, 2.75 and 2.79%; SE = 0.03), milk protein yield (63.7, 65.5, 65.5 and 65.5 g/d; SE = 1.95), forage intake (2.21, 2.25, 2.15 and 2.19, SE = 0.09) and BCS (2.75, 2.75, 2.72, 2.78; SE = 0.07).

Key Words: goat, conjugated linoleic acid, milk

T462 Requirements of magnesium, potassium and sodium for maintenance and growth of Boer crossbred kids. M. H. M. R. Fernandes[1], K. T. Resende[1], L. O. Tedeschi[2], J. S. Fernandes Jr.[1], and I. A. M. A. Teixeira*[1], [1]*Universidade Estadual Paulista/UNESP and INCT-CA members*, *Jaboticabal, SP 14870, Brazil*, [2]*Texas A&M University*, *College Station*

The requirements of magnesium (Mg), potassium (K) and sodium (Na) of goats have been assumed to be identical to those for cattle and sheep (3.5, 50, 15 mg/kg of BW, respectively). The objective of this study was to determine the requirements of Mg, K, and Na for maintenance and growth of 34 intact male crossbred kids (3/4Boer 1/4Saanen), varying BW from 20 to 35 kg. The comparative slaughter technique with 3 slaughter periods was used to determine the mineral requirements. A baseline (BL) group was comprised of 7 randomly selected kids, averaging 20 kg BW. The intermediate slaughter group was fed ad libitum and consisted of 6 randomly selected kids that were slaughtered when they reached 27.5 kg BW. The remaining kids (n = 21) were allocated randomly on d 0 to 3 levels of DMI (treatments were ad libitum or restricted to 70 or 40% of the ad libitum intake) within 7 slaughter groups. A slaughter group contained 1 kid from each treatment, and kids were slaughtered when the kid fed ad libitum reached 35 kg BW. Body components were weighed, ground, mixed, and subsampled for chemical analysis. Initial body composition was determined using equations developed from the composition of the BL kids. The diet DM consisted of 47% corn hay and 53% concentrate (0.95% Ca, 0.52% P, 0.19% Mg, 0.62% K, 0.22% Na). A digestion trial with 15 kids at 3 levels of intake was concurrently conducted to determine the apparent absorption coefficient and endogenous fecal and urinary losses. During the trial, all kids (n = 34) were fed once daily (0800) in individual pens with free access to water. The requirements of Mg, K, and Na for maintenance were 7.8 ± 7.0 mg/kg BW, 39.7 ± 0.38 mg/kg BW and 10.4 ± 0.35 mg/kg BW, respectively. The net Mg, K and Na requirements for growth ranged from 0.29 to 0.31 g/kg empty weight gain (EWG), 1.18 to 1.05 g/kg EWG and 0.67 to 0.62 g/kg EWG for 20 and 35 kg BW, respectively. These results indicated that Mg, K, and Na requirements for Boer crossbred, a meat type breed, are less than those recommended for cattle and sheep. Further studies are required to confirm these findings for growing goats.

Key Words: Boer, minerals, net requirement

T463 Calcium and phosphorous requirements for maintenance and growth of Boer crossbred kids. M. H. M. R. Fernandes[1], K. T. Resende[1], L. O. Tedeschi[2], J. S. Fernandes Jr.[1], and I. A. M. A. Teixeira*[1], [1]*Universidade Estadual Paulista/UNESP and INCT-CA members*, *Jaboticabal, SP 14870, Brazil*, [2]*Texas A&M University*, *College Station*.

Calcium (Ca) and phosphorous (P) play an important role in several metabolic functions. The net requirements of Ca and P for goat dairy breeds are 2 and 1.4 g/d (BW of 30 kg). The objective of this study was to determine Ca and P requirements for maintenance and growth of 34 intact male crossbred kids (3/4Boer 1/4Saanen) varying BW from 20

to 35 kg. The comparative slaughter technique with 3 slaughter periods was used to determine the mineral requirements. A baseline (BL) group was comprised of 7 randomly selected kids, averaging 20 kg BW. The intermediate slaughter group was fed ad libitum and consisted of 6 randomly selected kids that were slaughtered when they reached 27.5 kg BW. The remaining kids (n = 21) were allocated randomly on d 0 to 3 levels of DMI (treatments were ad libitum or restricted to 70 or 40% of the ad libitum intake). These kids were pair-fed in 7 slaughter groups. A slaughter group contained 1 kid from each treatment, and kids were slaughtered when the ad libitum treatment kid reached 35 kg BW. Body components were weighed, ground, mixed, and subsampled for chemical analysis. Initial body composition was determined using equations developed from the composition of the BL kids. The diet DM consisted of 47% corn hay and 53% concentrate (0.95% Ca, 0.52% P). A completely randomized design digestion trial was conducted in parallel with the comparative slaughter trial and used 15 kids at 3 levels of intake to determine apparent absorption coefficient and endogenous fecal and urinary losses. During the trial, all kids (n = 34) were fed once daily (0800) in individual pens with free access to water located in a masonry shed and protected from rain and wind. The Ca and P requirements for maintenance were 16.1 ± 29.1 mg/kg BW and 31.6 ± 14.3 mg/kg BW, respectively. The net Ca and P requirements for growth ranged from 6.7 to 7.0 g/kg empty weight gain (EWG) and 5.3 to 5.4 g/kg EWG for 20 and 35 kg BW, respectively. These findings suggested that net Ca and P requirements for growth of Boer crossbred, a meat type breed, might be lower than those requirements published for dairy goats.

Key Words: Boer, minerals, net requirement

T464 Blood mineral concentration of adult goats in a subtropical region of southern Mexico during the rainy and dry season. R. Rojo*, A. Z. M. Salem, F. Jiménez, S. Rebollar, J. L. Tinoco, B. Albarrán, J. F. Vázquez, D. Cardoso, J. Hernández, and F. González, *Centro Universitario UAEM-Temascaltepec*, *Temascaltepec, Estado de México, México*.

The aim of work was to evaluate the effects of season (rainy: RS; and dry: DS) and sample location of 3 different places (Rio Topilar: RT; El Devanador: ED; y San Pedro Limon: SPL) at the province of Tlatlaya in Mexico State on mineral status of blood plasma in crossbred adult goats (LW 35 ± 1.5 kg) during transition period under the semiarid rangeland of southern Mexico. Representative samples of 7 adult Creole goats were taken from each production unit (7 animals × 3 production unit) within each season (dry and rainy). Mineral concentrations (Ca, P, K, Mg, Na, Zn and Cu) in plasma were assayed using the Atomic absorption. Data were analyzed using one way ANOVA test; significant differences between means were tested by Tukey. Higher Ca and P concentrations were observed during the DS than RS ($P < 0.01$), with a lowest value in SPL during the DS. No significant differences ($P > 0.05$) were observed between seasons or production units in concentration of Mg, while Na concentration was affected by the production unit (P 0.05), and the highest values were during the DS. Lowest Zn concentration was observed during the DS in SPL (0.18 mg/dL), while Cu concentration was significantly ($P < 0.01$) increased during the same season than in RS (0.07 to 0.10 mg/dL, respectively). Generally, the concentration of K, Zn and P in goat plasma was above the recommended levels by NRC (2007), while the concentration of Ca, Mg, Na and Cu were below. Adult Creole goats during transition period under the semiarid rangeland of southern Mexico had a deficiency in some blood minerals such as K, Zn and P, and this maybe due to their native grazing behavior on browse shrubs and 3 foliages in the province of Tlatlaya in México State.

Key Words: adult goats, blood serum, mineral concentration

T465 Effect of copper and zinc on in vitro ruminal fermentation of total mixed ration in goats. J. F. Vazquez[1], R. Rojo*[1], D. Lopez[1], A. Z. M. Salem[1], J. M. Gonzalez[2], D. Colín[1], and J. L. Tinoco[1], [1]*Centro Universitario UAEM-Temascaltepec*, *Temascaltepec, Estado de México, Mexico*, [2]*Facultad de Agrobiología, Universidad Auténoma de Tlaxcala*, *Ixtacuixtla, Tlaxcala, México*.

One in vitro experiment was conducted with the objective of evaluate the effect of copper and zinc addition on some parameters of ruminal fermentation of total mixed ration (TMR) (14% CP, 25.6% NDF and 18.3% ADF) using ruminal inoculum of goats. The TMR was incubated during 96 h with 4 different supplementary treatments: Control, Cu (860 ppm), Zn (224 ppm), Cu-Zn (860–224 ppm) provided as mineral premixed at 3 per cent of TMR. One g of TMR with each treatment was incubated in serum botles with 90 mL nutritive solution and 10 mL ruminal fluid from goats. In vitro gas production (ml g^{-1} DM) after 24 (GP_{24}), 48 (GP_{48}) and 96 h (GP_{96}) of incubation, dry matter degradability (IVDMD: g/kg DM) were determined while *b* (asymptotic gas production (ml g^{-1} DM)), *k* (rate of gas production (/h)), lag phase (lag) and metabolizable energy (ME: MJ kg^{-1} DM) were estimated. Data were analyzed using the general lineal model (GLM) procedure in SAS in a complete random design and differences among means by Tukey test. Addition of Zn increased fraction B, but addition of Zn-Cu decreased this fraction. Treatments did not affect the fraction lag and IVDMD. Cu addition tended to increase the volume of GP at 24, 48 and 96 h of incubation. Cu treatment had the highest value for the fraction K and ME, while Zn appeared to have the lowest values. Addition of Cu in the diet improved gas production volume and fermentation efficiency in goats.

Table 1. In vitro ruminal fermentation parameters of total mixed ration with four different supplemental treatments

Parameters	Control	Zn	Cu	Zn-Cu	SEM	P <
b	273.5^{bc}	334.9^{a}	288.8^{b}	241.6^{c}	10.7l	0.01
k	0.014^{c}	0.008^{d}	0.037^{a}	0.019^{b}	0.00	0.01
lag	0.87^{a}	1.32^{a}	1.78^{a}	0.68^{a}	0.19	0.15
GP						
24	69.3^{c}	58.5^{c}	169.3^{a}	90.7^{b}	13.2	0.01
48	140.6^{bc}	114.0^{c}	237.0^{a}	153.2^{b}	14.1	0.01
96	202.6^{b}	182.9^{b}	291.0^{a}	210.0^{b}	12.8	0.01
IVDMD	724.3^{a}	714.1^{a}	707.0^{a}	703.3^{a}	4.09	0.30
ME.	15.1^{c}.	14.4^{c}.	21.9^{a}.	16.5^{b}.	0.90.	0.01.

Means in the same row with different superscripts differ (P<0.05).

Key Words: copper, goats, ruminal fermentation, zinc

T466 Nutritional supplementation does not improve the sexual response of goats managed in northern Mexico. F. G. Véliz*[1], C. A. Meza-Herrera[2], M. A. De Santiago-Miramontes[1], R. Rodríguez-Martínez[1], and M. Mellado[3], [1]*Universidad Autónoma Agraria Antonio Narro*, *Torreón, Coahuila, Mexico*, [2]*Universidad Autónoma Chapingo, Unidad Regional Universitaria de Zonas Áridas*, *Bermejillo, Durango, México*, [3]*Universidad Autónoma Agraria Antonio Narro*, *Buenavista, Saltillo, Coahuila*.

The objective was to determine if nutritional supplementation of native goats under an extensive management system in northern Mexico improves pregnancy rate in goats. Native multiparous goats (n = 79), were divided in 2 homogenous groups with respect to BW and body

condition. Both experimental groups grazed (11:00 to 17:00 h) rangeland and crop residues fields. Five days before and 20 d after breeding, the supplemented group (SS, n = 37) received a supplemental ration to provide 75% of its energy and protein maintenance requirements. The control group (CC; n = 24) received no supplementation during the experimental period. In March 20th, experimental groups were exposed to 4 male bucks, which were induced to an intense sexual activity by means of a photoperiodic treatment of 2.5 mo. Data were analyzed by means of Chi-squared test. More than 90% of goats in both experimental groups showed sexual behavior during the experimental period. In fact, during the first 6 d, 91% (38/42) of the CC-group exhibited estrual activity, while the SS-group exhibited corresponding values of 95% (35/37). The observed pregnancy and ovulatory rates were 1.26 and 64% and 1.15 and 75% in the CC and SS groups, respectively. Our results suggest that native multiparous goats under extensive-range production systems in Northern Mexico, receiving or not nutritional supplementation before or after breeding season, had similar productive and reproductive outcomes.

Key Words: nutritional supplementation, goat reproduction, male effect

T467 Seasonal reproductive activity of Nubian, Alpine and Criollo female goats exposed to natural photoperiod in a semiarid region of central-north Mexico. M. T. Rivera[1], M. O. Diaz-Gomez[1], M. Rincon[1], F. J. Escobar[1], C. F. Arechiga[2], H. G. Gamez[3], J. Urrutia*[3], and H. Vera-Avila[3], [1]*Universidad Autonoma de Zacatecas*, *Zacatecas, Mexico*, [2]*Universidad Autonoma de San Luis Potosi*, *San Luis Potosi, Mexico*, [3]*Instituto Nacional de Investigaciones Forestales, Agricolas y Pecuarias*, *San Luis Potosi, Mexico.*

Female goats in a temperate climate have showed a seasonal reproduction influenced by photoperiod and great differences have been observed among breeds: Alpine goats have showed a much shorter reproductive season than Nubian goats. It is not clear whether this behavior will persist under tropical conditions, where photoperiod variations are less accentuated. In this study, variation of reproductive activity of Nubian, Alpine and Criollo goats was examined in the semiarid region of central-north Mexico (San Luis Potosi State; 22° N latitude). The study was conducted at the UASLP-Goat Unit under natural photoperiod and temperate conditions during a whole year (from April to April). Female goats, Alpine, Nubian and Criollo (n = 8 of each breed), were included in the study and exposed to presence of 2 Alpine bucks kept in a separate barn, but close enough to detect their visual, olfactory and audible signals. Progesterone concentrations indicate that all goats showed a great variation in reproductive activity throughout the year, showing ovulatory cycles between September and February. Nubian goats showed a shorter breeding season (113.8 d), than Alpine (132.1 d) and Criollo goats (138.5 d; (P = 0.12). A slight variation on live body weight ($P > 0.05$) throughout the study allowed to assume that BW did not affect reproductive activity. Results indicate that Nubian, Alpine and Criollo goats kept at 22° N present a wide seasonal variation in ovulatory activity, which was not influenced by breed, despite the fact that these breeds have shown great differences in length of their reproductive season at higher latitudes. Alpine goats showed a higher number of ovulatory cycles than Criollo and Nubian goats (51 vs. 45 vs. 40; respectively). Induction of long ovulatory cycles (≥26 d) was greater for Criollo goats than Nubian or Alpine goats (25.5 vs. 10 vs. 2%; respectively). These results demonstrate that the main influence that photoperiod exerts on seasonal reproductive activity of female goats persist under tropical photoperiodic conditions.

Key Words: goats, seasonal reproduction, photoperiod

T468 Conditions to test electric fence modifications of cattle barb wire fence for goat containment. A. L. Goetsch*, G. D. Detweiler, R. Puchala, T. Sahlu, and T. A. Gipson, *American Institute for Goat Research, Langston University*, *Langston, OK*.

Two 6 × 6 Latin squares, each with 24 yearling meat goat doelings previously exposed to electric fence, were conducted to identify appropriate conditions to test electric fence modifications of cattle barb wire fence for goat containment. After overnight fasting, groups of 4 doelings were placed in 2.4 × 2.4 m pens without forage. Pens had 3 metal panel sides and 1 side with 5 strands of barb wire 31, 56, 81, 107, and 132 cm from the ground adjacent to a pasture with forage and browse. Intervals between the 6 periods of 2–3 d and 1 wk were assigned to the 2 squares. The 6 treatments in each square were 4 strands 15, 28, 43, and 58 cm from the ground at low voltage of 4–4.5 kV (4S-LV); 2 strands at 15 and 43 cm and high voltage of 8.5–9 kV (2S-HV); 2 strands at 15.2 and 43.2 cm and low voltage (2S-LV); 1 strand at low height of 15 cm and low voltage (1S-LH-LV); 1 strand at 43 cm and low voltage (1S-HH-LV); and 1 strand at 23 cm and high voltage (1S-MH-HV). Means were separated by least significant difference with a protected F-test. The percentage of doelings exiting after 2 (during continuous visual observation) and 6 h was similar between intervals (6.3 and 4.2% at 2 h (SE = 2.49) and 9.7 and 6.3% at 6 h (SE = 2.33)) for long and short intervals, respectively). Doelings receiving a first shock in 2 h did not differ between intervals (16.7 and 19.4% for long and short intervals, respectively; SE = 3.20). The percentage of doelings exiting at 2 and 6 h was not affected by fencing treatment ($P > 0.05$). Period of the squares affected ($P < 0.05$) the percentage of doelings shocked in 2 h (62.5, 29.2, 6.3, 6.3, 0, and 4.2%; SE = 4.92) and exiting pens after 2 (20.8, 8.3, 2.1, 0, 0, and 0%; SE = 3.24) and 6 h (27.1, 10.4, 6.3, 4.2, 0, and 0% for 4S-LV, 2S-HV, 2S-LV, 1S-LH-LV, 1S-HH-LV, and 1S-MH-HV, respectively; SE = 3.44). Low pen exit, particularly in latter periods, suggests desirability of more thorough prior training to electric fence. Memory of previous exposure to electric fence appeared substantial, implying need to evaluate longer intervals. The overnight fasting period may not have created an adequate impetus to test electric fence for pen exit.

Key Words: goats, fence, pasture containment

T469 Accuracy of calculated distances between consecutive fixes of GPS collars worn by goats. T. A. Gipson*, G. D. Detweiler, and A. L. Goetsch, *American Institute for Goat Research, Langston University*, *Langston, OK*.

Small ruminants have been fitted with GPS collars to estimate distance traveled in grazing studies; however, accuracy has not been assessed. To do so, a mobile stand was developed to hold 21 Lotek 3300 GPS collars (Lotek Wireless, Newmarket, Ontario, Canada) and was moved a prescribed distance between fixes on 4 azimuthally different courses (NE at 45°, S at 180°, W at 270°, and NW at 315°). Fixes were scheduled at 5-min intervals. Distances traveled on a course were 0, 10, 20, 30, 40, 50, 60, 70, 80, 90, and 100 m. Distances were replicated 3 times for each course and the order of the distances was randomized within each replicate. Two courses were run per day and each course was paired with every other course, for a total of 6 different dates. Fixes were downloaded and distances between fixes were calculated using spherical geometry. The BIAS was estimated as distance calculated from collars minus true distance and was analyzed using a repeated measures design (PROC MIXED; SAS). Dependent fixed effects included true distance (0 to 100 m), course (NE, NW, S, W), and the 2-way interactions. Collars and dates were considered random effects. There was no effect ($P > 0.10$) of course on BIAS. For true distance, BIAS was greatest for 0 m (7.6 m ± 0.36) and least for 60 m (0.5 m). Other estimates of BIAS were

intermediate at 10 (2.9 m), 20 (1.6 m), 30 (0.9 m), 40 (1.7 m), 50 (1.4 m), 70 (0.6 m), 80 (0.8 m), 90 (1.2 m), and 100 m (1.3 m). There were linear and quadratic ($P < 0.01$) effects on BIAS when all distances were analyzed. However, if 0 and 10 m distances were eliminated, the linear effect disappeared ($P > 0.10$) but the quadratic remained ($P < 0.05$). The ability of GPS collars to differentiate between when an animal is stationary or moving only a short distance between fixes appears very limited; however, if an animal is moving more than 20 m between GPS fixes, collar estimates are within 1.6 m of actual distance traveled.

Key Words: goats, GPS, distance

T470 Use of biometric measurements to estimate fetal mass in dairy goats. C. J. Härter*, I. A. M. Teixeira, L. D. Lima, H. G. O. Silva, A. R. Rivera, and K. T. Resende, *Universidade Estadual Paulista*, *Jaboticabal, SP, Brasil*.

An understanding of fetal mass is important to check for normal fetal growth. Moreover, it can be helpful for estimating nutritional requirements of pregnant females. The aim of this study was to estimate fetal mass based on biometric measurements. Data were obtained from 39 dairy female goats with an average BW = 50.59 ± 7.71, and body condition scored as 2.58 ± 0.59. After the pregnancy confirmation, female goats were distributed to treatments according to a 2 × 2 × 3 factorial design as follows: 2 breeds (Oberhasli and Saanen), 2 types of pregnancy (single and twin) and 3 gestational ages (80, 110 and 140 d). Multiple linear regression was used to analyze the data using SAS PROC MIXED. At pre-established pregnancy ages goats were slaughtered and the mammary gland and reproductive tract were removed and separated from the cervix, and the uterus, fetus, placenta, and placental fluid were dissected. After fetal removal, weights, body length in centimeters (BL), height at withers, height at rump, chest width, rump width, rump length, hearth girth (HG) and abdominal girth were recorded for fetuses. The slaughter procedures followed the recommendations of the ethics committee for animal experimentation. The biometric measurements highly correlated with fetal mass ($P < 0.001$) which allowed the creation of predictive equations for fetal mass. The best equations were generated using body length ($Y = -549.4 \pm 520.4 + 22.14 \pm 50.25\ BL + 3.296 \pm 1.12\ BL^2$ ($R^2 = 0.89$); and hearth girth ($Y = 103.0 \pm 305.2 - 54.18 \pm 30.31\ HG + 5.175 \pm 0.696\ HG^2$ ($R^2 = 0.94$), whereas Y = fetal mass (g). Fetal mass can be precisely estimated based on fetus biometry showing an interesting perspective of pregnancy management as biometric measurements can be further determined using ultrasound, similar to what has been demonstrated in humans.
Fapesp (2009/10125–0).

Key Words: biometry, fetal weight

T471 The relationship of real-time ultrasound body composition measurements, body weight and hip height with body condition score in mature Boer crossbred does. A. M. Duff*, J. A. Carter, C. A. Hughes, K. N. Gates, C. S. Ellason, W. S. Stewart, and F. R. B. Ribeiro, *Texas A&M University-Commerce*, *Commerce*.

The purpose of this study was to determine the relationship between real-time ultrasound (RTU) measurements of body composition, BW, and hip height (HH), with body condition score (BCS) in mature Boer crossbred does (n = 27). BCS was assessed visually using a 1 to 5 scale. The body composition traits measured by RTU were 12–13th rib *longissimus lumborum* muscle area (uLMA, mean = 9.08 cm^2), 12–13th rib fat thickness (uBF, mean = 0.27 cm), and ultrasound rump fat thickness (uRUMP, mean = 0.24 cm). Ultrasound measurements were taken using an Aloka 500 with a 12 cm 3.5 MHz transducer, and each animal′s hair was clipped to no longer than 0.64 cm, and vegetable oil was used as a coupling agent to enhance image quality. Data were analyzed using the Proc CORR and Proc REG procedures of SAS. BW was correlated ($P < 0.05$) to HH, uBF, uLMA and uRUMP (0.55, 0.44, 0.67, and 0.58, respectively). BCS was correlated ($P < 0.05$) to uBF, uLMA and uRUMP (0.83, 0.77, and 0.92, respectively), and HH was not correlated ($P > 0.05$) to any of the RTU traits measured. Linear regression to predict BCS was developed using a stepwise selection. The first variable to enter the model was uRUMP which accounted for 84% of the variation and HH entered next in the model, accounting for an additional 6% of the variation, with the full model accounting for 90% of the variation in BCS. Body condition scoring done before breeding is very important to ensure that animals have enough body reserves to go through gestation and lactation. Since uBF was not a good predictor of BCS evaluators should give more emphasis in palpation of the rump area rather than the back of the animal when evaluating goats for BCS in order for a better assessment of total body fat reserves. Results of this study suggest that BCS can be accurately predicted from uRUMP and HH.

Key Words: ultrasound, body composition, goat

T472 Relationship between participation in youth equine organizations and collegiate equine activities. M. Nicodemus*, *Mississippi State University*, *Mississippi State*.

Despite current economic uncertainties, youth equine organizations are flourishing. While University budgets cuts threaten elimination of equine programs due to relatively low enrollment, a potential rise in enrollment would justify program continuation. To determine whether a background in youth equine activities influences participation in collegiate equine activities, students enrolled in equine courses (n = 95) at Mississippi State University were asked to fill out a researcher-developed, 10-item survey instrument with questions focusing on youth and collegiate activities. Effect of youth equine activities on percentage of those students involved in equine collegiate activities was tested using a one-way ANOVA ($P < 0.05$). Less than half (30%) of surveyed students had participated in youth equine organizations with 4-H (40%) ranking the highest for those individuals. The majority (82%) of those with a youth background planned on a career in the equine industry with only 58% for those with no background. As for equine extra-curricular activities, 36% of those with a youth background were active compared with only 13% of those with no background. The majority (89%) of those with a youth background planned on taking another equine course with the other 11% unable to take another course due to graduation, while 39% of those with no youth background were not planning to take another equine course with the majority of those students (22%) not graduating. Even though those with a youth background had a strong equine handling foundation before college, 79% had taken or were currently taking a course with a hands-on laboratory. Overall, a youth equine background was found to influence the involvement in collegiate equine activities as although these students were the minority their involvement in collegiate equine activities (riding teams, judging teams, clubs, hands-on riding laboratory courses, hands-on non-riding courses, non-hands-on laboratory courses, and enrollment in multiple equine courses) was greater than those without ($P < 0.05$) suggesting the growth currently seen in youth equine organizations will result in a growth of students active in future collegiate equine activities.

Key Words: youth equine organizations, collegiate equine activities

T473 Free web applications for educational purposes. P. A. Curtis* and M. O. Kloepper, *Auburn University*, *Auburn, AL*.

Using free web applications costs you—nothing! This session will focus on free applications that the presenters use in face-to-face and distance education classes, encourage you to invest a little bit of time to learn about them and discover how they might be used for your educational purposes. Only free applications will be showcased. Discussion will be encouraged among attendees to suggest and share novel ways the various applications might be used.

T474 Applications of functional anatomy in farm animals using collaborative learning. H. G. Kattesh*, M. H. Sims, R. B. Reed, and F. M. Hopkins, *University of Tennessee*, *Knoxville*.

A multimedia program dedicated to the teaching of fundamental principles of functional anatomy in farm animals using a problem-oriented approach was produced and developed for web course distribution in promoting collaboration among students and faculty at other colleges and universities. Students are presented a series of lessons containing text, graphics, animation, and audio and video that involve the anatomy and physiology of the respiratory system in farm animals. Mastery level of the lessons is assessed using 20 randomly selected multiple-choice questions from the 10 lesson chapters. Three case studies of respiratory system abnormalities in animals of agricultural significance were documented. Expert prompts, including history and details pertinent to each case, are provided in video and text formats to aid the student in documenting initial observations. Upon successful completion of the lesson material, the student is permitted to enter conclusions about the nature of the abnormality. This information, along with the student's notes and quiz responses, is stored on the Blackboard Web site for subsequent review by the instructor. At the end of the program the expert will give a synopsis of the case. We have received favorable comments from our undergraduate, graduate and professional students regarding the program′s quality, format, and innovative nature. Using a designated Web site, syllabi from participating universities that offer a comparable course in farm animal anatomy and physiology will be solicited and published to facilitate interaction among the students and their instructors. Each instructor will facilitate discussion forums and web forms will be used to collect data on the learning process. Participation in this collaborative learning community should improve problem-solving skills of students as they practice applying physiologic concepts to their own observations and, at the same time, form partnerships with other undergraduate agricultural students to better utilize limited resources.

Key Words: collaborative learning, functional anatomy, respiratory system

T475 Measuring the impact of varied instructional approaches in an introductory animal science course. B. G. Bolt* and K. D. Layfield, *Clemson University*, *Clemson, SC*.

The objective of this study was to measure the impact of various teaching formats on a student's likelihood of correctly answering a knowledge-based question and to also assess any relationships between knowledge acquisition and self-perceived levels of engagement. Data were collected on students in the AVS 150, introductory animal science class (n = 155) at a southeastern university during the fall of 2008. Ten to 15 min of class time were allocated to use of one of 3 teaching formats. The 3 teaching formats were labeled as traditional lecture, technology-enhanced or Web-enhanced. At the conclusion of allocated time, students were posed a knowledge question, germane to the presented material and they were also asked to respond with a perceived level of engagement in classroom activities. The responses were collected via a 5-point Likert-type scale (1 = completely disaffected to 5 = completely engaged) using the i-Clicker audience response system. There was a significant difference ($P < 0.05$) in students reported level of engagement in traditional lecture (M = 3.41), Web-enhanced (M = 3.52) and technology-enhanced (M = 3.70). No significant relationships were identified between a student's level of engagement and the likelihood of answering a knowledge question correctly. This finding suggests that although students indicate a preference for how material is delivered, this preference did not impact academic performance.

Key Words: student engagement, teaching methods, undergraduate education

SYMPOSIA AND ORAL PRESENTATIONS

Animal Behavior and Well-Being: Sow Housing, Management, and Stress

409 Productivity and well being of pregnant sows in loose housing is affected by floor space allowance and dietary fiber content. A. R. Hanson*[1], A. E. DeDecker[2], J. L. Salak-Johnson[2], P. M. Walker[1], and J. P. Holt[1], [1]*Illinois State University*, *Normal,* [2]*University of Illinois*, *Urbana*.

As government mandates and public perceptions encourage the adoption of group housing, appropriate management strategies must be evaluated to determine their effect on sow well being and performance. To evaluate the effects of floor space allowance (FSA) and dietary fiber, a 10 mo study was conducted involving 6 trials (n = 40 sows/trial). Pregnant, mixed parity sows were housed 10 per pen with either 2.32m^2 (B) or 1.67m^2 (S) of FSA per sow. Sows were floor fed either a traditional corn-soy based control (C) or higher fiber diet (F). Sows were evaluated for BCS, BW and 10th rib backfat (BF) at d34 (start of trial), d65, and d90 of gestation. Sows were weighed and BCS at d110 of gestation (end of trial), and were scored for lesions at d34 of gestation (before mixing sows), every 2nd day for 2 weeks, and at d65, d76, d90, d110 of gestation to assess skin injury. Farrowing data were collected for each litter, including total birth and weaning weight, piglet mortality, number of pigs born, born alive, born dead and weaned. Data were analyzed by GLM procedures or mixed models, using repeated measures analysis when appropriate to measure effects across gestation days (GD). Sows were assigned to 1 of 3 parity groups (PG) for gilts entering parity 1 (G), sows entering parities 2–3 (M), and sows entering parity 4 or higher (H), respectively. There were significant PG by diet interactions for BCS change, weight gain, and ADG. Gilts lost more BF over gestation compared with other PG ($P < 0.05$). Sows in B pens tended to have higher ADG/period than those in S pens ($P = 0.09$). The HF sows had higher ADG/period than the other diet by PG classifications ($P < 0.05$). The FSA by GD interaction was significant, with S sows accruing lesions of higher severity compared with B sows at d36 ($P = 0.002$) and d76 of gestation ($P = 0.07$). Litter birth weight, and litter live birth weight were greater for higher parity sows ($P < 0.05$).These results indicate that a diet high in fiber can be fed to sows without detrimentally impacting performance, and that FSA may affect lesion severity.

Key Words: sow group housing, fiber, floor space allowance

410 Effects of fiber and floor space allowance on group kept dry sow well-being. A. E. DeDecker*[1], A. R. Hanson[2], P. M. Walker[2], and J. L. Salak-Johnson[1], [1]*University of Illinois*, *Urbana,* [2]*Illinois State University*, *Normal*.

Alternative housing systems for gestating sows is one of the most controversial welfare issues facing the swine industry, thus it is imperative that before implementing new systems that various components of group housing systems be fully evaluated. Therefore, the objective of this study was to evaluate the effects of dietary fiber (source of energy) and floor space allowance on immune and endocrine status, and behavior of sows during gestation. On d34 of gestation, 160 multiparous (parities 1–6) large white crossbred sows were randomly allotted to a dietary treatment (control or high-fiber supplemented diet) and a floor space allowance of either 1.7m^2/sow or 2.3m^2/sow. Group size was kept constant at 10 sows per pen. On d 34 and 90 of gestation both sow immune and endocrine statuses (n = 40 sows/treatment) were measured and for a 24h period between gestation d 75 and 105 sow behavior (n = 10 sows/treatment) was continuously observed using EZViewLog by Geovision. Data were analyzed using Proc MIXED with repeated measures and Chi-squared analysis (SAS). Both diet and days of gestation had an effect on sow immune status; with neutrophil phagocytosis and plasma cortisol being greater ($P < 0.05$) for sows fed a control diet when compared with sows fed a high-fiber diet. Whereas, concanavalin-A induced lymphocyte proliferation was greater ($P < 0.05$) for sows fed high-fiber compared with sows fed a control diet. On d90 of gestation, lymphocyte proliferation was greater ($P < 0.01$) for sows fed a high-fiber diet than for sows fed a control diet. Sow behavior was also affected by diet; with sows fed the high-fiber diet being engaged in more ($P < 0.001$) agonistic encounters than sows fed a control diet. Durations of oral-nasal-facial (ONF), standing, and eating behaviors were all greater ($P < 0.05$) for sows fed the control diet compared with sows fed the high-fiber diet. Moreover, sow behavior was affected by floor space allowance; sows kept at 1.7m^2/sow performed more ($P < 0.05$) ONF, standing, and eating behaviors than did sows kept at 2.3m^2/sow. These results indicate that fiber and floor space allowance can influence sow physiology and behavior which may ultimately impact sow well-being.

Key Words: fiber, well-being

411 Effect of alternative individual and group housing on dry sow performance and physiology. A. E. DeDecker*[1], A. R. Hanson[2], P. M. Walker[2], and J. L. Salak-Johnson[1], [1]*University of Illinois*, *Urbana,* [2]*Illinois State University*, *Normal*.

Sow housing is one of the most controversial issues facing the swine industry, but before implementing alternative systems, we must fully understand the impact that various housing types have on the well-being of gestating sows. Therefore the objectives of this study were to evaluate the effects of individual standard and turn-around stalls on sow performance and physiology during gestation (Exp.1), and to determine the effects of keeping sows in one of the 2 types of stall for first 30d of gestation and then moving sows to group-pens for the rest of gestation (Exp.2). Forty multiparous crossbred sows were allocated, based on body weight and parity, to a standard stall (STS; n = 10) or a turn-around stall (TAS; n = 10) for all of gestation (Exp.1); or a standard stall (STS-G; n = 10) or turn-around stall (TAS-G; n = 10) for 30 d of gestation and then moved to group-pens of 10 sows/pen, at floor space allowance of 2.32m^2/sow (floor fed; Exp. 2). On d 30 and 90 of gestation sow immune and endocrine statuses were measured. Performance measures and lesion scores (scale 1–7) were also assessed throughout gestation. Data were analyzed using Proc MIXED with repeated measures (SAS) and experimental unit was the sow. Fixed effects included parity, day of gestation, treatment and interactions. In Exp. 1, stall-type influenced sow performance and immune status; with lesion scores being greater ($P < 0.05$) among sows kept in TAS than sows kept in STS. Sows kept in STS had greater ($P < 0.05$) body condition score (BCS) than those

sows kept in TAS. Mitogen-induced lymphocyte proliferation was greater ($P < 0.05$) for sows kept in TAS than for sows kept in STS. In Exp. 2, Treatment influenced both performance and immune status of sows; BCS, back fat, and lesion scores all tended to be greater ($P < 0.10$) for sows kept in TAS-G than for sows kept in STS-G. Neutrophil phagocytosis and count, and total WBC count were all greater ($P < 0.05$) for sows kept in STS-G than for sows in TAS-G. In conclusion, these data indicate that type of individual stall throughout gestation and before group-pens can affect performance and immune status of the sow, thus affecting sow well-being.

Key Words: group, stall

412 Effect of alternative accommodations on sow behavior during gestation. A. M. Visconti*[1], A. E. DeDecker[1], A. R. Hanson[2], P. M. Walker[2], and J. L. Salak-Johnson[1], [1]*University of Illinois*, *Urbana*, [2]*Illinois State University*, *Normal*.

Currently there is a lack of scientifically-sound data to establish welfare-friendly guidelines on how to effectively manage gestating sows. Thus, to improve sow well-being, we must understand the impact that various housing systems have on the behavioral aspects of gestating sows. The objectives of this study were to determine the impact that keeping sows in either a standard or turn-around stall throughout gestation has on sow behavior (Exp. 1), and to evaluate the effects of keeping sows in either a standard or turn-around stall for first 30d of gestation and then moving sows to group-pens for remainder of gestation has on sow behavior (Exp.2). Post-mating, 30 multiparous white crossbred sows were randomly allotted to 2 treatments (TRT) either a standard traditional stall (STS; n = 5/TRT) or a turn-around stall (TAS; n = 5/TRT) for entire gestational period (Exp.1), or to a standard stall (STS-G; n = 10/TRT) or turn-around stall (TAS-G; n = 10/TRT) for 30 d and then moved to group-pen until d107 of gestation (Exp.2). Sow behavior was observed continuously from 0800 to 0900 h, 1200 to 1300 h, and 1600 to 1700 h on d6, 30, and 90 of gestation for Exp. 1 and on d30, 45, 65 and 90 for Exp. 2. Data were analyzed using Proc MIXED with repeated measures and Chi-squared (SAS). In Exp. 1, stall type and day of gestation affected behaviors. On d90, duration of standing and eating was greater ($P < 0.01$) for sows in TAS than for sows kept in STS. Duration of eating was greater ($P < 0.05$) for sows kept in STS on d30 than for sows in TAS. In Exp. 2, treatment and day of gestation both affected sow behavior. Duration of ONF was greater ($P < 0.05$) for sows kept in TAS-G compared with sows kept in STS-G. Frequency of aggression was greater ($P < 0.01$) for sows kept in TAS-G than sows in STS-G. Duration of lying on d45 and 90 was greater ($P < 0.05$) for sows kept in TAS-G compared with sows kept in STS-G. These data indicate that individual stall design throughout gestation and type of stall before group-housing can influence sow behavior; therefore further assessment of alternative accommodations is needed before implementation of alternative systems.

Key Words: behavior, sow

413 Effects of alternative housing systems on the well-being of gestating sows. A. E. DeDecker* and J. L. Salak-Johnson, *University of Illinois*, *Urbana*.

Housing systems for gestating sows is one of the most controversial welfare issues facing the swine industry. New systems are being implemented without scientifically evaluating the impact these alternative accommodations may have on sow well-being. The objectives were to evaluate the effects of 3 housing systems on sow physiology, performance, productivity and behavior. On d30 of gestation 36 multiparous sows were allocated to a standard crate (CRATE; control), a width adjustable crate (FLEX), or free access stall-pen (FREE). Immune and endocrine status, body condition and lesion scores, body weight, and back-fat depth were measured at weaning (d 0), various time points throughout gestation, and again at d110. Behavior was observed for 24h on d29, 30, 66, and 87 of gestation for block 1. Data were analyzed using Proc MIXED with repeated measures (SAS). Sows in the FREE system had greater ($P < 0.01$) body condition and lesion scores, body weight, and back fat depth than sows in either FLEX or CRATE systems. Sows in FLEX had greater litter size ($P < 0.10$) and piglet mortality rate ($P < 0.05$) than did sows in CRATE; while sows in FLEX had piglets with greater ($P < 0.01$) wean weight and rate of gain than did sows kept in either FREE or CRATE systems. Sows in FREE had less ($P < 0.05$) banded neutrophils than did sows in either FLEX or CRATE. On d31 (24 h later), all sows had greater ($P < 0.05$) lymphocyte and neutrophil counts, neutrophil chemotaxis, and concanavalin A- and lipopolysaccharide-induced lymphocyte proliferative responses than any other day of gestation. Sows kept in CRATE engaged in more oral-nasal-facial (ONF) behaviors than sows kept in other systems ($P < 0.05$). Sows in CRATE stood more ($P < 0.05$) than sows in all other treatments. Also, as day of gestation increased ($P < 0.05$), duration of ONF, sham-chewing, eating, and drinking behaviors all increased. These data indicate that alternative housing accommodations can affect immune status, physiology, performance, productivity and behavior of pregnant sows throughout gestation. Moreover, these data support the hypothesis that modifications of specific housing components within existing housing systems can affect sow well-being.

Key Words: behavior, immune

414 The effect of a repeated prenatal stressor and low-dose Ketamine on the anxiety and social behavior of pigs. B. L. Davis*[1] and M. A. Sutherland[2], [1]*Texas Tech University*, *Lubbock,* [2]*Ruakura Research Centre, AgResearch*, *Hamilton, New Zealand*.

The fetal programming hypothesis states that exposure to elevated glucocorticoid concentrations in utero can alter offspring development. Animals exposed to stress prenatally have been shown to display increased anxiety-like behavior coupled with a reduced ability to cope with stress. The objective of this research was to determine if exposure to stress prenatally would affect the social and anxiety-like behavior of pigs and whether an anxiolytic drug (Ketamine) would reverse these behavioral changes. Sows were allocated to one of 2 treatments; 1) Sows were given an injection of adrenocorticotropic hormone (ACTH; 100 IU i.m.) 3 times a wk during the last 5 wk of gestation (ACTH; n = 10), and 2) Sows were control handled (HAN; n = 10). At 6 mo of age, the female offspring from the ACTH (PNS; n = 20) and HAN (CON; n = 20) sows were tested for 10 min in an open-field test (OFT) to measure anxiety and for 30 min in a social test (ST) to measure social interactions. The ST involved observing the interactions between 2 pigs; the experimental pig and a naïve non-experimental pig. Pigs were tested in each behavioral test twice; 1 wk apart. Two h before testing, pigs were given either Ketamine (KET; 0.5mg/kg, i.m.) or saline (SAL) at the same dose. Videos from behavior tests were analyzed using Observer 7.0. Data were analyzed using the MIXED procedure of SAS. At 6 mo of age, PNS pigs tended ($P = 0.075$) to weigh less than CON pigs. In the OFT, PNS pigs spent more ($P < 0.05$) time in the middle squares and pigs given KET spent less ($P < 0.05$) time displaying escape behaviors compared with SAL pigs. In the ST, PNS pigs given KET tended to spend less time ($P = 0.065$) fighting and more time ($P < 0.05$) performing non-aggressive social touching than CON pigs given KET. In conclusion, exposure to elevated glucocorticoid concentrations in utero may affect

offspring growth and anxiety-like behaviors. Furthermore, low-dose KET appeared to have anxiolytic effects on pig behavior, especially among prenatally stressed pigs.

Key Words: stress, pigs, anxiety

415 Heart rate variability—A tool to differentiate positive and negative affective states in pigs? R. Poletto*[1], R. M. Marchant-Forde[1], J. N. Marchant-Forde[1], J. L. Rault[1,2], D. F. Hogan[3], and D. C. Lay Jr.[1], [1]*USDA-ARS-Livestock Behavior Research Unit*, *West Lafayette, IN,* [2]*Department of Animal Sciences, Purdue University*, *West Lafayette, IN,* [3]*Veterinary Clinical Sciences, Purdue University*, *West Lafayette, IN*.

Neurophysiological processes, such as autonomic nervous system activity, that mediate behavioral and physiological reactivity to an environment have largely been ignored in farm animal research. Heart rate variability (HRV) analysis is a clinical diagnostic tool used to assess affective states (stressful and pleasant) in humans, but its application is limited in farm animals. This experiment aimed to determine if HRV may be used to differentiate affective states in swine. Ten 4-mo-old barrows and gilts underwent surgery to place an intracardiac ECG lead attached to a biotelemetry device; pigs had a 3-wk recovery period before data collection. A negative state was induced by restraining pigs for 1 h in metabolism crates located in the same room, while a positive state was induced by allowing pigs′ access to the hallway for 10 min. Behavior and ECG data were recorded. For data analyses, a 512–beat section of HR inter-beat intervals was selected per pig while behaviorally inactive during restraint; or while performing a combination of play- and exploratory-like behaviors in the hallway. Data were analyzed using time and frequency domain analysis followed by a factorial analysis of test × sex with mixed models and Tukey's post hoc test. Average HR was lower for restraint than the hallway test (121.7 vs. 162.4 ± 4.4 bpm; $P < 0.01$), while RMSSD, index of vagal cardiac control, was higher for restraint than for hallway test (11.0 vs. 7.0 ± 1.0 msec; $P < 0.05$). Gilts had higher low frequency (LF) power than barrows (65.1 vs. 43.9 ± 4.0 msec^2/Hz; $P < 0.01$). High frequency (HF) power was lower in hallway than in restraint (4.2 vs. 14.1 ± 1.9 msec^2/Hz; $P < 0.01$). Sympathovagal balance (LF/HF) was higher during hallway test compared with restraint ($P < 0.01$). Gilts showed primarily sympathetic modulation of HR; while over both sexes, restraint resulted in greater parasympathetic control of cardiac function. Results indicate that HRV can be used to distinguish different degrees of activity/states in pigs. Further research will assist to identify distinct autonomic response patterns to different well-being states in farm animals.

Key Words: swine, heart rate variability, behavior

416 A combination of head/heart electric stunning is more effective than the head-only method in pigs. K. D. Vogel*[1], G. Badtram[2,3], J. R. Claus[3], T Grandin[1], S. Turpin[3], R. E. Weyker[3], and E. Voogd[4], [1]*Department of Animal Sciences, Colorado State University*, *Fort Collins,* [2]*Wisconsin Department of Agriculture, Trade, and Consumer Protection, Division of Food Safety*, *Madison,* [3]*Department of Animal Sciences, University of Wisconsin-Madison*, *Madison,* [4]*Voogd Consulting, Inc.*, *West Chicago, IL*.

Head-only electrical stunning is a reversible procedure that is effective for approximately 15 s. Shackle to bleed time in small slaughter facilities may exceed 30 s, primarily due to slow hoist speed. A 2-stage stunning method was proposed where head-only stunning for 3 s was followed by application of the same stunning apparatus to the cardiac region of the animal for 3 s while lying in lateral recumbency (head/heart). A paired-comparison study was performed on 89 pigs in a small Wisconsin slaughter facility to compare the head-only method applied for 6 s to the head/heart method. The study objective was to evaluate signs of return to sensibility, shackle to bleed time, blood lactate concentration, muscle pH, drip loss, and fresh meat color to validate the head/heart electrical stunning method for small slaughter plants. Incidence of corneal reflex was not different ($P > 0.05$) between head/heart (93.8%) and head only (85%) stunning. Nose twitching was more common ($P < 0.05$) in head only (26.5%) than head/heart (5%) stunning. The head/heart method eliminated rhythmic breathing, natural blinking, eye tracking to a moving object, and righting reflex, which were all observed in head-only stunned pigs. Blood lactate was not different ($P > 0.05$) between stunning methods (head only: 8.8 ± 0.7 mmol/L, head/heart: 7.8 ± 0.7 mmol/L). Shackle to bleed time did not differ ($P > 0.05$) between stunning methods (head only: 32 ± 1 s, head/heart: 33 ± 1 s). Mean time to loss of detectable heartbeat with the head-only method was 121 ± 5 s. No detectable heartbeat was observed with the head/heart method. Longissimus thoracis pH, color, and drip loss were not different ($P > 0.05$) between stunning methods. Farm of origin effects were observed in blood lactate, meat color, and drip loss. Farm effects can be generated by differences in genetics and management, which were not investigated in this study. This study determined that the head/heart electrical stunning method reduces the incidence of signs of return to sensibility without significant effect on meat quality, speed of plant operation, and blood lactate concentration.

Key Words: swine, stunning, welfare

417 Effects of pen size on the stress response of market weight pigs during loading and unloading. L. M. Gesing*[1], A. K. Johnson[1], K. J. Stalder[1], J. T. Selsby[1], M. Faga[2], A. Whiley[2], S. Abrams[2], H. Hill[2], R. Bailey[3], and M. J. Ritter[4], [1]*Iowa State University*, *Ames,* [2]*Iowa Select Farms*, *Iowa Falls,* [3]*JBS Swift and Co.*, *Marshalltown, IA,* [4]*Elanco Animal Health*, *Greenfield, IN*.

The objective of this trial was to determine the effects of pen size on the stress response and transport losses in market weight pigs. Twenty-six loads (~174 pigs/load) of pigs (n = 4522) were used in a complete randomized block design. Three commercial grow-finish sites were used over July and August. Each site had 2 rooms with both treatments represented in each room. The small pen (SP) treatment had 36 pigs/pen (0.59 m^2·pig^{-1}). The large pen (LP) treatment had 324 pigs/pen (0.59 m^2·pig^{-1}). To achieve large pens, 8 consecutive swing gates were kept open. During loading, all swing gates were closed in LP pens. Pigs from both treatments were sorted from pen mates at the time of loading, moved in groups of 4–6 using sort boards and electric prods if necessary, and loaded onto straight deck trailers. Treatments were randomly assigned to a deck, pigs were provided with ~0.42 m^2·pig^{-1}, and transported ~1 h to a commercial harvest facility. During loading and unloading, the number of pigs displaying open mouth breathing (OMB), skin discoloration (SD) and muscle tremors (MT) were recorded. At the plant, dead and non-ambulatory pigs (fatigued and injured) were recorded during unloading and total losses were defined as the sum of dead and non-ambulatory pigs. Data were analyzed using Proc Glimmix of SAS. MT at loading and injured and DOA at plant could not be run and will be presented descriptively. SP had lower incidences of OMB ($P = 0.0015$) and SD ($P = 0.0120$) during loading than LP. At loading MT was 0.04% SP vs. 0% LP. At the plant, LP had a lower incidence of SD ($P < 0.0001$) than SP; however, there were no ($P > 0.05$) differences between treatments for OMB, MT, fatigued, total non-ambulatory, or total losses. Incidence of injured pigs was 0% SP vs. 0.04% LP and there were no DOAs. In summary, pen size did not impact the incidence of transport losses.

Key Words: pen size, pig, transport loss

418 Effects of vehicle design on blood stress indicators and meat quality in pigs of three genotypes for two different travel distances. A. Vanelli Weschenfelder*[1,2], S. Torrey[3], N. Devillers[2], L. Saucier[1], and L. Faucitano[2], [1]*Université Laval*, *Sainte-Foy, Québec, Canada*, [2]*Agriculture and Agri-Food Canada*, *Lennoxville, Québec, Canada*, [3]*University of Guelph*, *Guelph, ON, Canada*.

This study aimed at evaluating the effects of vehicle design on stress response and meat quality traits of 3 different pig genotypes; namely Piétrain HALNn (A), Piétrain HALNN (B) and Duroc crossbreds (control; C). A total of 360 pigs (120 pigs/genotype) were transported either for a short or long distance (45 min and 7h, respectively) over a 6 weeks period. The vehicles were a 3-decked Pot-Belly (PB) trailer equipped with 2 internal ramps and a 3-decked Flat-Deck (FD) trailer equipped with moving decks and no internal ramps. For each group, blood samples were collected at exsanguination from a sub-sample of 144 pigs (4 pigs/genotype/vehicle/week) for the analysis of lactate and creatine phospho-kinase (CPK) concentrations, while meat quality was assessed in the Longissimus dorsi (LD) and Semimembranosus (SM) muscles of all 360 pigs (10 pigs/genotype/vehicle/week). Data were analyzed using the mixed model procedure of SAS. In the short distance journeys, CPK levels were higher ($P = 0.021$) in A pigs transported on the PB trailer compared with those transported on the FD trailer. Pigs transported on the PB trailer had higher ($P = 0.02$) pHu values in the SM muscle than those transported on the FD trailer. Yet, in the short distance study group, A pigs had lower ($P = 0.008$) pHu and higher ($P < 0.001$) drip loss in the LD muscle compared with B and C pigs. Concurrently, the LD muscle of A and B pigs was paler (higher L* value; $P = 0.002$) than that of C pigs. A pigs also had higher L* and drip loss values ($P = 0.04$ and $P < 0.001$, respectively) in the SM muscle. In the long distance transportation, no effect of vehicle type was found on blood stress indicators ($P > 0.05$). Nonetheless, A and B pigs had higher lactate ($P = 0.003$) and CPK levels ($P < 0.001$) than C pigs. Regarding meat quality parameters, differences between genotypes were similar to those found in the short distance travel study. Overall, the use of PB trailer for short distance transportation and of HALn carrier pigs are not recommended from an animal welfare and meat quality improvement perspective.

Key Words: transport, pigs, stress

419 Effects of pasture versus stall housing on cortisol and DHEA concentrations in young Quarter Horses. S. M. Garey*, T. H. Friend, L. R. Berghman, A. L. Adams, and C. L. Terrill, *Texas A&M University*, *College Station*.

Adaptation of horses to long-term stall housing has not been thoroughly investigated. The objective of this study was to determine if cortisol or dehydroepiandrosterone (DHEA) differed among groups of young horses when housed in individual stalls versus in a group on pasture. Eighteen 2- to 3-yr-old Quarter Horses were randomly assigned to either stall or pasture housing for 21 d. The 3.05 × 3.05 m stalls had solid concrete side and rear walls with a small ventilation window, while the front allowed horses to view the alley of the barn. The stalled horses were allowed 15 min of exercise 3 d per week. The 9 pasture horses were on a novel 0.2 km^2 pasture. All horses were fed concentrate 2 times per day, pastured horses had coastal grass, and stalled horses had coastal hay. After 21 d, all horses were combined on pasture and observed for 7 d. Jugular blood samples were drawn at 24 h and 0.5 h before treatment, then every 12 h for 3 d, every 24 h for 5 d, and every 48 h for the final 13 d. On d 22, blood samples were collected at 0.5 h before combining the horses, 12 h and 24 h post-combination, then every 24 h for the remaining 6 d. Plasma was analyzed by ELISA to determine cortisol and DHEA concentrations. A mixed model repeated measures ANOVA with unstructured covariance determined treatment and time of sampling effects. Overall, stalled horses had significantly higher cortisol concentrations (5.11 ng/mL) than pastured horses (3.62 ng/mL, $P < 0.0001$), although no significant differences were observed in DHEA ($P = 0.08$). No significant differences were observed in cortisol concentrations between treatment groups during the pre-treatment sample periods ($P = 0.29$), however, average cortisol concentration of stalled horses during the treatment period (4.73 ± 1.08 ng/mL) was significantly higher ($P < 0.0001$) than pastured horses (3.23 ± 1.08 ng/mL). In conclusion, differences between the treatment groups were initially slight, and became more exaggerated over the treatment period. These results suggest that isolation in an individual stall over an extended period of time causes changes in cortisol that merit further investigation.

Key Words: housing, stall, cortisol

420 Use of infrared thermography to measure inflammation associated with castration and anti-inflammatory drugs. L. A. González*[1], K. S. Schwartzkopf-Genswein[2], E. Fierheller[3], E. Janzen[3], N. Caulkett[3], and T. A. McAllister[2], [1]*University of Manitoba*, *Winnipeg, Manitoba, Canada*, [2]*Agriculture and Agri-Food Canada*, *Lethbridge, Alberta, Canada*, [3]*University of Calgary*, *Calgary, Alberta, Canada*.

Angus bulls (n = 48; initial BW 301 ± 3 kg) were randomly assigned to 1 of 6 treatments according to a 3 × 2 factorial design to study the effect of castration method and pain medication on eye (ET) and scrotal area temperature (ST). Castration (Cast) treatments consisted of sham (C), band (B), and surgical (S) castration. Pain medication (Med) treatments consisted of either lactated ringer solutions (NM) or pain mitigation drugs (M). Drugs used were 2% lidocaine with epinephrine injected at 10 mL into each testicle plus 10 mL subcutaneously at the scrotal base, and a subcutaneous injection of flunixin meglumine (2.2 mg/kg BW) in the neck of calves. Maximum ET and ST were measured with an infrared camera on day −1, 0, 2, 5, 7, 14, 21, and 35 relative to castrations. Data were analyzed with a mixed-effects regression model considering the fixed effects of covariate (d −1), Cast, Med, and Day as repeated measure, the random effect of Pen, and all possible interactions. Maximum temperature of the scrotal area was affected by Cast ($P < 0.001$), Cast × Med ($P < 0.05$), and Cast × Day ($P < 0.001$). S calves had greater temperature than C and B at d 2, 5, and 7 after castration ($P < 0.05$). In contrast, B had greater temperature than S and C at d 21 and 28, and greater than C at d 14 and 35 ($P < 0.05$). MB calves had lower ($P < 0.05$) ST compared with NMB but this was not the case in S and C ($P > 0.10$), values being 36.0, 35.3, 35.2, 35.5, 34.2, and 34.7 ± 0.32°C for BNM, BM, SNM, SM, CNM, and SM, respectively. Cast and Med did not significantly influence ET ($P > 0.10$). Based on ST, S produces inflammation during the first week whereas B produced inflammation during wk 3 and 4 after castration. However, neither Cast nor Med resulted in systemic inflammation because no differences in ET were observed. The medication protocol used in the present study reduced local inflammation in band castration only.

Key Words: bull inflammation, castration method, pain medication

421 Influence of cattle temperament on stress hormones and IgG concentrations in Angus-cross calves. R. C. Vann*[1], N. C. Burdick[2], J. G. Lyons[2], T. H. Welsh, Jr.[2], and R. D. Randel[3], [1]*MAFES-Brown Loam Research Station*, *Raymond, MS,* [2]*Texas AgriLife Research*, *College Station,* [3]*Texas AgriLife Research*, *Overton*.

The objective of this study was to determine the influence of temperament on concentrations of cortisol, epinephrine, norepinephrine, and

IgG in Angus-cross calves. Calves from 2005 and 2006 were selected based on temperament score measured 28 d before weaning and at weaning. Based on temperament score the 10 calm, 10 intermediate and 10 temperamental calves from each sex (steers and heifers in 2005, bulls and heifers in 2006) were selected from each calf crop (n = 120). Blood was collected 28 d before weaning, weaning, 28 and 56 d post-weaning to determine serum cortisol and IgG, and plasma epinephrine (EPI) and norepinephrine (NE) concentrations. Data were analyzed using the MIXED procedure of SAS specific for repeated measures. Sources of variation included temperament, sex, day and year. Concentrations of EPI and NE were greater in 2005 than 2006 ($P = 0.004$). Cortisol concentrations were lower in calm (25.9 ± 0.9 ng/mL, $P < 0.001$) compared with intermediate or temperamental calves (35.5 ± 0.7 and 32.7 ± 0.9 ng/mL, respectively). Heifers had greater ($P < 0.001$) cortisol concentrations (37.2 ± 0.7 mg/mL) with steers being intermediate (34.2 ± 1.2 ng/mL) and bulls having lower concentrations (22.7 ± 1.3 ng/mL). Calm had lower ($P < 0.001$) EPI concentrations (389 ± 65 pg/mL) than intermediate (613 ± 64 pg/mL) and temperamental calves (788 ± 64 pg/mL). Concentrations of EPI declined over the 4 collection times ($P < 0.002$). Temperamental had greater concentrations ($P < 0.001$) of NE (754 ± 53 pg/mL) and NE did not differ between calm and intermediate calves (461 ± 53 and 470 ± 53 pg/mL, respectively). Concentrations of NE differed ($P = 0.012$) over the 4 collection times and were not influenced by sex. Concentrations of IgG were influenced by the following interactions: temperament × sex ($P < 0.002$) and sex × day ($P < 0.02$). In summary, there appears to be a relationship between temperament and concentrations of stress hormones. In addition, sex influenced concentrations of cortisol and EPI whereas, both temperament and sex influenced IgG.

Key Words: cattle, temperament, stress hormones

Animal Health Symposium: Accounting for Diseased Animals in Research Trials (Outliers, Treatments, Interactions)/ Disease Induction by Treatment?

422 Factors influencing onset of disease and subsequent effects on feedlot performance. R. M. Enns*[1], R. L. Weaber[2], H. Van Campen[1], and G. H. Loneragan[3], [1]*Colorado State University*, *Fort Collins*, [2]*University of Missouri*, *Columbia*, [3]*West Texas A&M University*, *Canyon*.

Prevention and treatment of disease in the dairy and beef industries increases production costs for producers. For researchers, disease symptoms often lead to the removal of animals from study outcomes. Removal of these animals from research trials may bias study results if susceptibility to disease is genetically related to outcomes of interest. Failing to correct performance records for factors that induce phenotypic variation can downwardly bias heritability estimates and diminish the power to detect quantitative trait loci. A more complete understanding of factors influencing onset of infectious disease, including genetic contributors, and the resulting influence of these diseases on subsequent animal performance and recovery time lag is warranted. Due to the variable nature of incidence of disease, estimation and quantification of factors contributing to disease susceptibility is often clouded by issues associated with specificity, sensitivity, and exposure to pathogens. Bovine respiratory disease (BRD) represents the largest proportion of disease incidence in feedlot cattle and results from the interactions of stress level, immunological status and response, and the presence of infectious organisms. Stress and immunological response have been reported to have heritable components. Feedlot personnel rely on animals exhibiting clinical signs of BRD for diagnosis and initiation of treatment. Yet, when lung lesion scores are collected at harvest and combined with treatment records a substantial portion of untreated animals have lung lesions while a noteworthy portion of calves treated do not exhibit lung damage. Taken alone, diagnosis and treatment of BRD is related to lower feedlot ADG, carcass weight, and quality. These effects seem to be dependent upon timing of treatment relative to slaughter with effects on recovered animals diminishing with longer periods on feed. A more complete understanding of the environmental and genetic factors contributing to the occurrence of BRD could lead to a reduction in disease frequency and better methodologies for predicting and accounting for impacts on animal performance in research studies.

Key Words: cattle, bovine respiratory disease, health

423 Reporting standards for randomized controlled trials in cattle: Improving the quality of research. I. A. Gardner*[1], A. M. O'Connor[2], J. M. Sargeant[3], J. S. Dickson[4], and M. E. Torrence[5], [1]*University of California, Davis,* [2]*Iowa State University*, *Ames,* [3]*University of Guelph*, *Guelph, Ontario, Canada*, [4]*Iowa State University*, *Ames,* [5]*USDA-ARS*, *Beltsville, MD*.

Design, analysis and reporting of randomized, controlled trials with production, health, and food safety outcomes in livestock presents unique challenges that may not be adequately addressed in published trial reports or in the CONSORT statement (Consolidated Standards of Reporting Trials of 22 items, available www.consort-statement.org). A consensus meeting of 24 experts (biostatisticians, epidemiologists, food safety researchers, and livestock production specialists) resulted in development of an extension of the CONSORT statement. The new statement is called REFLECT (www.reflect-statement.org/statement/). Thirteen items on the CONSORT checklist were modified as well as the inclusion of one additional item: item 1 (title and abstract), item 3 (participants), item 4 (interventions), item 5 (objectives), item 7 (sample size), item 8 (randomization sequence allocation), item 9 (allocation concealment), item 10 (randomization implementation), item 11 (blinding/masking), item 12 (statistical methods), item 13 (participant flow), item 15 (recruitment), and item 20 (interpretation). The additional item proposed was a new sub-item for item 4 (challenge trials). The consensus group also proposed terminology to describe study subjects to make the language more consistent with common usage in livestock production. Implications of these new standards for trials in dairy herd health and production medicine will be discussed with a focus on statistical methods to account for censored and missing observations and cluster designs.

Key Words: randomized controlled trials, statistical methods, censoring

424 Accounting for diseased animals in research trials. G. D. Snowder*, *National Center for Foreign Animal and Zoonotic Disease Defense*, *College Station, TX*.

Unfortunately, livestock on research trials frequently experience pathogenic or metabolic diseases. Sick or deceased research animals often present a dilemma for investigators by influencing the statistical power and/or conclusions of the study. A decision tree approach is recommended for determining appropriate handling of data from such animals. When the treatment effect is associated with the disease, the disease effect should be included in the statistical analyzes. When the disease is not associated with the treatment then it must be determined whether the animal is a statistical outlier which may be adjusted for or an anomaly that could be discarded. There are several different statistical approaches to adjusting data sets to account for outliers, but the interpretation of adjusted data can be difficult to comprehend. The most critical factor in accounting for diseased animals is the number of experimental units (animals) in a treatment or block. In trials with large numbers of experimental units ($n > 30$) per treatment, data from a few sick or deceased animals are frequently deleted. This approach is justified when statistical tests indicate large differences between treatment means and/or measures of variation for the healthy animals. When these statistical differences are small, one may consider inclusion of data from sick or diseased animals that have been properly adjusted or accounted for. When the number of experimental units per treatment is small, the decision to delete sick or deceased animals becomes critical. Depending on the response variable(s) measured, covariate analysis or sub-treatment group analysis may be considered. A decision tree approach with options for statistical methods will be presented for various scenarios to handle data from sick or deceased animals in research trials.

Key Words: statistics, sick, outliers

ARPAS-Ruminant Nutrition Joint Symposium: Nutrition Models–Where Are We Going in the Next Decade?

425 The role of models in animal nutrition: Research and field applications. J. A. Metcalf* and N. S. Ferguson, *Nutreco Canada Inc*, *Guelph, Ontario, Canada*.

Mechanistic mathematical models are essential to the interpretation of data from scientific experimentation, since they can be used to explain and predict outcomes. The more inclusive the theory behind the model, the more accurately the outcome can be explained or predicted, while at the same time being at risk of error due to inadequacy in the theoretical framework or scientific understanding. Nevertheless a sound biological model offers a powerful tool which requires that the parameters used to design and/or drive the model be fully understood by the user. Modeling and experimental design can be used together in research models, with the model used to identify areas where further investigation is required, while the experimental results can be used either to validate or further develop the model. There are many models used in practical animal nutrition, usually relating to diet formulation, predicting growth and the interaction of nutritional parameters with genetics and environment. Successful field models are those which have a sound mechanistic basis, allowing the incorporation of new technologies, such as rumen active feed additives or digestibility analyses. These technologies must be rigorously tested so that the impact on the model is predictable under field conditions, and training for the users requires that they understand the limitations of the model. Applied models which incorporate financial impacts, such as carcass grading or milk composition, as well as the cost of the nutrition, are essential for better decision making on farm. One extension of this is the ability to generate multiple solutions by allowing nutritional inputs to vary, in order to demonstrate to the producer the cost of changing objectives on milk production or growth. A frequent failing of applied models is at the user interface. Focusing on the ease of use by providing adequate default settings and a logical approach to diet formulation or evaluation can increase the usefulness of a model, and is an area which is undervalued.

Key Words: mechanistic modeling, nutritional models, diet formulation

426 Nitrogen recycling and rumen degradable protein requirements: Quantitative updates to describe microbial requirements, sources, and applications in ration formulation. M. E. Van Amburgh*, E. B. Recktenwald, D. A. Ross, R. J. Higgs, T. R. Overton, and L. E. Chase, *Cornell University*, *Ithaca, NY*.

Estimating the requirements for ruminal nitrogen (N) is a function of microbial demands driven by the availability of rumen fermentable carbohydrates for microbial growth. To improve overall efficiency of use and to reduce the environmental impact of N from cattle, we need to refine our estimates of ruminal N demand and supply to minimize urinary N excretion. The ruminant is an obligate recycler of N designed to conserve N in times of limitations in an effort to maintain an optimal microbial population. The objective of this abstract is to present a quantitative description of the demand and supply of ruminal N for a field application model. Recent work has indicated that recycled N to meet ruminal demands are greater and more constant than previously considered, are a function of intake N and are supplied as ammonia N and peptide N. Further, the current characterization of soluble protein into non-protein N and true protein has under-estimated the peptide content of the soluble protein fraction of feeds, particularly of forages, which has confounded not only estimations of rumen available N, but also metabolizable protein supply. Urea N synthesis is directly related to N intake and review of our work and the literature shows the conversion of intake N into urea N generally ranges from 50 to 70%. The proportion of N intake that reenters the gastrointestinal tract (GIT) as urea-N in the dairy cow is on average 30–45%. Microbial capture of the recycled N is of greatest interest and what impacts efficiency of use. Other sources of rumen available N are endogenous N and microbial turnover. Measurements of endogenous N flows through the rumen range from 5 to 15% of the total N supply, contribute to the rumen available N supply as peptides, are taken up by the microbes and constitute up to 15% of the microbial protein supply, which is comparable to the amount of bacterial N coming from recycled urea N. In addition, the use of N by protozoa and the interaction of protozoa with the bacterial pool will also be discussed.

Key Words: recycled N, RDP, modeling

427 Tackling the variable efficiencies in post-absorptive amino acid utilization. M. D. Hanigan*[1] and E. C. Titgemeyer[2], [1]*Virginia Polytechnic Institute and State University*, *Blacksburg,* [2]*Kansas State University*, *Manhattan*.

Productive performance of all animals including ruminants is nutrient dependent. While excess energy can be stored in times of excess, the ability to store amino acids (AA) is extremely limited. Thus, performance declines when AA supplies are limiting and excess AA are degraded when supply exceeds demand. Matching AA supply and tissue needs thus requires an accurate representation of the efficiency with which absorbed AA are utilized. The current NRC ruminant models assume that conversion of absorbed AA to product is high and constant when supply is at or below requirements. However, there is significant evidence that efficiency of conversion is moderate and variable. The assumption of constant efficiency is predicated on the concept of a single limiting nutrient. That paradigm dictates that productive output will increase in a linear manner in response to a nutrient until another nutrient becomes limiting or genetic potential is reached at which point productive responses will abruptly cease. In this scenario, the metabolic machinery remains constant and substrate supply dictates the rate of production. However, emerging work on the regulation of protein synthesis within the cell clearly supports the role of both AA and energy status as regulators of protein synthesis and AA extraction from blood resulting in continuously variable metabolic efficiency and demand. Further these data are not supportive of the single limiting nutrient approach. We have begun to build models representing both the substrate and regulatory effects of AA, energy yielding substrates, and hormones at the tissue level. These lower level models must be aggregated across tissues and consolidated into a postabsorptive system that is capable of predicting efficiencies for at least the essential AA over a range of conditions. Such a system should allow diet formulation to achieve animal N efficiencies of 40% or greater which will dramatically reduce N loss to the environment and may reduce feed costs.

Key Words: amino acid, requirement model, ruminant

428 VFA production and absorption: Modeling the impacts on energy availability. A. Bannink*[1], J. France[2], J. L. Ellis[2], and J. Dijkstra[3], [1]*Animal Sciences Group, Wageningen UR*, *Lelystad, the Netherlands*, [2]*Centre for Nutrition Modelling, University of Guelph*, *Guelph, Ontario, Canada*, [3]*Wageningen University*, *Wageningen, the Netherlands*.

Current feed evaluation systems aim to match supply and requirement for various nutrients. These systems are largely empirically based and fail to address the underlying mechanisms causing variation in feed digestion and nutrient absorption. Modeling exercises were undertaken to evaluate these mechanisms with a distinct representation of rumen, small intestine and large intestine functioning. Volatile fatty acids (VFA) are the main source of metabolizable energy and propionic acid the main glucose precursor. Their accurate estimation is a prerequisite to understanding variation in ruminant performance. Published VFA prediction methods differ in approach, type of information used, and level of detail represented. Substrate fermented (or bypassing rumen fermentation) is estimated from rates of outflow and degradation. The type of rumen VFA produced is mostly associated with the type of substrate fermented or some general dietary characteristics. But, details of rumen fermentation processes or intraluminal conditions are rarely taken into account. Also, the concepts used and presumptions made in rumen modeling efforts may restrict the possibilities to apply these representations of VFA production. The large intestine delivers a minor fraction of total VFA production (on average some 10%) but variation in hindgut fermentation is large and should be taken into account to obtain accurate estimates of the total tract VFA production. The absorption of VFA depends on the amount of VFA produced as well as on intraluminal conditions and rumen wall characteristics. Intraluminal state and VFA absorption rate are mutually dependent, rumen epithelia strongly adapt to intraluminal conditions, and intraluminal state affects rumen fermentation as the source of VFA. This means that for an understanding of the contribution of enteric fermentation to feed digestion and energy absorbed as VFA, these aspects need to be considered simultaneously.

Key Words: digestibility, VFA, modeling

429 Predicting dry matter intake responses: Modeling the influence of cattle management. R. J. Grant*[1], T. P. Tylutki[2], and P. D. Krawczel[1], [1]*William H. Miner Agricultural Research Institute*, *Chazy, NY*, [2]*AMTS LLC*, *Cortland, NY*.

Prediction of dry matter intake (DMI) may be improved by combining measures of the animal physical and social environment with traditional inputs such as body weight, milk production, stage of lactation, or dietary energy density. Rudimentary attempts have been made to adjust DMI predictions directly and indirectly based on environmental factors such as temperature, humidity, wind speed, degree of muddiness, hair coat, and distance walked. In the next decade, nutritional models will increasingly incorporate inputs such as stocking density, grouping strategy, and parity effects that characterize key components of the social environment and influence the animal response to diet. For instance, research shows that short-term daily DMI is unaffected by pen stocking density of stalls and feed manger, but feeding rate within a meal may be increased by up to 25%. Consequently, dynamic models will be required to accurately predict the impact of varying stocking densities on feeding, rumen conditions, and performance. Commingling primi- and multiparous cows often reduces the daily DMI of the younger, subordinate animals and also affects feeding rate and meal patterns. An input for parity will be useful in static and dynamic nutritional models. Time budget analysis of eating and resting times will ensure that adequate time is available for predicted daily DMI. Inputs related to the feeding environment such as feeding frequency and feed availability also affect DMI. The feeding environment specifically determines achievable DMI, in contrast to predicted DMI, and future models must accurately capture the key inputs and how these environmental factors influence feeding behavior and DMI. Currently, research that evaluates the effects of the social and physical environment on behavioral responses as well as DMI is limited, but it will be needed to improve nutritional models over the next decade. The Cornell Net Carbohydrate Protein System model (version 6.1) will be used to illustrate what may be implemented now and in the future to better predict DMI with a specific focus on dairy cattle.

Key Words: dry matter intake, nutrition models, social and physical environment

430 Application of a crossbred model reveals additional genetic variation in reproduction traits of commercial females. S. Bloemhof*[1,2], E. F. Knol[1], A. Kause[2], and I. Misztal[3], [1]*IPG, Institute for Pig Genetics B.V.*, *Beuningen, the Netherlands*, [2]*Animal Breeding and Genomics Centre, Wageningen University*, *Wageningen, the Netherlands*, [3]*Department of Animal and Dairy Science, University of Georgia*, *Athens*.

The objective of our study was to estimate genetic parameters for litter size and farrowing rate in a data set of 2 pure lines and the corresponding crossbreds. Data were obtained from the TOPIGS database and included 91,461 cycle records from 23,432 sows on 33 farms in Spain and Portugal collected from 2003 to 2008. Sows originated from two lines, namely Yorkshire (D) and Large White (I), and from their crosses (DI). Traits studied were litter size (1 to 29) and farrowing rate (0 or 1). Litter size was analyzed using a linear animal model and farrowing rate was analyzed using a threshold model. Both models included fixed effects of parity and number of inseminations, and random effects of herd-year-month, service sire, permanent environment, and the additive animal effect. Within-line and crossbred variance components were estimated via Gibbs sampling. Within-line heritability estimates for litter size were 0.05±0.01 for line D, 0.11±0.01 for line I, and 0.08±0.02 for line DI. Heritability estimates for litter size, obtained from the crossbred model, were 0.06±0.01 for line D, 0.11±0.01 for line I, and 0.14±0.03 for line DI. Genetic correlations for litter size were 0.81±0.15 between line D and line DI, and 0.85±0.06 between line I and line DI. Within line heritability estimates for farrowing rate were 0.06±0.01 for line D, 0.07±0.01 for line I, and 0.02±0.01 for line DI. Heritability estimates for farrowing rate, obtained from the crossbred model, were 0.07±0.01 for line D, 0.07±0.01 for line I, and 0.10±0.04 for line DI. Genetic correlations for farrowing rate were 0.57±0.57 between line D and line DI, and 0.50±0.25 between line I and line DI.
Estimates for genetic variation in litter size almost doubled (0.76 to 1.36) and for farrowing rate more than quadrupled (0.02 to 0.12) when pure line data were added to the crossbred dataset. Genetic correlations between pure line and crossbred data were (considerably) less than unity. These results indicate that pig breeders are advised to introduce crossbred data in their routine evaluations to increase genetic progress at commercial level.

Key Words: pig breeding, crossbred model, reproduction

431 Genetics-nutrition interactions influencing wool spinning fineness in Australian crossbred sheep. A. E. O. Malau-Aduli* and B. Holman, *School of Agricultural Science/TIAR, University of Tasmania*, *Hobart, Tasmania 7001, Australia*.

Our objective in this study was to investigate the interactions between sire genetics, supplement and gender on spinning fineness (SF) in crossbred sheep either grazing or supplemented with dietary protein. Correlations between SF and other wool traits were also investigated. We utilized 5 sires (Texel, Coopworth, White Suffolk, East-Friesian and Dorset) and mated them with 500 Merino ewes at a ratio of 1:100 in individual paddocks. Five hundred of the F1 progeny were raised on rye grass until weaning at 12 weeks of age. Forty of the weaners with initial BW range of 23–31kg (average of 27 ± 3.2 kg) were subjected to a supplementary feeding trial that lasted for 6 weeks. They were randomly assigned to 4 treatment groups in a 5 × 2 × 2 × 2 factorial experimental design representing 5 sire breeds, 2 supplementary feeds (canola and lupins), 2 feeding levels (1 and 2% BW) and 2 sexes (ewes and wethers). SF of the wool was commercially measured at the Australian Wool Testing Authority. The data were statistically analyzed in SAS using MIXED models procedures with sire fitted as a random effect, while sire breed, supplement, level of supplementation and gender and their interactions were fitted as fixed effects. We found highly significant interactions between sire breed × level of feeding ($P < 0.0043$) and sire breed × gender ($P < 0.019$) on SF that ranged from 22.7 ± 0.16 microns in White Suffolk-sired progeny to 25.1 ± 0.21 in East-Friesian crosses. Coopworth-sired sheep supplemented with either canola or lupins at 1%BW recorded the highest spinning fineness. There were significant correlations between SF and wool fiber diameter (0.93), CV of fiber diameter (−0.40), wool curvature (−0.12) and wool yield (0.10). We concluded that the significant interactions between sire genetics and nutrition would impact on choices sheep farmers make in selecting sires and supplementary feeding levels to achieve desirable spinning fineness in their crossbreds. The correlations between spinning fineness and other wool traits should be taken into account when designing breeding programmes.

Key Words: spinning fineness, wool, sheep

432 Effects of index selection and sire breed on crossbred lamb growth and finishing. G. C. Márquez*[1], W. Haresign[2], M. H. Davies[3], R. Roehe[4], L. Bünger[4], G. Simm[4], and R. M. Lewis1,4, [1]*Virginia Polytechnic Institite and State University*, *Blacksburg,* [2]*Aberystwyth University*, *Wales, UK*, [3]*ADAS Rosemaund*, *Preston Wynne, England, UK*, [4]*Scottish Agricultural College*, *Edinburgh, Scotland, UK*.

A lean growth index (LGI) was developed in the UK for terminal sire sheep to increase carcass lean weight keeping fat constant. High and low LGI rams were progeny tested to evaluate the effectiveness of the LGI in improving growth and carcass of their crossbred progeny reared commercially. From 1999 to 2002, Charollais (CH), Suffolk (SF) and Texel (TX) rams were selected for high or low LGI score, differing 5 SD on average. Across years, 15 high and 15 low LGI sires from each breed (90 total) were mated to 4,800 crossbred ewes at 3 farms in the UK. Most rams were used for 2 mating seasons, with some rotated among farms to create genetic links. Live weight of 6,515 lambs was recorded at birth (BWT), 5 weeks (5WK), 10 weeks (10WK), and finishing (FWT) at approximately 11% subcutaneous fat. Data were analyzed with a mixed model in SAS to investigate effects of sire index and breed on body weight and finish age (FAGE). Fixed effects were sire index and breed, their interaction, sex, dam breed, dam age, birth-rearing rank, farm and year, and their interaction. Covariates were d within lambing season for BWT, age for 5WK and 10WK, and subcutaneous fat percentage for FAGE and FWT. Rearing dam and residual were fitted as random effects. Lambs from high vs. low LGI sires were 0.07 ± 0.017, 0.3 ± 0.06, 0.4 ± 0.08, and 1.1 ± 0.1 kg heavier at BWT, 5WK, 10WK, and FWT, respectively. The SF sired lambs were heavier at BWT, 10WK and FWT ($P < 0.05$), while SF and TX lambs were heavier than CH lambs at 5WK ($P < 0.01$). High and low LGI sires did not differ for FAGE ($P > 0.1$), and TX sired lambs finished faster ($P < 0.01$). Birth-rearing rank influenced FAGE ($P < 0.01$): single born and reared lambs finished at 119 ± 1.9 d, multiple born, single reared at 154 d ± 2.1 d, and multiple born and reared at 189 ± 1.1 d. Multiple born and reared lambs from high LGI sires required 2.5 ± 1.2 more d to finish, with breed differences persisting. Selection of sires on LGI produced lambs that were heavier at all ages, and at finish. Irrespective of sire LGI, lambs reared

as singles took the same time to finish but offspring of high LGI lambs sires reared as multiples finished significantly later.

Key Words: sheep, selection index

433 Inclusion of the inbreeding coefficient into models for genetic evaluation of dairy cattle. C. A. García-Munguía, A. Ruíz-Flores*, R. Núñez-Domínguez, R. Ramírez-Vlaverde, and R. López-Ordaz, *Universidad Autónoma Chapingo*, *Chapingo, México, México*.

The objective was to evaluate the effect of the inclusion of the inbreeding coefficient (F) into the models to predict breeding values (BV) of Jersey (J) and Brown Swiss (BS) Mexican dairy cattle. In J the conventional model that included the fixed effect of herd-year-season, and the random genetic additive, permanent environmental, and residual effects; was compared with an alternative model that additionally included F. In BS the models also included the linear covariable of upgrading level, and the linear and quadratic covariables of age of cow at calving. The traits analyzed in J were milk (MY), fat and protein yields per lactation, and the percentages of fat and protein (%P) in milk. In BS only MY was studied. The analyses were done using an animal model and the MTDFREML program. The pedigrees for J and BS included 21,026 and 101,861 animals. Several criteria to compare the results from the alternative models were used. The effect of the inclusion of F into the models depended on the criterion of comparison and the trait. The most notorious change was for the BV for %P in J; the BV for the other traits remained essentially the same with the 2 models in both breeds. The percentage of coincidence among the top 100 sires evaluated with the 2 models ranged from 90 to 98% for all traits. The regression coefficients of BV and their accuracies from the conventional model on the BV and their accuracies from the alternative model ranged from 0.96 to 1.10, and from 1.00 to 1.01, respectively. For the 2 alternative models, the variance components and h^2 estimates were essentially the same. The results suggest that inclusion of F into the models to evaluate genetically Jersey and Brown Swiss Mexican dairy cattle is not necessary.

Key Words: inbreeding coefficient, genetic evaluation, Brown Swiss

434 Jersey-sired and Montbeliarde-sired crossbred heifers compared to pure Holstein heifers for survival and fertility from birth to first parturition. A. R. Hazel*, L. B. Hansen, B. J. Heins, A. J. Seykora, D. G. Johnson, and J. G. Linn, *University of Minnesota*, *St. Paul*.

Jersey x Holstein crossbred (JH) heifers (n = 91) were compared with pure Holstein (HO) heifers (n = 87). Also, Montbeliarde × Holstein crossbred (MH) heifers (n = 66) and Montbeliarde/(Jersey x Holstein) crossbred ((MJH) heifers (n = 101) were compared with HO heifers (n = 188) for survival to 90d, 365d, and to first parturition; days to first service; first service conception rate; interval from first to last service; number of services; age at conception; and gestation interval to first calving. The heifers were born at 2 research facilities of the University of Minnesota, and JH and HO contemporary heifers were born from September 2001 to June 2003, and MH, MJH and contemporary HO heifers were born from September 2003 to May 2008. JH heifers were mated to Montbeliarde AI sires, MH heifers were mated to Jersey AI sires, and MJH and HO heifers were mated to HO AI sires. Independent variables for all traits included breed group. Also, 2-breed versus 3-breed crossbreds nested within breed group was an independent variable for the MO crossbreds. Additionally, effects of location and year of birth were considered. JH and HO heifers did not differ significantly for survival to 90d, 365d, or to first parturition. MH (94.2%) and MJH (94.2%) were similar to HO (91.3%) heifers for survival to 90d. For survival to 365d and to parturition, MH and MJH were similar to HO heifers. Age at first breeding tended ($P < 0.07$) to be less for JH (437d) compared with HO (445d) heifers. MJH (429d) were significantly ($P < 0.05$) younger at first breeding than HO (440d) heifers. For first service conception rate, MH (63.5%) were significantly higher than HOL (48.4%) heifers. Age at conception was significantly ($P < 0.05$) less for JH (462d) than HO (484) heifers. MJH were significantly ($P < 0.01$) younger at conception than HO heifers (457 d versus 480 d). The MH heifers, carrying Jersey-sired calves, and the MJH heifers, carrying HO-sired calves, had longer ($P < 0.01$) gestation length than pure HO heifers (280 d versus 278 d, respectively).

Key Words: crossbreeding, survival, Montbeliarde

435 Productivity over five lactations of Normande, Montbeliarde, and Scandinavian Red crossbreds compared to pure Holsteins in commercial dairies in California. B. J. Heins* and L. B. Hansen, *University of Minnesota*, *Saint Paul*.

Normande (NM) × Holstein (HO) crossbreds (n = 245), Montbeliarde (MO) × HO crossbreds (n = 494), and Scandinavian Red (SR) × HO crossbred (n = 328) cows were compared with pure HO (n = 380) cows for 305-d milk, fat, and protein production and SCS during their first 5 lactations. Cows were housed in 7 commercial dairies in California and calved from June 2002 to January 2009. All HO sires and HO maternal grandsires of all cows were required to have a code assigned by the National Association of Animal Breeders to assure they were sired by AI bulls. The SR was a mixture of Swedish Red and Norwegian Red. Best Prediction was used to calculate actual production (milk, fat, and protein) for 305-d lactations. Adjustment was made for age at calving and milking frequency, and records less than 305 d were projected to 305 d. Independent variables for statistical analysis were the fixed effects of parity, herd-year-season (4-mo seasons within the 7 herds) nested within parity, the genetic level of HO maternal grandsire (linear), genetic group, parity nested within genetic group, and cow within genetic group, which was a random effect. During first lactation, the SR × HO (637 kg) cows were not significantly different from the pure HO (646 kg) cows for fat plus protein production; however, the NM × HO (597kg) cows and the MO × HO (623 kg) cows had significantly ($P < 0.05$) lower fat plus protein production than pure HO cows. Pure HO cows were significantly ($P < 0.05$) higher for fat plus protein than all crossbred cows during second and third lactation. Pure HO (808 kg) cows had significantly ($P < 0.05$) greater fat plus protein than NM × HO (723 kg) and SR × HO (774 kg) cows during fourth lactation. The MO × HO and SR × HO cows were not significantly different from pure HO cows for fat plus protein production during fifth lactation. Pure HO cows and all crossbred cows were not significantly different for SCS for first to fourth lactation, however, during fifth lactation the NM × HO (3.70), MO × HO (3.46), and SR × HO (3.74) cows had significantly ($P < 0.05$) less SCS than pure HO (4.14) cows.

Key Words: crossbreeding, heterosis, production

436 Death rates, survival rates to 5th lactation, and profitability of Normande, Montbeliarde, and Scandinavian Red crossbreds compared to pure Holsteins. B. J. Heins* and L. B. Hansen, *University of Minnesota*, *Saint Paul*.

Normande (NM) × Holstein (HO) crossbreds (n = 251), Montbeliarde (MO) × HO crossbreds (n = 503), and Scandinavian Red (SR) × HO crossbred (n = 321) cows were compared with pure HO (n = 416) cows for death rate and survival to calving a second, third, fourth, and fifth time. Cows were housed in 6 commercial dairies in California and

calved from June 2002 to January 2009. All HO sires and HO maternal grandsires of cows were required to have a code assigned by the National Association of Animal Breeders to assure they were sired by AI bulls. The SR was a mixture of Swedish Red and Norwegian Red. All cows had the opportunity to calve at least 3 times. Four cows (2 HO and 2 SR) did not have the opportunity to calve a fourth time, and 71 cows (10 HO, 4 NM × HO, 33 MO × HO, and 24 SR × HO) cows did not have the opportunity to calve a fifth time. A chi-squared test was conducted for all traits. Ten of 1,075 crossbred cows (0.9%) died before first observation for milk recording, however, 15 of 416 pure HO (3.6%) died before first observation for milk recording. Pure HO (5.3%) cows had significantly ($P < 0.05$) higher death rate on farm than NM × HO (1.2%) cows, MO × HO (2.0%) cows, and SR × HO (1.6%) cows during the first 305-d of first lactation. All crossbred groups had ($P < 0.01$) significantly more cows calving a second, third, fourth, and fifth time than pure HO cows. For pure HO cows, 77% calved a second time; 59% calved a third time, 35% calved a 4 time, and 18% calved a fifth time. Percentage of cows calving a second, third, fourth, and fifth time for NM × HO (88%, 70%, 51%, 28%) cows, MO × HO (88%, 70%, 52%, 32%) cows, and SR × HO (86%, 69%, 50%, 28%) cows were significantly higher than pure HO cows in all cases.

Key Words: crossbreeding, heterosis, reproduction

437 Production, reproduction, health and growth traits in backcross Holstein x Jersey and their Holstein contemporaries. D. W. Bjelland*, N. M. Esser, K. A. Weigel, and P. C. Hoffman, *University of Wisconsin*, *Madison.*

A total of 172 purebred Holsteins and 177 backcross Holstein x Jersey dairy cattle were compared for production, reproduction, health, and growth traits. These animals were born between 2003 and 2006 and were housed in the University of Wisconsin - Madison experimental herd. All animals had Holstein dams, which had been mated to either Holstein sires to produce purebred Holsteins or Jersey × Holstein crossbred sires to produce the backcross animals. Traits were analyzed using a linear mixed model with effects of season of birth, age of dam, pen number as a heifer, sire, birth year of sire, and days in milk. Holsteins had significantly ($P < 0.05$) greater 305-d milk yield (9230 vs. 8311 kg), 305-d mature equivalent milk yield (10836 vs. 9632 kg), peak daily milk yield (35 vs. 32 kg), total milk yield (8913 vs. 7682 kg), and total protein yield (284 vs. 267 kg) compared with the crossbreds. Days open (152 vs. 162 d), services per conception as a heifer (1.43 vs. 1.40) or first parity cow (1.70 vs. 2.03) did not differ, but the proportion of first parity births with calving ease score ≥3 was significantly less in Holsteins than in crossbreds (11 vs. 32%). Health traits included incidence of scours and respiratory problems as a heifer and incidence of mastitis, feet problems and injury during first lactation. Holsteins had a significantly higher incidence of injury (39 vs. 22%) and scours (30 vs. 23%) and a lower incidence of respiratory problems (5 vs. 18%). Holsteins were significantly heavier (630 vs. 559kg), with greater hip height (145 vs. 139 cm), body length (167 vs. 163 cm), heart girth (205 vs. 198 cm), and hip width (55 vs. 53 cm) at 22 mo of age. Results of this study suggest that backcross Holstein × Jersey have decreased production but fail to demonstrate an advantage in health and reproduction when compared with purebred Holsteins.

Key Words: crossbreeding, backcross, Jersey

438 Multibreed genomic evaluation of dairy cattle. K. M. Olson*[1] and P. M. VanRaden[2], [1]*Virginia Polytechnic Institute and State University*, *Blacksburg,* [2]*Animal Improvement Programs Laboratory, ARS, USDA*, *Beltsville, MD*.

Multibreed models are currently used in traditional USDA dairy cattle genetic evaluations of yield and health traits, but within-breed models are used in genomic evaluations. Multibreed genomic models were developed and tested using all 19,686 genotyped bulls included in the official August 2009 USDA genomic evaluation. The data were divided into training and validation sets. The training data set were comprised of bulls that were proven (had daughter information) as of November 2004 and totaled 5,331, 1,361, and 506 Holstein, Jersey, and Brown Swiss, respectively. The validation data set had 2,477 Holstein, 410 Jersey, and 182 Brown Swiss bulls that were unproven (no daughter information) in November 2004 and proven by August 2009. A common set of 43,385 single nucleotide polymorphisms (SNP) were used for all breeds. Three methods of multibreed evaluation were investigated. Method 1 estimated SNP effects separately within-breed and was tested by multiple regressions to predict daughter deviations of bulls of another breed. Method 2 estimated a common set of SNP effects from combined genotypes and phenotypes of all breeds. Method 3 solved for correlated SNP effects within each breed estimated jointly using a multitrait model. Multiple regressions were used to test across-breed genomic predicted transmitting ability (GPTA) with within-breed GPTA and parent average (PA). A few effects were significant with method 1, mostly for Jerseys and Holsteins, but estimates were small compared with within-breed GPTA and PA. Across-breed GPTA from method 2 were significant for certain traits in some breeds; correlations between within-breed GPTA and across-breed GPTA ranged between 0.91 and 0.93. Results from method 3 were significant and adjusted coefficient of determinations for protein yield (the only trait tested for method 3) were highest of all methods for all breeds. However, compared with the current within-breed genomic model, method 3 increased the adjusted coefficient of determination by only 0.0097, 0.0042, and 0.0017 for Brown Swiss, Jerseys, and Holsteins, respectively.

Key Words: dairy cattle, genomic evaluation, multibreed

Food Safety: Poultry Aspects

439 Hide and pen floor contamination and transmission of *Escherichia coli* O157:H7 among feedlot steers. K. Stanford*[1], T. P. Stephens[1], and T. A. McAllister[2], [1]*Alberta Agriculture and Rural Development*, *Lethbridge, Alberta Canada*, [2]*Agriculture and Agri-Food Canada*, *Lethbridge, Alberta Canada*.

Super-shedders, cattle shedding at least 10^4 colony forming units (CFU) of *E. coli* O157:H7, elevate risks of contaminating the food chain and maintaining the organism in cattle populations. As detecting super-shedders in cattle populations is laborious and time-consuming, a study was conducted to evaluate the role of hide and pen-floor contamination by model super shedders (MSS) in transmission of *E. coli* O157:H7 to penned cattle. Steers (n = 48) negative for *E. coli* O157:H7 for 3 wks were allocated to 6 pens, with 2 replicate pens per treatment. Treatment A consisted of 3000 g of feces inoculated with 10^6 CFU spread in artificial fecal pats on the pen floor for d 0 through 4 and 14 through 18 of the study. For treatment B, 100 g of the feces was spread on the perineum of 1 MSS per pen and the remaining feces spread on the pen floor similar to treatment A. Treatment C differed from B in that 50 g of feces was spread on the perineum and 50 g on the brisket of the MSS. Fecal samples, perineal swabs (500 cm^2 area of the rump), freshly voided fecal pats and manila rope samples were collected during the 56 d experimental period. More positive rope samples were found in treatments B and C as compared with A ($P < 0.05$) and steers within treatments B and C were 1.3 times more likely ($P < 0.05$) to shed *E. coli* O157:H7 in their feces than steers in treatment A. Even though loads of *E. coli* O157:H7 were similar in pens, results indicate a heightened importance of hide as compared with pen floor contamination for transmission of this organism to cattle. As cattle within treatments B and C were persistently colonized with *E. coli* O157:H7, this model would be suitable for future studies investigating mitigation of *E. coli* O157:H7 transmission by super-shedders.

Key Words: *Escherichia coli* O157:H7, feedlot cattle, super-shedder

440 Feed supplementation with caprylic acid reduces *Campylobacter* colonization in market aged broiler chickens without altering cecal microbial populations. I. Reyes-Herrera*[1], F. Solis de los Santos[1], M. Hume[2], K. Venkitanarayanan[3], A. M. Donoghue[4], I. Hanning[1], M. F. Slavik[1], V. F. Aguiar[1], J. H. Metcalf[1], P. J. Blore[1], and D. J. Donoghue[1], [1]*Dept. Poultry Science, University of Arkansas,*, *Fayetteville,* [2]*Food and Feed Safety Research Unit, Southern Plains Agricultural Research Center, USDA-ARS*, *College Station, TX,* [3]*Dept. Animal Science, University of Connecticut*, *Storrs,*[4]*Poultry Production and Product Safety Research Unit, USDA-ARS*, *Fayetteville, AR*.

Campylobacter is a leading cause of food-borne illness in the United States and epidemiological evidence indicates that poultry products are a significant source of human infections. Caprylic acid is an 8-carbon medium chain fatty acid which has been reported by our laboratories to reduce *Campylobacter* colonization in chickens. The mechanism of action of caprylic acid, however, has not yet been determined but may be due to changes in the intestinal microflora. To evaluate this possibility, cecal microbial populations were evaluated using denaturing gradient gel electrophoresis (DGGE) in market age broiler chickens fed caprylic acid. In the first trial (n = 40 per trial) chicks were assigned to 4 treatment groups (n = 10 birds per treatment group): Positive controls (*Campylobacter*, no caprylic acid) with or without a 12 h feed withdrawal before slaughter; 0.7% caprylic acid supplemented in feed for the last 3 d of the trial with or without a 12 h feed withdrawal before slaughter. Treatments were similar for Trial 2, except caprylic acid was supplemented for the last 7 d of the trial. On d 14 of age, chicks were orally challenged with *C. jejuni* and on d 42, ceca were collected for DGGE and *Campylobacter* analysis. Caprylic acid supplemented for 3 or 7 d at 0.7% reduced *Campylobacter* compared with the positive controls (approx. Three log reduction), except for the 7 d treatment with a 12 h feed withdrawal period. DGGE profiles of the cecal content showed that caprylic acid had little, if any, effect on the cecal microbial community. The results of this study indicate that caprylic acid′s ability to reduce *Campylobacter* does not appear to be due to changes in cecal microflora.

Key Words: *Campylobacter*, caprylic acid, DGGE

441 Evaluating the prevalence and distribution of *Campylobacter* in newly constructed broiler houses. K. N. Eberle*[1], J. L. Purswell[2], J. D. Davis[1], C. D. McDaniel[1], and A. S. Kiess[1], [1]*Mississippi State University*, *Mississippi State,* [2]*USDA-ARS Poultry Research Unit*, *Mississippi State*.

In 2009, the USDA Food Safety and Inspection Service announced the development of new pathogen reduction performance standards for *Salmonella* and *Campylobacter* both on-farm and in the processing plant. The objective of this study was to evaluate the prevalence and distribution of *Campylobacter* in 3 newly constructed broiler houses for the first 4 flocks placed to determine the necessity for on-farm regulation. Litter and fecal samples were collected from each house at 0, 28, and 48 d of production. Samples were serially diluted and spread onto Campy Cefex agar plates. Two 40-mL water samples were collected each production day and filtered through a 0.45 µm membrane before being placed onto a Campy Cefex agar plate. All plates were purged with a microaerophilic gas and incubated for 36 h at 42°C. Individual plates were screened for characteristic *Campylobacter* colonies and suspect colonies were confirmed using a latex agglutination kit. An additional 50 g of litter was collected from the evaporative cooling inlets, middle, and tunnel ventilation fans to determine litter moisture and pH. Inside and outside temperature and humidity were collected using a weather station. Out of 2300 litter, 900 fecal, and 45 water samples, only 5, 6 and 1 of the collected samples respectively were confirmed *Campylobacter* positive. Litter moisture was different depending on location: the middle contained a higher moisture level (37%) than the evaporative cooling inlets (33%) and tunnel ventilation fans (34%) ($P < 0.05$). Litter pH was not different for day, location or flock. Temperature and humidity averaged 26.8°C and 69.3% inside and 27.6°C and 60.6% outside. In conclusion the newly constructed houses did not show a high prevalence of *Campylobacter*. Litter moisture and humidity were at levels conducive for *Campylobacter* growth. The high litter pH and low temperatures, along with other on-farm management strategies, may have suppressed the ability of *Campylobacter* to colonize the litter.

Key Words: *Campylobacter*, litter, broiler house

442 Colonization of marker and field strains of *Salmonella* Enteritidis and Typhimurium in antibiotic pretreated and non-pretreated laying hens. J. F. Hannah*[1], J. L. Wilson[1], N. A. Cox[2], L. J. Richardson[2], J. A. Cason[2], and R. J. Buhr[2], [1]*University of Georgia, Department of Poultry Science*, *Athens*, [2]*USDA, ARS, Richard Russell Research Center*, *Athens, GA*.

A study was conducted to evaluate the effects of a vancomycin (VNC) pretreatment on the ability of marker (nalidixic acid-resistant) *S*. Enteritidis (SE^M), field *S*. Enteritidis (SE^F), or marker *S*. Typhimurium (ST^M) to colonize within the intestinal and reproductive tracts and translocate to other internal tissues of laying hens. In each of 3 trials, caged hens (76, 26, and 33 wk-of-age) were divided into 6 groups designated to receive SE^M, SE^F, or ST^M, and half pretreated with VNC (n = 12). VNC treated hens received 0.5 mL for 5 d to inhibit gram-positive bacteria. On d 6, all hens were challenged orally, intravaginally and intracolonally with *Salmonella* and placed into separate floor pens on new wood shavings. Two wk post-inoculation, all hens were killed and samples aseptically collected from the ceca, spleen, liver/gallbladder (LGB), upper (URT) and lower (LRT) reproductive tracts, and ovarian follicles, and cultured for *Salmonella*. Results for the 3 hen ages were combined, and Chi-squared and Fisher's exact test were used to identify significant differences ($P < 0.05$) in colonization. Among tissues sampled, there were no significant differences in SE^M, SE^F, and ST^M colonization between VNC pretreated and non-pretreated hens. For the ceca, spleen, and LGB samples, SE^F (83, 100, and 100%) and ST^M (100, 73, and 91%) colonization was significantly greater than SE^M (8, 0, and 8%) colonization in non-pretreated hens. For VNC pretreated hens, SE^F (92, 92, and 83%) and ST^M (100, 75, and 83%) colonization among ceca, spleen, and LGB samples was significantly greater than SE^M (36, 0, and 0%) colonization. Overall colonization of *Salmonella* in the LRT samples was relatively low, ranging from 8 to 42% and SE^F and ST^M were isolated from 8 and 18% URT samples, respectively. Only SE^F (8–17%) was isolated from the ovarian follicles. In conclusion, the VNC pretreatment had no significant effect on the level of colonization of SE^M, SE^F, or ST^M in the tissues evaluated, and these results may provide further understanding of *Salmonella* ecology within laying hens.

Key Words: *Salmonella* colonization, vancomycin, laying hens

443 Evaluation of *Campylobacter* challenge route (in ovo vs. crop) and feed additives to reduce cecal *Campylobacter* in broilers. T. A. Scott*, J. E. de Oliveira, and E. Hangoor, *Provimi Feed Solutions*, *Sint-Stevens-Woluwe, Belgium*.

The objective was to compare challenge route to establish *Campylobacter* in the ceca of broilers and then the efficacy of additives to reduce this reservoir of contamination. Twelve treatment groups (8 cages of 7 male Ross 308 broilers) were evaluated, representing 2 challenge routes (in ovo E17d; gavage to the crop at 3d post hatch) and 6 additives (None, Antibiotic, Adhesion, Probiotic, MCFA and Organic acid). Based on preliminary experiments the optimum in ovo dose of *Campylobacter jejuni* was determined to provide cecal colonization; one half of the chicks were thus infected and then randomized in respective cages separated from other cages by solid plastic sheets 30cm in height. The remaining cages were housed with chicks from the same egg source, but hatched in a commercial hatchery to avoid cross contamination. All chicks were given ad libitum access to feed (6 diets) and water. A basal mash diet, formulated to meet or exceed the NRC broiler requirements was divided into 6 groups and remixed with appropriate feed additive, the chicks were maintained on diets to 18d of age. At 3 d, a excreta (collected on paper for 4 h) sample from each cage was used to establish presence of *Campylobacter*; all cages from in ovo chicks, except those fed an antibiotic were 100% positive; only 3 of the 48 non challenged cages were positive demonstrating low cross contamination. Body weight (18d) was significantly impacted by challenge route (3d Crop > in ovo) and additive (Antibiotic > MCFA = Organic Acid = None = Adhesion > Probiotic), and reflected similar differences in feed intake and FCR. At 11 and 18 d of age 4 broilers/cage (32 / treatment) were monitored for presence of *Campylobacter* by cloacal swab and cecal content swab, respectively. There were no significant differences in number of contaminated birds due to challenge route, although this was numerically higher for in ovo treated birds. Only the Antibiotic diet caused a significant reduction in *Campylobacter* at 11 and 18d of age, the None treated diet was numerically the highest, but not different from Organic Acid = Adhesive = Probiotic = MCFA.

Key Words: *Campylobacter*, in ovo challenge, broilers

444 The efficacy of the natural plant extracts, thymol and carvacrol, against *Campylobacter* colonization in broiler chickens. K. Arsi*[1], J. H. Metcalf[1], I. Reyes-Herrera[1], A. M. Donoghue[2], K. Venkitanarayanan[3], P. J. Blore[1], A. C. Fanatico[1], and D. J. Donoghue[1], [1]*Dept. Poultry Science, University of Arkansas*, *Fayetteville,* [2]*Poultry Production and Product Safety Research Unit, USDA-ARS*, *Fayetteville, AR,*[3]*Dept. Animal Science, University of Connecticut*, *Storrs*.

Campylobacter is one of the most common causes of foodborne bacterial gastroenteritis in the US. Case control studies have demonstrated that consumption or handling of raw or under-cooked poultry products can be directly linked to human campylobacteriosis. Incidence of *Campylobacter* in broiler flocks can range from 70 to 100%, thus a reduction of this pathogen in poultry would greatly reduce the incidence of human disease. Unfortunately, most treatments fail to produce consistent reductions in *Campylobacter* colonization in chickens. Natural plant extracts, such as thymol and carvacrol, have been tested against pathogens like *Salmonella, E. coli, Shigella, Listeria* but their ability to reduce *Campylobacter* in chickens has not been reported. The objective of this study was to determine the efficacy of different concentrations and combinations of thymol and carvacrol in feed to reduce *C. jejuni* in broilers. To evaluate in vivo efficacy, day of hatch birds were feed 0% (controls) or 0.0625, 0.125, 0.25, 0.5, 1.0 or 2.0% thymol or carvacrol or combinations of both (n = 10 chicks/dose). Birds were orally challenged with 5 different *C. jejuni* strains at d 3 and at d 10, cecal samples were collected for *Campylobacter* enumeration. Four different trials were conducted. Data were analyzed by ANOVA using the GLM procedure of SAS and a probability of $P < 0.05$ was required for statistical significance. Significant reductions of *C. jejuni* were observed with 0.25% or 2% thymol, and for 1% or 2% carvacrol. A 2-log reduction was observed with the combination of 0.5% thymol and 0.5% carvacrol. However, treatments did not always produce consistent reduction in *C. jejuni* between trials. These results justify the potential application of these compounds to control *Campylobacter* in chickens, but additional experiments are required to determine the most consistently effective concentrations and combinations of these plant extracts.

Key Words: *Campylobacter*, natural plant extracts, carvacrol/thymol

445 Probability of identifying different *Salmonella* serotypes in poultry samples. J. A. Cason*, N. A. Cox, R. J. Buhr, D. V. Bourassa, and L. J. Richardson, *Russell Research Center, USDA/ARS*, *Athens, GA*.

Recent work has called attention to the unequal competitive abilities of different *Salmonella* serotypes in standard broth culture and plating media. Such serotypes include Enteritidis and Typhimurium that are specifically targeted in some regulatory and certification programs because they cause a large proportion of human salmonellosis. Common lab methods recommend selecting 3 to 5 colonies per plate, but surveys show that many laboratories pick and identify only 1 probable *Salmonella* colony from poultry samples. To explore the implications of *Salmonella* serotypes surviving and growing at different rates during culture and

isolation, spreadsheet formulas were used to calculate binomial and multinomial probabilities of picking serotypes present at various ratios on plates, assuming that 100% of picked colonies are *Salmonella*. When 2 serotypes are present in equal numbers, 6 colonies must be picked to have a 95% probability of finding both serotypes. To identify 3 serotypes under the same conditions, 11 colonies must be picked. If a serotype is outnumbered 10 to 1 by another serotype on a plate, a ratio that has been reported in the scientific literature, 32 colonies must be picked to have a 95% probability of finding the minority serotype. Relatively small survival and growth rate differences can produce large changes in the likelihood of picking a colony of a particular serotype even when that serotype was present in the original sample in equal numbers, so picking one colony per plate can give a distorted picture of what serotypes are in samples. Given the labor and expense of isolating and serotyping suspect *Salmonella* colonies, methods are needed for culturing specific serotypes of interest.

Key Words: *Salmonella*, serotypes, colonies

446 The effect of electrostatic polarization ultraviolet light filters on *Enterobacteriaceae*, and *Salmonella* spp. bacteria in a broiler processing plant hang room. J. C. Butler*, P. A. Curtis, C. R. Kerth, D. E. Conner, and L. K. Kerth, *Auburn University*, *Auburn, AL*.

Poultry processing hang rooms are one of the dirtiest areas of a processing plant. To determine the bioaerosols in the hang room of a particular processing plant, 3 electrostatic polarization light filters utilizing UV light were mounted on 3 different walls of the hang room. Over a period of 24 sampling days, the filters were turned on or off and air and settle plate samples were taken of the air in the room to test for Glucose- and Lactose-fermenting *Enterobacteriaceae*, and *Salmonella spp.* Relative humidity, temperature and wind speed were also taken inside and outside the hang room and number of workers in the room and number of fans on were also noted. Samples were taken every 0, 3, 6, or 9 h into the processing shift. *Enterobacteriaceae*, (Lactose and Glucose) levels were not affected ($P > 0.05$) by filter position. *Salmonella* was low in counts sampled for at all positions, but were not different from one another when comparing position location within the bacteria. The filters had no impact on airborne *Enterobacteriaceae*, (Lactose) during sampling hours 0, 3, and 9 ($P > 0.05$). Results showed a significant decrease for both *Enterobacteriaceae*, bacteria at the 9h sampling period. These results may be indicative of a shift change occurring in between the 6 and 9h where new workers were introduced to the environment. *Salmonella* positive counts were not significantly different regardless of filter use or hour. In general, all of the bacterial counts were low, only reaching approximately 2 logs at their highest. The environmental factors accounted for did not attribute to a large amount of variation for any bacteria sampled. Although, position of the filters were highly correlated for both *Enterobacteriaceae*, types.

Key Words: poultry, bioaerosols, *Enterobacteriaceae*

447 Role of lauric acid-potassium hydroxide concentration on bacterial contamination of spray washed broiler carcasses. A. Hinton Jr.*, J. Cason, R. Buhr, and K. Liljebjelke, *Russell Research Center*, *Athens, GA*.

A series of experiments were conducted to examine reductions in bacterial contamination of broiler carcasses washed in a spray cabinet with various concentrations of lauric acid (LA)-potassium hydroxide (KOH) solutions. Fifty eviscerated carcasses and 5 ceca were obtained from the processing line of a commercial poultry processing facility. An inoculated cecal paste was prepared by mixing 5 g of cecal contents with 0.3 mL of a bacterial suspension containing 10^8 cfu/mL each of antibiotic resistant strains of *Escherichia coli*, *Salmonella* Typhimurium, and *Campylobacter coli*. A 0.1 g portion of the inoculated cecal paste was applied to the skin of each carcass and allowed to dry for 15 min. Inoculated carcasses were then divided into 5 groups of 10 carcasses each, and groups were spray washed with water, 0.25% LA-0.125% KOH, 0.5% LA-0.25% KOH, 1% LA-0.5% KOH, or 2% LA-1% KOH at 80 psi (552 kPA) for 15 s. Washed carcasses were rinsed for 15 s with sterile, deionized water to remove excess LA-KOH before whole carcass rinses were performed for 2 min in 200 mL of sterile phosphate buffered saline. Total plate count bacteria (TPC) and antibiotic resistant *E. coli*, *Salmonella* Typhimurium, and *C. coli* in the rinsates were enumerated, and the pH of the rinsates was measured. Findings indicated that significantly fewer TPC bacteria, *E. coli*, and *Salmonella* Typhimurium were recovered from carcasses washed with 2% LA-1% KOH than from carcasses washed in water. Furthermore, significantly fewer *C. coli* were recovered from carcasses washed in 1% LA-0.5% KOH than from carcasses washed in water, and no *C. coli* were recovered from carcasses washed in 2% LA-1% KOH. The pH of rinsates from carcasses washed in water, LA-0.125% KOH, 0.5% LA-0.25% KOH, 1% LA-0.5% KOH, or 2% LA-1% KOH was 7.27, 7.41, 7.57, 8.00, and 9.94, respectively. Findings indicate that the concentration of LA-KOH plays an important role in the ability of this antibacterial surfactant to reduce bacterial contamination of broiler carcass.

Key Words: lauric acid, potassium hydroxide, spray washing

448 Antimicrobial effect of sodium metasilicate on *Salmonella enterica* serovar Typhimurium and psychrotrophs in ready to cook, skin-on chicken breast meat stored at 4 ± 1°C. C. S. Sharma*, S. K. Williams, and G. E. Rodrick, *University of Florida*, *Gainesville*.

The objectives of this study were to determine the antimicrobial effects of sodium metasilicate (SMS) against *Salmonella* Typhimurium and psychrotrophic organisms in fresh ready to cook skin-on chicken breasts, and to ascertain the effects of the treatments on pH. The chicken breasts were inoculated with *S.* Typhimurium (ATCC 14028), treated with 0% SMS and no inoculum (negative control), 0% SMS and inoculum (positive control), 1% and 2% SMS (w/w), packaged and stored at 4 ± 1°C. All samples were analyzed in duplicate after 0, 1, 3, 5 and 7 d of storage for recovery of *S.* Typhimurium, psychrotrophic organisms and pH measurements. The whole experiment was repeated 3 times. Treating the breast meat with 1% and 2% SMS resulted in low ($P < 0.05$) *Salmonella* counts when compared with the positive control. Chicken breasts treated with 1% and 2% SMS resulted in 1.1 to 1.4 and 2.5 to 4.1 log cfu/g reductions of *S.* Typhimurium, respectively, as compared with positive controls. Psychrotrophic counts for breast meat treated with 2% SMS were lower ($P < 0.05$) than the control samples on all sampling days except d 0. The pH values were higher ($P < 0.05$) for all SMS treatments when compared with the negative and positive controls. This study revealed that SMS could function to control the pathogen *S.* Typhimurium, and extend the shelf life of poultry by retarding the growth of psychrotrophic bacteria, which are the primary spoilage organisms in fresh poultry.

Key Words: sodium metasilicate, *Salmonella*, psychrotrophs

449 Antimicrobial effect of sodium metasilicate marinade on *Salmonella enterica* serovar Typhimurium and psychrotrophs in ready to cook skinless and boneless chicken breast meat stored at 4 ± 1°C. C. S. Sharma*, S. K. Williams, and G. E. Rodrick, *University of Florida*, *Gainesville*.

The objectives of this study were to determine the antimicrobial effects of sodium metasilicate (SMS) marinades against *Salmonella* Typhimurium and psychrotrophic organisms in fresh marinated ready to cook skinless and boneless chicken breast meat, and to ascertain the effects of the treatments on pH. The chicken breasts were inoculated with *S.* Typhimurium (ATCC 14028), marinated in solutions containing either 0% SMS and no inoculum (negative control), 0% SMS and inoculum (positive control), 1% or 2% SMS, packaged and stored at 4 ± 1°C. All samples were analyzed in duplicate after 0, 1, 3, 5 and 7 d of storage for recovery of *S.* Typhimurium, psychrotrophic organisms and pH measurements. Chicken breasts marinated with 1% and 2% SMS had lower ($P < 0.05$) *Salmonella* counts when compared with the positive control at 3 d storage and through 7 d. Chicken breasts treated with 1% and 2% SMS resulted in 0.83 to 0.91 and 1.04 to 1.16 log cfu/g reductions of *S.* Typhimurium, respectively, after 3 d through 7 d of storage as compared with positive controls. The psychrotrophic counts were similar ($P > 0.05$) for all treatments. The pH values for 1% and 2% SMS treatments were higher ($P < 0.05$) when compared with the controls. This study revealed that SMS could function to control the pathogen *S.* Typhimurium, but had no effect on reducing the spoilage microflora when it was used in the marinade.

Key Words: sodium metasilicate, *Salmonella*, psychrotrophs

450 Aviplus treatment improves growth efficiency in broilers and swine but does not affect intestinal populations of experimentally inoculated *Salmonella*. T. R. Callaway*[1], E. Grilli[2], T. S. Edrington[1], N. Krueger[1], R. Anderson[1], D. W. Pitta[3], W. E. Pinchak[3], and A. Piva[2], [1]*USDA/ARS, Food and Feed Safety Research Unit*, *College Station, TX,* [2]*University of Bologna*, *Bologna, Italy*,[3]*Texas A&M University Agrilife Research Station*, *Vernon*.

Organic acids improve growth efficiency in food animals, and can impact the microbial ecology of the gastrointestinal tract. Thus it has been suggested that they could be used to reduce foodborne pathogenic bacterial populations before animals enter the food chain. This study was undertaken to determine the effect of a commercial microencapsulated organic acid product on populations of experimentally inoculated Salmonella populations in swine and broilers. Broiler chicks (n = 192 in 2 replications; 1 d of age) were artificially inoculated with 10^6 CFU S. Typhimurium and randomly assigned to 0g, 0.2 kg, 2 kg, or 10 kg Aviplus/1000 kg feed diets. Feed consumption and weights were measured daily for 7 d. Salmonella populations were analyzed upon sacrifice but no differences in cecal Salmonella populations were found. Aviplus treatment at 0.2 kg/1000 kg feed increased ($P < 0.05$) pen weight, average body weight and average daily gain across the study. Aviplus inclusion at 0.2, 2, and 10 kg/1000 kg feed reduced ($P < 0.05$) feed to gain ratios as well. In another study, newly weaned pigs (7 d of age; n = 24) were blocked by sex and were randomly assigned to either 0g, 3 kg, or 30 kg Aviplus /1000 kg feed diets and fed for 14 d and were weighed and feed intake was measured daily. Pigs were artificially inoculated with 10^7 CFU S. Typhimurium and fecal samples were collected daily for 5 d until sacrifice. Intestinal contents from the rectum, cecum and ileum were collected, as well as ileocecal lymph nodes. No differences in Salmonella populations were found in any compartment, though rectal populations were reduced in swine fed 30 kg Aviplus/1000 kg feed. Feed efficiency (feed to gain) in pigs were increased ($P < 0.05$) by 3 kg Aviplus/1000 kg feed treatment, and ADG and BW was increased by 30 kg Aviplus/1000 kg feed treatment. Collectively, our results indicate that while Aviplus does not affect artificially inoculated Salmonella populations in vivo in these short-term studies, Aviplus treatment increased the feed efficiency of broiler chicks and newly weaned swine.

Key Words: food safety, organic acids

451 Aviplus treatment reduces *E. coli* and *Salmonella* populations in pure and mixed ruminal culture fermentations. T. R. Callaway*[1], E. Grilli[2], and A. Piva[2], [1]*USDA/ARS, Food and Feed Safety Research Unit*, *College Station, TX,* [2]*University of Bologna*, *Bologna, Italy*.

Foodborne pathogenic bacteria can live in the intestinal tract of cattle, swine and poultry and can be transmitted to humans through the food supply or indirectly through animal/fecal contact. Organic acid products have been used as non-antibiotic modifiers of the gastrointestinal fermentation of food animals to improve animal health and performance. However, the impact of these organic acid products on foodborne pathogens remains unknown. Therefore, this study was designed to examine the effects of a commercial organic acid product on populations of the foodborne pathogens, *Escherichia coli* O157:H7 and Salmonella Typhimurium. Pure cultures (2×10^3 CFU/mL) of each pathogen were added to tubes that contained water-solubilized Aviplus added at of 0, 0.1, 0.5, 1, 2, 5, and 10% (w/v; n = 4). Water-solubilized Aviplus reduced ($P < 0.05$) the growth rate and final populations of *E. coli* O157:H7 and S. Typhimurium in pure culture at concentrations greater than 2% w/v. In further in vitro studies, *E. coli* O157:H7 and S. Typhimurium were added to mixed ruminal bacterial fermentations collected from cattle fed a pasture-based diet. The in vitro fermentations contained water-solubilized Aviplus at concentrations of 0, 1, 2, 5, and 10% (w/v; n = 2) and were incubated for 24 h. Aviplus addition reduced ($P < 0.05$) final populations of *E. coli* O157:H7 and S. Typhimurium in the ruminal fluid at concentrations >5% w/v. The A:P ratios from the in vitro ruminal fermentations were reduced ($P < 0.05$) by solubilized Aviplus treatment and total VFA production was not affected, but methane and ammonia concentrations were decreased. Organic acid products, such as Aviplus, can alter the intestinal microbial ecology and enhance animal productivity and health. Under in vitro conditions, solubilized Aviplus can be used to reduce populations of pathogenic bacteria. Intervention strategies to reduce foodborne pathogens that can improve animal performance have the advantage of a food safety intervention that pays for itself financially.

Key Words: food safety, *Salmonella*, organic acids

452 Lamb and cow performance when fed corn silage that has reduced ferulate cross linking. H. G. Jung*[1,3], D. R. Mertens[2], and R. L. Phillips[3], [1]*USDA-ARS*, *St. Paul, MN,* [2]*USDA-ARS*, *Madison, WI,* [3]*University of Minnesota*, *St. Paul*.

Ferulate-mediated lignin/hemicellulose cross linking in grasses reduces in vitro NDF digestibility (IVNDFD). Impact of ferulate cross linking on animal performance was examined in lamb digestibility and dairy cow performance trials using the seedling ferulate ester (*sfe*) corn mutant that reduces cross linking and improves IVNDFD. Digestibility of control (W23) and 2 near-isogenic *sfe* (M04–4 and M04–21) silages was determined with lambs fed ad lib and restricted. Each silage was fed to 4 lambs as the sole ingredient. The same silages were fed to lactating cows in 37% corn silage diets formulated for 29% diet NDF and 70% of NDF from corn silage. A 28-d lactation trial was conducted with 14 cows per diet. Feed intake and milk production were determined. Both trials were analyzed as a randomized complete block using PROC MIXED. Orthogonal contrasts were used to compare W23 to *sfe* lines combined and M04–21 only. The *sfe* silages had fewer ferulate cross links than W23 (0.96, 0.86, and 0.81% of NDF in W23, M04–4, and M04–21, respectively), but the *sfe* mutants had higher NDF and ADL, and lower starch concentrations than W23. The IVNDFD of MO4–21 silage after 24-, 48-, and 96-h was greater than W23, while M04–4 IVNDFD was only greater after 24 h. Lamb ad lib silage intake was greater ($P < 0.05$) for W23 than *sfe* lines combined, but M04–21 did not differ from W23. Digestibility of DM was greater ($P < 0.05$) for W23 than *sfe* at ad lib but not restricted intake, whereas silages did not differ for NDF or starch digestibility at either intake. Lambs were less selective against NDF when fed *sfe* silages ad lib ($P < 0.05$) or restricted ($P < 0.10$). Intake (21.8, 23.4, and 23.3 kg/d for W23, M04–4, and M04–21, respectively) and milk production (38.9, 39.3, and 41.6 kg/d for W23, M04–4, and M04–21, respectively) were greater ($P < 0.01$) for cows fed the *sfe* containing diets. Diet refusals indicated cows selected less against NDF in the *sfe* diets than for W23 diets. The data suggest reduced ferulate cross linking in corn silage had a small positive impact on ruminant performance.

Key Words: ferulate, corn silage, NDF

453 Impact of brown midrib trait and seeding rate on chemical composition and in vitro gas production of pearl millet silage. F. Hassanat*[1], A. Mustafa[2], P. Seguin[3], and R. Berthiaume[1], [1]*Agriculture and Agri-Food Canada*, *Sherbrooke, QC, Canada*, [2]*Department of Animal Science, McGill University*, *Montreal, QC, Canada*, [3]*Department of Plant Science, McGill University*, *Montreal, QC, Canada*.

The impact of brown midrib trait and seeding rate on chemical composition, and in vitro gas production of millet (*Pennisetum glaucum*) silage was investigated in a 2 × 3 completely randomized factorial block design. Regular (RM, variety CFPM101) and brown midrib (BM, variety CFPBMR) millet were seeded at rates of 5, 10, and 15 kg ha^{-1}. Forages were harvested at vegetative stage (pre boot, 2m average height, 8 fully developed leaves) and ensiled in mini-silos for 28 d. Chemical composition of silages was determined as well as in vitro gas production profiles using 24 h incubation in Ankom^{RF} gas production monitoring system. Michaelis-Menten model was used to estimate gas production parameters. Chemical composition of solid and liquid incubation residues was used for degradability calculations. Results showed that both millet cultivars produced well preserved silage with an average pH of 4.2 and 120 g kg^{-1} lactic acid. Brown midrib millet silage contained 5.3% less neutral detergent fiber (NDF), and 32% less acid detergent lignin ($P < 0.05$) than RM. Treatments had no effect on crude protein content, which averaged 130 g kg^{-1}. Asymptotic gas production was similar between the 2 millet types, while degradation rate was 40% higher ($P < 0.05$) for BM than RM. Thus, brown midrib trait reduced ($P < 0.05$) time to degrade 50% and 75% of the silage substrate by 2 and 6 h, respectively. In vitro true dry matter degradability and NDF degradability were 3 and 5% higher ($P < 0.05$) for BM than RM silage. Acetic, propionic and butyric acid concentrations in the liquid residue were all higher ($P < 0.05$) for BM than RM. Microbial protein production efficiency per g substrate was 9% higher ($P < 0.05$) for BM than RM. This is supported by post incubation medium ammonia concentration, which was higher ($P < 0.05$) for RM than BM silage. Seeding rate had no impact on chemical composition or in vitro gas production parameters of millet silage. Quality of BM silage was superior to that of RM silage by providing more substrate for microbial growth and more volatile fatty acids for energy production.

Key Words: millet, brown midrib, in vitro gas production

454 Exogenous fibrolytic enzyme or anhydrous ammonia effects on digestion kinetics of steers fed bermudagrass harvested at two regrowth intervals. J. J. Romero*, A. T. Adesogan, M. A. Zarate, O. C M. Queiroz, J. H. Han, J. H. Shin, C. R. Staples, and W. F. Brown, *University of Florida*, *Gainesville*.

The objectives were to compare effects of fibrolytic enzyme (ENZ, Biocellulase A20) and anhydrous ammonia (AMN, 4% of DM) treatment of 5 and 13-wk regrowths of bermudagrass hay on digestion kinetics in steers. Six individually housed, ruminally-cannulated Brangus steers (BW 216 ± 6 kg) were used in an experiment with a 6 × 6 Latin square design with a 3 (additives) x 2 (regrowth intervals, RI) factorial arrangement. Steers were fed hay in ad libitum amounts supplemented with 2 kg of sugar cane molasses and 0.8 kg of distillers grains daily. In each period, after 14 d of adaptation, ruminal liquid volume, dilution rate, VFA, NH_3-N, and pH were quantified and in situ ruminal DM degradation was measured in triplicate in steers fed the incubated hay. The 5-wk hay had a longer ($P < 0.001$) in situ lag time (2.8 vs. 1.5 h) and contained less ($P < 0.05$) soluble (12.7 vs. 13.6%) and indigestible (40.9 vs. 43.5%) fractions and more ($P < 0.001$) potentially digestible fraction (46.4 vs. 42.9%) than the 13-wk hay. Proportion (mol / 100 mol) of ruminal acetate was greater ($P = 0.002$; 58.3 vs. 56.5) and butyrate was lower ($P = 0.001$; 16.1 vs. 17.8) for steers fed the 5-wk vs. 13-wk hay. Ammoniation increased ($P < 0.05$) concentrations of total VFA (155 vs. 144 mM) and ruminal NH_3-N (15.1 vs. 11.4 mg/dl) and the potentially digestible fraction (50.3 vs. 42.7%) and decreased ($P < 0.05$) the molar proportion of propionate (17.9 vs. 19.1 mol / 100mol) and the indigestible fraction (34.6 vs. 45.3%). Ammoniation also increased the degradation rate of the 13 wk hay (7.4 vs. 5.6% / h; AMN × RI interaction, $P = 0.04$). Enzyme treatment did not affect any of these measurements. Ruminal fluid volume, dilution rate and turnover time were unaffected by additives or RI. Ammoniation improved the digestion kinetics of the hays but enzyme application did not.

Key Words: forage, enzyme, ammonia

455 Effect of chopping or cubing on apparent digestibility of hay when fed to steers. R. Willcutt*[1], B. J. Rude[1], and J. Davis[2], [1]*Animal & Dairy Sciences, Mississippi State University*, *Starkville,* [2]*Agricultural & Biological Engineering, Mississippi State University*, *Starkville*.

Resurged interest in pelleting (cubes) grass has been a result of the push to decrease reliance upon fossil fuels, thereby the cubes can be co-fired in coal furnaces to generate energy production. As such, these cubes may have a dual function that will allow grass producers to determine optimum marketing of cubes based upon economic incentive for either energy production or animal feed. The objective of this study was to evaluate the apparent digestibility of chopped or chopped and cubed hay and its value as a feedstuff for ruminants. Angus (n = 6), Hereford (n = 3), and Charolais (n = 3; total n = 12; 226 ± 19.3 kg) steers were stratified by breed and then randomly assigned into 3 treatment groups: 1) long stem hay; 2) chopped (approx. Fifteen cm) hay; and 3) chopped and then cubed hay. Steers were adapted to their respective diets for14 d, after which they were placed in metabolism crates for 10 d and allowed ad-libitum access to diets and water. The first 3 of the 10 d were used for adaptation to the crates followed by 7 d of data collection. All data was analyzed using the GLM procedures in SAS. There was no difference ($P > 0.05$) for DM intake of the steers consuming the 3 diets (between 4.0 and 4.3 kg/d; 1.8 and 1.9%BW/d). Apparent digestibility of DM (between 61 and 71%, SEM = 3.3), organic matter (between 63 and 73%, SEM = 7.9), NDF (between 63 and 72%, SEM = 3.3), ADF (between 60 and 70%, SEM = 3.9), hemicellulose (between 66 and 75%, SEM = 2.8), and energy (63 and 71%, SEM = 3.2) were not different ($P > 0.05$) among the 3 diets. However, steers consuming long stem hay digested more ($P = 0.0302$) CP (65%, SEM = 5.6) than those consuming chopped hay (39%, SEM = 5.6) with those consuming cubed hay had an intermediate value (51%, SEM = 5.6). Additionally, Steers fed long stem and chopped hay (68 and 63%, respectively, SEM = 3.8) digested more ($P = 0.0071$) fat than those fed cubed hay (47%, SEM = 3.8). For hay producers that are interested in cubing hay for the fuel market, it appears that when prices for cubes used as fuel are reduced, selling cubed hay as a feed may be a viable alternative.

Key Words: cubed hay, digestibility, beef cattle

456 Effect of cutting time and conditioning method on cattle preference for trefoil–grass hay. R. Berthiaume*[1], A. F. Brito[2], and C. Lafreniere[1], [1]*Agriculture & Agri-Food Canada*, *Sherbrooke, QC, Canada*, [2]*University of New Hampshire*, *Durham.*

Ruminants prefer forages cut in the afternoon. However, PM–cut could increase losses due to rainfall, prolonged wilting time, leaching and respiration. Maceration, an intensive mechanical conditioning applied to herbage, can enhance field drying, reduce wilting time and improve animal performance. We hypothesized that maceration would have different effects when applied to forages cut in PM vs. AM. A trefoil-grass field was divided in 4. Half was cut at 18:00(PM) with a mower conditioner. Fifty percent of the PM cut herbage was macerated after 12 h and left to wilt. The other half of the field was cut at 06:00 (AM) the next morning with 50% of the AM cut herbage macerated after 4 h and left to wilt. The 4 hays were field dried, baled at the same time, and chopped before their use. Two preference trials were conducted with the same 6 growing steers. The first trial was conducted in October 2008 whereas the second was conducted in February 2009. During adaptation, hays were offered alone as meals. In the experimental phase, every possible pair of hays (n = 6) was randomly presented for a meal to each of the 6 steers over 6 consecutive days. Dry matter intake was measured after 2, 4, 8, and 24 h. Data were analyzed by multidimensional scaling and by ANOVA with a model including hay and animal effects. During the first trial steers showed a preference for PM over AM-cut hay at every time points ($P = 0.006$). Steers ingested 222, 177, 133 and 38% more DM ($P \leq 0.0001$) from PM than AM-cut hay after 2, 4, 8 and 24 h. In the second trial steers showed no preference for PM over AM-cut hay ($P = 0.51$). Nevertheless, DMI was 57, 60 and 51% higher ($P \leq 0.007$) for PM over AM-cut hay after 2, 4 and 8 h. DMI after 24h was not affected by cutting time. In both trials, there was no effect of maceration and no interaction between cutting time and maceration. Maceration had no effect on the preference of cattle for trefoil–grass hay whether it was cut in the PM or AM.

Key Words: feeding preferences, dry matter intake, conditioning

457 Acceptability of teff hay by horses. S. McCown*, M. Brummer, J. Earing, S. Hayes, and L. Lawrence, *University of Kentucky*, *Lexington*.

Teff hay *(Eragrostis tef)* is a summer annual forage that has recently been introduced to the equine industry in the United States. Teff hay has been fed to horses in parts of the US; however, its relative acceptability compared with other hays has not been reported. Therefore, a study was conducted to evaluate the acceptability of 2 different teff hays when compared with midmaturity alfalfa (A) or timothy (TIM) hay. Two teff varieties were used: Horse Candi (HCT) and Tiffany (TT). The HCT was planted June 8, 2009, and harvested August 16, 2009, in the late heading stage. The TT was planted June 2, 2008, and harvested on July 11, 2008, in the early heading stage. The acceptability of both types of teff was compared with A in experiment 1 (E1) and to TIM in experiment 2 (E2) using 2-choice preference tests. Each experiment used 4 mature mares that had been previously acclimated to individual 3 × 15 m partially covered pens. Mares were offered a different combination of 2 hays each day, so each mare received all combinations in the experiment. The 2 hays were offered in side-by-side hay nets in the pens for 2, 1 h periods on 3 consecutive days. In the first period, 4 kg of each hay was offered to the mares. After an hour, the hay nets were taken away for 1 h. The mares were then offered new hay nets for 1 h with the same hay combination, but with the right-left positions reversed. Hay nets were weighed to determine intake of each hay. In E1, mares consumed more A than HCT (1.66 kg A vs 0.24 kg HCT; $P < 0.05$; SE = 0.25), more A than TT (1.74 kg A vs 0.16 kg TT; $P < 0.05$; SE = 0.25), and more TT than HCT (1.08 kg TT vs 0.24 kg HCT; $P < 0.05$; SE = 0.25). In E2, mares consumed more TIM than HCT (1.54 kg TIM vs 0.12 kg HCT; $P < 0.05$; SE = 0.16), more TIM than TT (1.04 TIM vs 0.66 kg TT; $P < 0.05$; SE = 0.16), and more TT than HCT (0.65 kg of TT vs 0.33 kg HCT; $P < 0.05$; SE = 0.16). When given a choice, mares chose A and TIM over either variety of teff. The mares did discriminate between the 2 teff hays. The reason for the difference in preference between TT and HCT has yet to be determined.

Key Words: preference, horse, hay

458 Nutritive value of North American grasses during establishment. A. E. Lee*[1,4], J. P. Muir[3], B. D. Lambert[1,3], J. L. Reilley[2], and T. R. Whitney[4], [1]*Tarleton State Univ.*, *Stephenville, TX*, [2]*Kika de La Garza PMC*, *Kingsville, TX*, [3]*TX AgriLife Research*, *Stephenville*, [4]*TX AgriLife Research*, *San Angelo*.

Non-native grass species currently used by ranchers can become invasive. To promote the use of native warm-season grasses as forage, more nutritive information is needed. In the spring of 2007 (establishment year), seeds from 3 native grasses [plains bristlegrass (*Setaria vulpiseta* Scribn. and Merr., PBG); multiflower false rhodesgrass (*Chloris pluriflora* Fourn., MFR); and pink pappusgrass (*Pappophorum bicolor* Fourn., PPG)] were collected in south Texas. Plants were then grown in a greenhouse and transplanted into plots (n = 1 to 2/species) within block (n = 4) located in Stephenville, TX, with either no fertilizer or a single spring application of N (67 kg/ha) and P (127 kg/ha) fertil-

izer. During July to November (2007) and April to November (2008), monthly clippings were taken to evaluate effects of fertilization on forage N, NDF, and ADF and in vitro organic matter digestibility (IVOMD) using fistulated steers and goats. During both years, a species × treatment × month interaction ($P < 0.10$) was observed for N. During year 1, N in PBG increased ($P = 0.04$) in September due to fertilization, but average species N increased ($P = 0.02$) due to fertilization in July and September. During year 2, N in PBG increased in July, but unexpectedly decreased in October ($P < 0.04$) due to fertilization. No species × month interaction ($P = 0.19$) was observed for NDF during year 1, but was observed ($P < 0.001$) during year 2. A species × month interaction ($P < 0.001$) was observed for ADF during both years. An animal × species x month interaction ($P < 0.001$) was observed for IVOMD for both years. The IVOMD determined using rumen fluid from goats was greater ($P < 0.02$) for all species during July, October, and November of year 1 and greater ($P < 0.05$) for MFR and PPB during April and May of year 2. Differences in nutrient characteristics and digestibility need to be considered when utilizing these grass species.

Key Words: fiber, native grasses, digestibility

459 Effects of different manure sources and urea on chemical composition of three tropical pasture grasses. O. M. Arigbede*[1,2], U. Y. Anele[1,2], K.-H. Südekum[2], J. A. Olanite[1], A. O. Oni[1], P. A. Dele[1], and J. O. Bolaji[1], [1]*University of Agriculture*, *Abeokuta, Nigeria*, [2]*University of Bonn*, *Bonn, Germany*.

A study was carried out to investigate the effects of different fertilizer types on chemical composition of 3 tropical grasses. The grasses were established in the small ruminant paddocks on the teaching and research farm, University of Agriculture, Abeokuta, Nigeria. The grasses were cut at 10 cm above ground level and sampled 4 weeks before the commencement of the trial and subsequently on monthly basis. A 4 × 3 factorial design was adopted with 4 treatments (control - no manure, urea - 150 kg/ha, caged layers droppings - 250 kg/ha, compost manure - 350 kg/ha) and 3 grass species (*Panicum maximum* (local), *P. maximum* (Ntchisi), and *Pennisetum purpureum*) with 3 field replicates. About 1 kg of each grass species from every plot were cut at 10 cm above ground level, weighed, and oven-dried at 65°C to a constant weight. The plots were maintained weed-free through manual weeding. Manure application generally improved ($P < 0.05$) the chemical composition of the grasses when compared with the urea fertilized and unfertilized ones. Differences ($P < 0.05$) existed between the major nutrient contents with the grasses fertilised with caged layer droppings recording the highest CP concentration (161, 168, and 150 g/kg DM) and the lowest NDF (ash-free) concentration (388, 363, and 448 g/kg DM) for *P. maximum* (local), *P. maximum* (Ntchisi), and *P. purpureum*, respectively. The nutrient contents of the 3 grasses did not differ ($P > 0.05$) between grasses fertilized with caged layer droppings or compost manure. There was also no difference ($P > 0.05$) in the ash content of grasses from the 4 treatments. The use of organic manure proved more effective in enhancing the chemical composition of tropical pasture grasses when compared with those under urea fertilization. Therefore, based on this study organic manure is recommended as a tool for organic ruminant livestock production grazing systems.

Key Words: tropical grass, chemical composition, fertilizer

460 In vitro ruminal fermentation characteristics of anthocyanidin accumulating Lc-alfalfa. A. Jonker*[1,2], M. Gruber[2], Y. Wang[3], and P. Yu[1], [1]*Department of Animal and Poultry Science, College of Agriculture and Bioresources, University of Saskatchewan*, *Saskatoon, SK, Canada*, [2]*Saskatoon Research Centre, Agriculture and Agri-Food Canada*, *Saskatoon, SK, Canada*, [3]*Lethbridge Research Centre, Agriculture and Agri-Food Canada*, *Lethbridge, AB, Canada*.

Transformed Lc-progeny were previously found to have a decrease initial rate of N and DM degradation but did not survive winter conditions in western Canada. Therefore, the objective of this study was to determine the effect of winter hardy Lc-progeny expressing different phenotypes on in vitro fermentation characteristics. To develop winter hardy Lc-progeny, 3 non-winter hardy transgenic T0 Lc-alfalfa populations 88–19, 88–09 and 88–01 were crossed with 3 winter hardy alfalfa varieties Rangelander, Rambler and Beaver, respectively and harvested at a vegetative pre-bud stage. The Lc-plants were subsequently phenotyped into 3 groups per population in the field based on colors, green (Gr), light purple-green (LP) and purple-green(PG), Ground (1 mm) freeze-dried samples were compared in quad duplicate for their ruminal fermentation characteristics with their non-transgenic (NT) parents using a in vitro gas production technique. The results were analyzed in a completely randomized design with repeated measurement in Proc Mixed of SAS. Anthocyanidin concentration was 0, 103.9, 108.4 and 282.5 µg/g DM in NT, Lc-Gr, Lc-LP and Lc-PG alfalfa, respectively. The NT-alfalfa had the highest ($P < 0.05$) and Lc-Gr alfalfa the lowest ($P < 0.05$) cumulative gas production after 48 h. Average gas production per h, fractional degradation rate (K_d) and half time to maximum gas production were all higher ($P < 0.05$) in NT-alfalfa compared with the 3 Lc-alfalfa phenotypes. At 48-h incubation, concentration of methane in total gas was lower ($P < 0.05$) and concentration of propionic acid was higher ($P < 0.05$) in Lc-LP alfalfa compared with NT-alfalfa, whereas production of total volatile fatty acids (VFA) was similar between Lc-LP and NT-alfalfa. It was also observed that branch chain VFA concentration was higher ($P < 0.05$) and NH3 concentration lower ($P < 0.05$) for the 3 Lc-phenotypes compared with NT-alfalfa after 48-h incubation. In conclusion, all 3 Lc-alfalfa phenotypes accumulated anthocyanidin and fermentation profiles differed between the 3 phenotypes and between non-transgenic alfalfa and Lc-alfalfa.

Key Words: anthocyanidin-accumulating alfalfa, in vitro ruminal fermentation, methane

461 Revisiting heat damaged-protein and ruminal degradation kinetics in heated hays. W. K. Coblentz*[1], P. C. Hoffman[2], and N. P. Martin[3], [1]*US Dairy Forage Research Center*, *Marshfield, WI*, [2]*University of Wisconsin*, *Madison,* [3]*US Dairy Forage Research Center*, *Madison, WI.*

Previous studies utilizing conventional (45-kg) hay bales have shown that acid-detergent insoluble CP (ADICP), ruminal CP degradation rate (K_d), and rumen degradable protein (RDP) are related to various measures of spontaneous heating in simple linear relationships that frequently exhibit relatively high r^2 statistics. However, large-round bales often attain much greater maximum internal bale temperatures (MAX) during storage than conventional 45-kg bales, and these greater temperatures may persist for longer durations of time. Our objective was to use regression techniques to relate ADICP, K_d, and RDP to spontaneous heating within large-round bales of mixed alfalfa-orchardgrass hay, and then to compare these responses to the simple linear relationships observed commonly within conventional 45-kg bale packages. Changes in concentrations of ADICP (poststorage – prestorage; ΔADICP) during storage increased with heating degree days >30°C (HDD), and were best explained with a nonlinear model [$Y = 14.9 – (15.7*(e^{-0.0000019*x*x})$); $R^2 = 0.934$]. A similar quartic response ($Y = -0.000053x^4 + 0.012x^3 – 1.00x^2 + 35.7x - 470.9$; $R^2 = 0.975$) was observed for the regression of ΔADICP on MAX. Changes in K_d during storage (ΔK_d) were best explained with

cubic models for regressions on both HDD ($R^2 = 0.939$) and MAX ($R^2 = 0.876$), and these changes represented an approximate 50% rate reduction in severely heated hays relative to prestorage controls. Within ranges of heating most commonly encountered under field conditions, changes in RDP during storage (ΔRDP) declined in mostly linear relationships with HDD or MAX. However, when severely heated hays also were considered, the relationships became cubic ($Y = -0.0000000079x^3 + 0.000028x^2 - 0.027x + 1.1$; $R^2 = 0.802$) for HDD and quadratic ($Y = 0.025x^2 - 3.04x + 86.5$; $R^2 = 0.734$) for MAX. Generally, responses for ADICP, K_d, and RDP in large-round bales were consistent with the linear nature observed previously within conventional 45-kg bales at low-to-modest increments of heating, but exhibited more complex relationships when heating became more extreme.

Key Words: spontaneous heating, ADICP, ruminal kinetics

462 Effects of spontaneous heating on estimates of energy from alfalfa-orchardgrass hays stored in large-round bales. W. K. Coblentz*[1] and P. C. Hoffman[2], [1]*US Dairy Forage Research Center*, *Marshfield, WI*, [2]*University of Wisconsin*, *Madison*.

Using the summative approach to estimate total digestible nutrients (TDN), truly digestible fiber can be estimated from inputs of: i) protein-corrected NDF and acid-detergent lignin (LIG-METHOD); or ii) protein-corrected NDF and 48-h neutral detergent fiber digestibility (NDFD-METHOD). Our objectives were to assess the relationship between TDN and spontaneous heating, and to describe any differences that may result specifically from the 2 methods of estimating truly digestible fiber. During 2006 and 2007, mixed alfalfa (*Medicago sativa* L.)-orchardgrass (*Dactylis glomerata* L.) hays were obtained from 3 harvests at the same 8.2-ha research site. Following storage of the hays, both options for estimating truly digestible fiber (LIG-METHOD or NDFD-METHOD) were then used via the summative approach to estimate the total concentrations of TDN (TDN-LIG or TDN-NDFD, respectively). Estimates of both TDN-LIG and TDN-NDFD were related to heating degree days >30°C accumulated during storage by various regression techniques. Changes (poststorage – prestorage) in TDN-LIG that occurred during storage (ΔTDN-LIG) were best fitted with a nonlinear decay model in which the independent variable was squared [$Y = (11.7 * e^{-0.0000033*x*x)} - 11.6$; $R^2 = 0.928$]. For changes in TDN-NDFD (ΔTDN-NDFD), a quadratic regression model provided the best fit ($Y = 0.0000027x^2 - 0.010x + 0.4$; $R^2 = 0.861$). Generally, ΔTDN-LIG was 2.0 to 4.0 percentage units lower (more negative) than ΔTDN-NDFD when heating degree days >30°C exceeded 500. For regressions on maximum internal bale temperature, both ΔTDN-LIG ($Y = -0.38x + 16.3$; $r^2 = 0.954$) and ΔTDN-NDFD ($Y = -0.25x + 10.2$; $r^2 = 0.848$) were best fitted by linear models with heterogeneous ($P < 0.001$) slopes and intercepts. In general, TDN-NDFD was greater in heated hays than TDN-LIG, largely because the relationship between NDFD and spontaneous heating was poor. In contrast, TDN-LIG declined more rapidly with spontaneous heating, largely because the LIG-METHOD for estimating truly digestible fiber was sensitive to changes in concentrations of both protein-corrected NDF and acid-detergent lignin.

Key Words: alfalfa hay, spontaneous heating, TDN

Immunology and Pathology Symposium: Immunity, Nutrition, Genomics, and Gut Microbiota

463 Direct fed microbial supplementation alters hosts' immune response and repartitions energy to the immune system. M. D. Koci* and W. J. Croom, *North Carolina State University*, *Raleigh*.

Direct fed microbials (DFMs) are used in animals and humans as dietary supplements to improve health. In recent years, increased scrutiny by the Food and Drug Administration, regarding the use of subtherapeutic levels of antibiotics in food animal production has stimulated new interest in DFMs. Currently, our understanding of the mechanism(s) of action of DFMS and the factors that influence their effects on health and performance is limited. This is due to our incomplete understanding of how the gut microflora and the hosts' tissues communicate; the effects of DFMs on host animal metabolism; our limited understanding of the dynamics regulating the microbial ecosystem in the gut, and our inability to culture and/or identify the majority of the organisms living in the host′s intestine. In spite of these challenges, contemporary studies, using different host species, demonstrate DFMs can, and do, augment health. Although the extent of biological activity varies among different model consortia, there appear to be common mechanisms. These include the prevention of colonization of pathogenic and opportunistic organisms, enhancement of nutrient digestion and absorption, and increased immune function. Research in our laboratory suggests DFMs can mediate changes in host tissue energy partitioning which may help facilitate enhanced immune response. Collectively, published studies underscore both the complexity of the DFM/host interaction, and the need for a greater understanding of how intestinal physiology and immunity are interrelated.

Key Words: direct fed microbials, immunity, animal health

464 Role of antibiotics on gut microbiota and incidence of gangrenous dermatitis in commercial broilers. G. Ritter*[1], G. Siragusa[2], S. Dunham[2], and A. Neumann[2], [1]*Mountaire Farms Inc.*, *Millsboro, DE,* [2]*Danisco*, *Waukesha, WI*.

Gangrenous dermatitis (GD) is a bacterial translocation disease of commercial broilers and turkeys caused by *Clostridium perfringens* (CP) and *Clostridium septicum* (CS). In affected birds, CP/CS that are part of the normal gut flora of poultry escape from the gut and invade target tissues of skin, liver and joints producing rapid toxicosis and death. The incidence of GD in a 1.5M birds per week commercial broiler complex was tracked for 5 years. Increased incidence of GD during the study period was positively correlated to feeding programs containing ionophore coccidiostats (polyether antibiotics) included in grower feed diets fed to broilers from 19 to 28 d of age. A gastrointestinal (GIT) microbiota field study was conducted on 6 GD endemic commercial broiler farms. Four farms were fed a diet including ionophore grower feed (correlated with high incidence of clinical GD) and 2 farms were fed grower feed without ionophores that is not associated with clinical expression of GD. GIT bacterial communities in birds on each farm were characterized using molecular techniques of 16S cloning/sequencing and terminal restriction fragment length polymorphism (T-RFLP) from pooled gut samples collected from 6 presumably healthy birds at 16, 24, 25 and 41 d of age. Results of 16S cloning/sequencing revealed that birds fed ionophores in grower feed had the most *Clostridiaceae* and least *Lactobacillaceae* in their GITs while birds not fed ionophores had the least *Clostridiaceae*. T-RFLP results showed differences in bacterial community profiles and individual T-RFLP peaks between treatment groups. These observed differences may be important to GD disease development and clinical expression.

Key Words: gangrenous dermatitis, antibiotics, commercial broilers

465 Antibiotics disrupt the microbiota-host-pathogen interaction. B. Willing*, *University of British Columbia*, *Vancouver, BC Canada*.

The mucosal immune system is essential for protecting the host from a steady barrage of bacterial, fungal, and viral pathogens that it encounters. However, proper functioning of the mucosal immune system requires continual stimulation by a resident gastrointestinal microbiota. When a healthy microbiota is absent as a consequence of antibiotic therapy or other disturbances, the mucosal immune system fails to control pathogens allowing the host to become sick. Each bacterium affects the immune system in a different way, therefore the effects of an antibiotic regimen on the mucosal immune system are dependent upon which bacteria the antibiotic targets. Understanding the changes in mucosal immunity and how they relate to deviations in gut bacteria will be important in the development of strategies to bolster the mucosal immune system and promote intestinal health.

Key Words: antibiotics, microbiota, host-pathogen

466 Nutrigenomics: Understanding how nutrients influence host innate immunity and modulate host-pathogen interaction. H. Lillehoj*[1], S.-H. Lee[1], D.-K. Kim[1], and D. Bravo[2], [1]*Beltsville Agricultural Research Center, USDA-Agricultural Research Service*, *Beltsville, MD,* [2]*Pancosma S.A.*, *Grand Saconnex, Geneva, Switzerland*.

With anticipated human population growth to 9.5 billion in 2050 (2.5 people every second), we need more efficient and safe animal production system to meet the demands for high-protein meat products. In 2006, the European Union banned antibiotics growth promoters in animal feed due to increasing concerns with the drug uses and resistances for human antibiotics. This new constraints for animal and pharmaceutical industry was the driving force for a new thrust in research to find alternative non-drug dependant strategies for growth promoting and disease control for farm animals. Recently, there has been increasing interest and research activities on the nutrition-based strategy to enhance host immunity, especially using plant-derived products in clinical medicine. However, there is very limited information on the use of phytonutrients in veterinary medicine and knowledge on the nutrient-host gene interaction in poultry is scarce. To best utilize the available information in nutrition, immunity and gut microbiota for developing alternative disease control strategies against poultry diseases, we are applying new technology in nutrigenomics to develop dietary immunomodulation strategy as an alternative to antibiotics in poultry disease control.

Key Words: nutrigenomics, host-pathogen, poultry

Lactation Biology 1

467 The effect of milk accumulation on gene expression in bovine mammary gland. E. H. Wall*[1], J. P. Bond[2], and T. B. McFadden[1], [1]*Department of Animal Science, University of Vermont*, *Burlington,* [2]*Vermont Genetics Network Bioinformatics Core, University of Vermont*, *Burlington*.

We hypothesized that accumulation of milk would influence gene expression in the mammary gland of lactating dairy cows. To test this hypothesis, we enrolled 4 multiparous Holstein cows (150 ± 10 DIM) in a half-udder milk stasis experiment. On d 1 of the experiment, right udder halves were milked at 0430 h and 1430 h. On d 2 of the experiment, right udder halves were milked at 0430 h and mammary biopsies were obtained from both udder halves immediately thereafter. At the time of biopsy, it had been 24 h since left udder halves had last been milked. Using Affymetrix GeneChip Bovine Genome Arrays, we identified 32 genes that were differentially expressed between left (full) and right (empty) udder halves (fold change >1.5; $P < 0.05$). Four of the genes were downregulated in response to milk stasis, whereas 28 were upregulated. Differentially expressed genes were associated with extracellular matrix remodeling, tight junction formation, regulation of blood flow, and apoptosis. In addition, 4 of the differentially expressed genes had been previously identified as candidates for local regulation of milk production in dairy cows. Expression of 2 of these candidates, early growth response-1 (EGR-1) and thrombospondin-1 (THBS-1), was validated using real-time quantitative RT-PCR. Consistent with microarray results, both genes were upregulated in response to 24-h of milk stasis ($P < 0.03$). Immunofluorescence was used to localize expression of EGR-1 protein, which was restricted to epithelia and was uniformly distributed. We conclude that accumulation of milk alters gene expression in the bovine mammary gland. In particular, EGR-1 and THBS-1 have emerged as strong candidates for local regulation of milk production in dairy cows.

Key Words: gene expression, mammary gland, milk stasis

468 Expression of ER stress pathways genes in bovine mammary tissue during the lactation cycle. G. Invernizzi*[1,2], M. Bionaz[1], G. Savoini[2], and J. Loor[1], [1]*University of Illinois*, *Urbana-Champaign,* [2]*University of Milan*, *Milan, Italy*.

Endoplasmic reticulum (ER) has a crucial role in cellular metabolism. Recent studies uncovered a tight relationship between ER stress pathways and lipogenic transcription factors. Mammary gland is subject to extreme metabolic loads at the onset of lactation. Recently, it was discovered that X-box binding protein 1 (XBP1) and eukaryotic translation initiation factor 2-α kinase 3 (PERK) play critical roles in regulating the expression of lipogenic transcription factors such as PPARγ and SREBF1. Furthermore, evidence from non-ruminant cell systems has shown that $p58^{IPK}$ ((DnaJ (Hsp40) homolog, subfamily C, member 3 (DNAJC3)) interacts with PERK to inhibit its eIF2α kinase activity. The latter is induced during the unfolded protein response (UPR) by an ER stress response element in its promoter region. Quantitative real-time RT-PCR of $p58^{IPK}$, PERK and XBP1 in mammary biopsy tissue (n = 5 at each time) was performed at −15, 1, 15, 60 and 240 d relative to parturition. Expression of $p58^{IPK}$ showed peaks ($P < 0.05$) at d 15 and 240 after calving with the highest expression at d 240 (2-fold vs. −15 d). Expression of PERK was similar to $p58^{IPK}$ at d 15 and was significantly increased (1.5-fold) at d 240. A possible unfolded protein response accompanying the sharp increase in milk production after calving (d 15) as well as apoptosis at late lactation (240 d) can partly explain the responses of PERK and $p58^{IPK}$. Preliminary results suggest that the mammary gland experiences ER stress at different stages of the lactation cycle. Further studies could explain better the role of XBP1 in regulation of the ER stress pathways through splicing mechanisms rather than mRNA expression.

Key Words: ER stress, lactation cycle, bovine mammary tissue

469 Effect of dexamethasone and age at induction on milk yields of heifers induced into lactation. A. L. Magliaro-Macrina*[1], A. C. W. Kauf[1], D. A. Pape-Zambito[1], and R. S. Kensinger[2], [1]*The Pennsylvania State University*, *University Park*, [2]*Oklahoma State University*, *Stillwater*.

The objectives of the present study were to determine if age or dexamethasone administration on d 1 and 2 of milking would affect milk production in heifers induced into lactation using estradiol and progesterone. Nonpregnant Holstein heifers at 14 (n = 20; 354 ± 38 kg BW) and 18 mo of age (n = 20; 456 ± 30 kg BW) were randomly assigned to dexamethasone (DEX) or control (CON) treatment groups in a 2 × 2 factorial arrangement with age and DEX as the 2 factors. Heifers were induced into lactation with daily subcutaneous injections of estradiol–17B and progesterone (75 and 250 μg/kg BW/d, respectively) on treatment d 1 to 7. They also received bST every 14 d beginning on treatment d 1. Milking began on treatment d 18 (= d 1 of lactation). DEX (10 mg) was administered on d 1 and 2 following the a.m. milking. CON heifers did not receive DEX. Milk yield from d 2 to 15 of lactation of heifers receiving DEX (7.8 kg/d) was greater ($P < 0.05$), than that of CON heifers (6.0 kg/d) but was similar thereafter until 200 DIM (17.9 kg/d). Milk production to d 11 was similar for 14 and 18 mo old heifers, but milk yield was greater for 18 (19.1 kg/d) than for 14 mo animals (16.7 kg/d) through 200 DIM ($P < 0.01$). Milk fat percent was greater over d 1 to 21 of lactation in DEX (4.48) vs. CON heifers (3.49, $P < 0.01$); milk lactose percent was higher ($P < 0.05$) in DEX (4.40) than CON (4.15) through d 21 of lactation. Day 1 to 7 mean IgG concentration and mass were greater ($P < 0.05$) for 18 (48.1 mg/ml; 41.8 g mass) vs. 14 mo (32.3 mg/ml; 30.0 g mass) old heifers. DEX treatment did not affect IgG content. There were no DEX × age interactions. Administration of DEX to heifers induced into lactation increased d 2 to 15 milk production compared with heifers that did not receive DEX, but not after 15 DIM. DEX appeared to stimulate mammary cell differentiation but did not change the rate of decline of milk IgG concentrations. Higher milk yield and IgG content in 18-mo-old heifers might be due to greater mammary epithelium and/or increased body mass.

Key Words: induced lactation, dexamethasone, dairy heifers

470 Effect of intramammary infusions of fluoxetine (FLX) and 5-hydroxytryptophan (5-HTP) on milk secretion rate and composition in lactating Holstein cows at dry-off. R. J. Collier*1,3, J. L. Collier[1], L. L. Hernandez[2], and N. D. Horseman2,3, [1]*University of Arizona*, *Tucson,* [2]*University of Cincinnati*, *Cincinnati, OH,* [3]*Amelgo*, *Covington, KY*.

Serotonin (5-HT), produced in mammary epithelial cells negatively feeds back on milk secretion via 5-HT receptors in mammary tissue. We hypothesized that increasing 5-HT concentration in milk via inhibiting its reuptake, (FLX) or by increasing the precursor for 5-HT synthesis, 5-HTP would accelerate milk yield at dry-off. Multiparous Holstein cows (45) milked 3x daily and producing at least 20 kg/d were randomly

assigned to once a day milking and one of 3 intramammary treatments (15 cows each) for 3 d. Each infusion was followed by prophylactic antibiotic (Today) on d1 and 2 and Quartermaster and Orbeseal on d 3. The control group (C) received the carrier (sterile H20 and oil at 9:1) The FLX group received 5 mg of FLX and carrier. The 5-HTP group received 5 mg of 5-HTP and carrier. Milk yield and composition samples were obtained daily. Blood samples were obtained by tail venipuncture on d 2 to 4. Rate of milk yield decline was greater for FLX and 5-HTP groups (9.5 and 10.0 kg) compared with C (7.5 kg) on d-1 following initiation of treatments ($P < 0.01$) and did not differ after. Milk lactose, protein and fat % were unaffected by treatment but milk Na:K ratio was increased to 2.8 in FLX treated animals d-2 post-infusion compared with 1.44 in C and 1.78 in 5-HTP treated animals ($P < 0.01$). Plasma lactose was increased 2-fold in FLX treated animals on d-1 post-infusion compared with C and 5-HTP animals ($P < 0.001$). Udder surface temperatures declined as milk yield declined in all animals ($P < 0.001$) and was lower in FLX treated animals than C and 5-HTP treated animals ($P < 0.003$). Rectal temperatures were also reduced in FLX treated animals ($P < 0.03$). We conclude that decrease in milk secretion during the first 24 h after reduction in milking rate from 3x to 1x was accelerated in FLX treated animals. Increase in the milk Na:K ratio and plasma lactose in the FLX groups suggest these treatments altered tight junction function post-dryoff.

Key Words: serotonin, lactation inhibition, dry-off

471 Acute fluoxetine administration accelerates mouse mammary gland involution. L. L. Hernandez*[1], R. J. Collier[2,3], and N. D. Horseman[1,3], [1]*University of Cincinnati*, *Cincinnati, OH,* [2]*University of Arizona*, *Tucson,* [3]*Amelgo*, *Covington, KY*.

Serotonin (5-HT) acts via autocrine-paracrine mechanisms on mammary epithelial cells in a variety of species. In human and bovine mammary epithelial cells, inhibition of the 5-HT reuptake transporter (SERT) with selective 5-HT reuptake inhibitors (SSRIs) exhibit disruption of tight junctions and decreased milk protein mRNA expression. SSRIs act to increase the cellular exposure to 5-HT by preventing reuptake of 5-HT by the cell and eventual degradation. This experiment set out to determine the in vivo effects of fluoxetine (FLX) treatment on lactation in mice. We utilized 7 ICR mice, approximately at 8–10 d of lactation and treated with either a single i.p. injection of sterile saline (CTRL; n = 3) or 40 mg/kg body weight FLX (n = 4). At the time of injection, the number 1, 3, 5 and 7 glands were sealed and the number 2, 4, 6 and 8 glands were left open. Mothers were then returned to their pups for 24 h. After 24 h, lactating dams were sacrificed and the number 1–8 glands were collected from all mothers. Mammary glands were stored in 4% paraformaldehyde overnight, and paraffin embedded and processed for hematoxylin and eosin staining at the Cincinnati Children's Hospital Pathology Research Core. Representative photographs were taken of each gland from each animal and analyzed for alveolar area and number of epithelial cells shed into the alveolar lumen using NIH ImageJ software. The alveolar area and number of epithelial cells shed of 6 alveoli per mammary gland were used for the analysis. Alveolar area was increased in FLX sealed glands relative to CTRL sealed glands ($P = 0.0028$) and in FLX open glands relative to CTRL open glands ($P = 0.04$). The number of epithelial cells shed into the luminal space was increased in FLX sealed glands compared with CTRL sealed glands ($P = 0.0166$) and FLX open glands compared with CTRL open glands ($P = 0.0395$). Results indicate that mammary gland involution was accelerated by systemic FLX treatment in both open and sealed glands compared with CTRL injections.

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Key Words: serotonin, lactation, fluoxetine

472 Effects of early ovariectomy on caprine mammary gland parenchyma during prepuberty. L. Finot[1,2], Y. Yart[1,2], and F. Dessauge*[1,2], [1]*INRA UMR 1080 Dairy Production*, *35590, Saint Gilles, France*, [2]*Agrocampus UMR 1080 Dairy Production*, *35000, Rennes, France*.

In ruminants, ovarian hormones (estradiol and progesterone) are absolutely essential for normal mammary development. From birth to puberty, the mammary parenchyma undergoes rapid growth characterized by cell proliferation and expansion of a ductal network into the surrounding fat pad. The objectives of this study were to increase the understanding of biological mechanisms underlying mammary growth and to investigate the role of ovary secretions during early prepubertal caprine mammogenesis. Alpine young goats were ovariectomized (OVX; n = 9) or sham operated (SHAM; n = 9) at 3 periods before puberty (P1 = 1 mo, P2 = 2 mo and P3 = 3 mo after birth). Goats were harvested at 9 mo of age to remove the mammary gland. Ovariectomy did not influence mammary gland weight at any experimental period. Histological observations revealed that adipose tissue was widely represented compared with secretory tissue (parenchyma) in OVX goats. Morphological analysis of mammary tissues indicated that parenchymal structures of OVX goats were negatively affected by ovariectomy with limited lobules and undeveloped ducts. Ovariectomy at P1 and P2 reduced estrogen receptor α at both the transcriptional (P1 = −85% and P2 = −90%) and translational (P1 = −65% and P2 = −70%) levels. In P1 and P2 periods, ovariectomy strongly affected cell-cell adhesion molecules and extracellular matrix protease activities. Lower expression of E-Cadherin (P1 = −78%; P2 = −76%), Pan-Cadherin (P1 = −60%; P2 = −43%) and P-Cadherin (P1 = −86%; P2 = −75%) was accompanied by a decrease of α and β catenins. In addition, the metalloproteinase MMP2 activity was significantly reduced in ovariectomized animals (P1 = −13% and P2 = −8%). No effects were observed with ovariectomy at 3 mo (P3). In conclusion, ovariectomy at 2 mo of age was the most critical for parenchymal development. These findings suggest that ovary secretions are required to initiate mammary epithelial cell proliferation in prepubertal goats.

Key Words: caprine mammary gland, ovariectomy, estrogen

473 Role of miR–15a in the mammary gland and mammary epithelial cells of dairy cows. H. M. Li, C. M. Wang, and Q. Z. Li*, *Key Laboratory of Dairy Science of Education Ministry, Northeast Agricultural University*, *Harbin, China*.

MicroRNAs (miRNAs) are a class of small non-coding RNAs consisting of 18–25 nucleotides. They regulate the expression of target genes at the post-transcriptional level by degradation or translational inhibition of the complementary mRNA target sequences. The role of miRNA in mammary gland development and lactation is relatively unknown. In this study, qRT-PCR was used to detect the expression of miR-15a and its target gene growth hormone receptor (GHR) in virgin, pregnancy, lactation and involution physiological stages in the mammary gland of Holstein dairy cows, and 3 cows were sampled at each physiological stage. The results revealed that miR-15a and GHR followed the same expression pattern across different physiological states. The expression of miR-15a and GHR was only increased significantly in the sixth month of pregnancy. In the other developmental periods, the expression of miR-15a and GHR was low. To determine the relationship between miR–

15a and GHR, bovine miR-15a was transfected into bovine mammary epithelial cells (BMEC, a cell culture line established by our laboratory). Experiments were replicated 3 times. After miR-15a was overexpressed by transfection, the extent of the miR-15a were 8.4-fold relative to the endogenous miR-15a and the expression of GHR mRNA and protein decreased ($P < 0.01$ and $P > 0.05$, respectively). Flow cytometry showed that over-expression of miR-15a inhibited the proliferation of mammary epithelial cells ($P < 0.01$). In conclusion, these results revealed that miR-15a inhibited the proliferation of mammary epithelial cells as well as the expression of GHR mRNA and protein level. Therefore, this miRNA may play an important role in mammary gland physiology.

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Key Words: miR-15a, GHR, mammary epithelial cell

474 Expression of let–7g in development, lactation and involution of the murine mammary gland. Y. Li, L. Tian, C. M. Wang, and Q. Z. Li*, *Key Laboratory of Dairy Science of Education Ministry, Northeast Agricultural University*, *Harbin, China*.

Micro RNAs (miRNAs) play important roles in the development, lactation and involution of the mammary gland. To identify key miRNAs implicated in mammary gland physiology, healthy female kunming mice in different mammary cycle stages were used (12 time points: virgin 28d, virgin 35d, virgin 49d, pregnancy 2d, pregnancy 9d, pregnancy 13d, lactation 2d, lactation 9d, lactation 13d, involution 2d, involution 5d, involution 10d;and 6 mice were used for each time point). The fourth pairs of abdominal mammary gland tissues were prepared under sterile condition and used for microarray (miRCURY LNA Arrays) and qRT-PCR analysis. Total RNA isolated from mammary gland tissues collected across 12 time points was covalently labeled with Hy3, respectively, and hybridized to the array. The microarray contained 4 replicate subarrays. The data analysis used Genepix Pro 6.0, and GeneSpring 7.2 was used for further data analysis. qRT-PCR was used to confirm the microarray results. Finally, the data were analyzed with SPSS by ANOVA. Expression levels of let-7g changed with the mammary cycle. Microarray and qRT-PCR produced similar results for the expression of let-7g, which exhibited significant changes during the mammary cycle. The microarray showed that let-7g was down-regulated in glands collected during pregnancy compared with virgin and involuting glands ($P < 0.05$). qRT-PCR showed that the expression of let-7g was lower in pregnancy ($P < 0.01$), and was relatively higher in virgin, lactating and involuting glands. To identify genomic targets of let-7g, an algorithm named miRanda and Pic Tar was used. The results showed that let-7g target genes were important transcription factors, such as Myc, Map3k1, Map4k3, and Stat3, which play significant roles in the mammary gland. In conclusion, let-7g was identified as a potential regulator of murine mammary gland development, lactation and involution.

This work was supported by the National High Technology Research and Development Program of China (Grant No. 2006AA10Z1A4).

Key Words: mammary gland, miRNAs, let-7g

475 Effect of heat stress during the dry period on mammary gland development of dairy cattle. S. Tao*, J. W. Bubolz, B. C. do Amaral, M. J. Hayen, S. E. Johnson, and G. E. Dahl, *University of Florida*, *Gainesville*.

Heat stress during the dry period affects immune status, alters hepatic metabolism and decreases milk production in the subsequent lactation. However, cellular mechanisms involved in the mammary response are unclear. Our objective was to evaluate the effects of heat stress during the dry period on mammary gland development of multiparous cows. Cows were dried off 46 d before expected calving and assigned to 2 treatments, heat stress (HT, n = 15) or cooling (CL, n = 14). Average THI during treatment was 76.6 for all cows, but CL cows had sprinklers and fans that came on when ambient temperatures reached 21.1 0C, whereas HT cows were in the same barn without fans or sprinklers. Rectal temperature (RT) was measured twice daily (0730 and 1430 h) and respiration rates (RR) recorded at 1500 h on a Mon-Wed-Fri schedule from dry-off to calving. After parturition, all cows were housed in a free-stall barn with sprinklers and fans. Milk yield was recorded daily to 147 DIM. Mammary biopsies were taken at dry-off, −20, +2 and +20 d relative to calving from a subset of cows (HT, n = 7, CL, n = 7) and infiltrated with paraffin. Numbers of Ki67 immunopositive epithelial and stromal cells were measured in 4-μm mammary tissue sections from each animal. Total cell numbers were measured following hematoxylin histology and percent proliferation was calculated as Ki67+/ total × 100. Compared with HT cows, CL cows had lower morning and afternoon RT (38.6 vs. 38.8 0C, 39.0 vs. 39.40C, $P < 0.01$, respectively) and lower RR (46 vs. 78 breaths/min, $P < 0.01$). Relative to HT cows, CL cows produced more milk (36.5 vs. 31.6 kg/d, $P < 0.06$). Compared with HT, CL cows had a higher percentage of proliferative epithelial cells at −20 d relative to calving (3.3 vs. 1.3%, $P < 0.05$), but there was no difference in labeled stromal cells ($P > 0.1$). We conclude that heat stress abatement during dry period improves milk production in the subsequent lactation possibly by increasing mammary epithelial cell proliferation during the dry period.

Key Words: heat stress, mammary gland, epithelial cell

476 Characterization of bovine glucose transporter 1 kinetics and substrate specificities in *Xenopus laevis* oocytes. P. A. Bentley[1], Y. Misra[1], A. D. Morielli[2], and F.-Q. Zhao*[1], [1]*Lactation and Mammary Gland Biology Group, Department of Animal Science, University of Vermont*, *Burlington,* [2]*Department of Pharmacology, College of Medicine, University of Vermont*, *Burlington*.

Glucose is essential for milk production as it serves as both a substrate for lactose synthesis and as an energy source. Glucose uptake in the bovine mammary gland therefore plays a key role in milk synthesis. Facilitative glucose transporters (GLUTs) mediate glucose uptake in the mammary gland. GLUT1 is the major facilitative glucose transporter expressed in the bovine gland and has been shown to localize to the basolateral membrane of mammary epithelial cells. GLUT1 is therefore thought to play an important role in glucose uptake during lactation. The objective of this study was to determine the kinetic properties of bovine GLUT1 transport using the *Xenopus* oocyte model. Bovine GLUT1 was expressed in *Xenopus* oocytes by microinjection of in vitro transcribed cRNA and was found to be localized to the plasma membrane, which resulted in increased glucose uptake. This bGLUT1-mediated glucose uptake was dramatically inhibited by specific facilitative glucose transport inhibitors, cytochalasin B and phloretin. Kinetic analysis of bovine GLUT1 was conducted under zero-trans conditions using radio-labeled 2-deoxy-D-glucose and the principles of Michaelis-Menten kinetics. Bovine GLUT1 exhibited a Km of 7.69 ± 1.7 m*M* for 2-deoxy-D-glucose. Transport by bovine GLUT1 was inhibited by mannose and galactose, but not fructose, indicating that bovine GLUT1 may also be able to transport mannose and galactose. Our data provide insight into potential functional properties of GLUT1 in transporting glucose across mammary epithelial cells for milk synthesis.

Key Words: glucose uptake, milk synthesis, glucose transporter

Meat Science and Muscle Biology: How Does Pre- and Postnatal Muscle Development Affect Meat Composition, Quality and Value?

477 Coordinating myogenesis and angiogenesis: a novel role for the satellite cell in skeletal muscle growth. R. P. Rhoads*, K. L. Flann, and R. E. Allen, *University of Arizona*, *Tucson*.

The cellular basis for postnatal muscle growth and hypertrophy has been realized over the past several decades. Skeletal muscle is extremely responsive to environmental and physiological cues by modifying growth and functional characteristics in accordance with the demands placed on it. This ability extends to instances of injury or trauma, where skeletal muscle exhibits the capacity to regenerate despite being largely composed of post-mitotic, multi-nucleated fibers. The plasticity of skeletal muscle results, in large part, from a population of resident stem-like cells, often referred to as satellite cells. When needed, satellite cells proceed through a terminal differentiation program culminating in fusion competency to participate in myogenic activities. The importance of satellite cell activity to skeletal muscle growth and hypertrophy is underscored when events leading to disruptions in myonuclear accumulation occur during critical growth or repair phases leading to muscle growth deficits that cannot be overcome. Although traditionally viewed exclusively in a myogenic role, new efforts have revealed novel roles, based on spatial, temporal and functional characteristics, ascribed to the satellite cell during muscle growth and repair. For example, the satellite cell location within the skeletal muscle niche and ability to produce numerous growth factors suggest communication between myogenic and angiogenic cell types exist. Recent experiments provide evidence that activated satellite cells initiate a potent pro-angiogenic program that may participate in vascularization of skeletal muscle. Coordination of myogenesis and angiogenesis may therefore be accomplished through the secretion of soluble factors by activated satellite cells.

Key Words: skeletal muscle, satellite cell, angiogenesis

478 The energy metabolism impacts that come along with muscle fiber type and its effect on postmortem metabolism. T. M. Scheffler, J. M. Scheffler, S. Park, A. L. Grant, and D. E. Gerrard*, *Department of Animal and Poultry Sciences, Virginia Tech*, *Blacksburg*.

The meat industry has reduced the variation in product quality through modifications in animal handling protocols and implemented procedures that mask some negative quality attributes. Even so, however, carcasses with poor meat quality remain an inefficiency in the food production chain. Understanding meat quality development, therefore, is of utmost concern to the animal industry. Meat quality development is largely impacted by the rate and extent of postmortem metabolism. Recall muscle consists of a heterogeneous population of muscle cells, which collectively dictate the overall biochemical and contractile nature of muscle. The relationship between these interdependent muscle characteristics is difficult to separate given their intimate function within muscle fibers. Yet, depending on the physiological status of the animal, muscle has the ability to modify its functional characteristics to accommodate a myriad of cues. We have studied this "plastic" nature of muscle to address how muscle fiber type-specific characteristics affect muscle growth and meat quality development. We have utilized repartitioning agents, transgenic mice, and natural mutations to manipulate muscle to better understand underlying mechanisms controlling growth, adaptation, and metabolism. The capacity for lean growth may be determined by muscle fiber type composition, yet various pathways are responsible for this response. Indeed, integration of various signals, such as nutrient availability, energy status, hormones, is necessary to match precisely supply and demand. Moreover, the response to these cues is different in various fiber types and during different phases of growth. AMP activated protein kinase (AMPK) may be key in integrating these cues; it modulates multiple energy production and consumption pathways, and regulates protein turnover. Understanding these mechanisms that contribute to regulation of muscle hypertrophy and contractile and metabolic phenotype are important for optimizing the quantity and quality of meat.

Key Words: meat, muscle, energy

479 How growth and body composition can affect the quality of poultry meat? C. Berri*, E. Le Bihan-Duval, and M. J. Duclos, *INRA, UR083 Recherches Avicoles*, *Nouzilly, France*.

Although poultry products are diverse, the general trend is for portioned and further processed products to increase their market share. In this context, technological quality of poultry meat is an important aspect. In poultry, the processing ability of meat is highly related to the acidification process occurring in muscle post-mortem. This later is mainly determined by the amount of resting glycogen in the muscle at death and by the stress susceptibility of the bird before slaughter. Several studies highlighted the great impact of growth rate and body composition on these parameters in chicken. Indeed, selection for greater body weight or muscle development has induced histological and biochemical modifications of the muscle tissue. More precisely, in fast-growing broiler lines, as fiber size increased muscle glycogen reserve at death decreased and as a consequence breast meat exhibited higher ultimate pH, darker color and reduced drip loss. It has also been observed that lean chickens showed a comparatively lower level of glycogen stores than fat chickens, with again positive consequences on ultimate pH, color and water holding capacity of breast meat. Even though the genetic determinism of meat quality traits as well as the possibility to modulate them by nutrition have been established, the molecular mechanisms involved in chicken meat quality variations are still poorly described. Recently, several genomic programs allowed identifying QTL regions as well as genes and molecular pathways controlling muscle post-mortem metabolism and meat quality. These approaches constitute a promising way to better control and improve chicken breast meat properties. It would allow developing useful breeding tools, such as molecular markers, to select birds with expected meat properties, and help optimizing rearing practices, via the study of gene regulation.

Key Words: poultry meat, growth, genomics

480 ASAS Early Career Award Presentation: Prenatal muscle development affects beef composition and quality. M. Du*, *Department of Animal Science, University of Wyoming*, *Laramie*.

The quality of beef is determined by its marbling and tenderness. Marbling (intramuscular fat) is associated with the number and size of adipocytes. While the size of adipocytes can be increased during the fattening stage, the number of intramuscular adipocytes is largely determined during the late fetal and early postnatal stages. Adipogenesis inside skeletal muscle which forms intramuscular adipocytes are the sites for marbling fat accumulation. On the other hand, connective tissue which is synthesized by fibroblasts contributes to the background toughness of beef. Pre-natal skeletal muscle development involves myogenesis, adipogenesis and fibrogenesis, all of which are mainly derived

from mesenchymal stem cells (MSC). Switching the commitment of MSC from myogenesis to adipogenesis will increase intramuscular adipocytes, but to fibrogenesis will promote intramuscular collagen accumulation. Maternal nutrition and physiological status such as inflammation affects the differentiation of MSC to myogenesis, adipogenesis and fibrogenesis, which could permanently alter the amount of intramuscular fat and connective tissue in offspring skeletal muscle and thus the quality of beef

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Key Words: prenatal, meat, quality

481 Effect of *Origanium vulgare* on ruminal fermentation, nutrient utilization, and production in dairy cows. J. A. Tekippe*[1], A. N. Hristov[1], K. S. Heyler[1], T. W. Cassidy[1], V. D. Zheljazkov[2], and G. A. Varga[1], [1]*Pennsylvania State University*, *University Park,* [2]*Mississippi State University, NMREC*, *Verona*.

A lactating cow trial was conducted to study the effects of dietary addition of oregano (*Origanium vulgare* L.; 0, control vs. 500 g/d, OV) on ruminal fermentation, total tract digestibility, manure emissions, N losses, milk taste, and dairy cow performance. Eight primiparious and multiparious Holstein cows (80 ± 30 DIM; 6 of the cows were ruminally cannulated) were used in a switch over design with 2, 21-d periods. Cows were fed once daily. The OV material was top-dressed to the TMR. Intake of DM averaged 26 ± 0.83 kg/d and did not differ between treatments. Apparent total tract digestibly of DM, OM, NDF, ADF, crude protein, and total nonstructural carbohydrates did not differ between treatments. Rumen pH and concentration of total and individual VFA, acetate:propionate ratio, and total free amino acids concentration were also not affected by treatment. Ruminal ammonia concentration was increased by OV compared with the control (5.3 vs. 4.3 mmol/L; $P < 0.001$). Blood urea N and glucose concentrations were not affected by treatment. Average milk yield, milk fat, protein, and lactose concentrations, MUN, and SCC were unaffected by diet. Milk sensory parameters were also not affected by treatment. Fat-corrected (3.5%) milk yield and 3.5% FCM feed efficiency were increased ($P = 0.03$ and <0.001) for OV compared with the control (42.2 vs. 40.7 kg/d and 1.63 vs. 1.53 kg/kg, respectively). Ruminal microbial N flow, urinary and fecal N losses, and manure ammonia, methane, and carbon dioxide emissions were similar between treatments. Under the current experimental conditions, supplementation of dairy cow diet with 500 g/d of *Origanium vulgare* did not affect ruminal fermentation, nutrient digestibility, and manure gas emissions. However, there is a potential for increased FCM and feed efficiency of FCM.

Key Words: *Origanium vulgare*, rumen fermentation, milk production

482 Effect of prostaglandin $F_{2\alpha}$ on growth of *Staphylococcus aureus* associated with bovine mastitis. C. A. Autran*[1], A. Ahmadzadeh[1], B. Shafii[1], M. A. McGuire[1], and J. C. Dalton[2], [1]*University of Idaho*, *Moscow,*[2]*University of Idaho*, *Caldwell R & E, ID*.

Some fatty acids inhibit the growth of mastitis-causing *Staphylococcus aureus*. The objective of this study was to determine the bacteriostatic and bactericidal effects of prostaglandin$F_{2\alpha}$ ($PGF_{2\alpha}$) on *S. aureus*. Tryptic soy broths were inoculated (1:100) with an *S. aureus* (Novel) overnight culture and subsequently treated with 0, 0.3, 0.6, 1.2 and 2.4 mg/mL of $PGF_{2\alpha}$ (dinoprost tromethamine). Cultures were incubated for 24 h at 37°C (with shaking at 250 rpm), and sampled at 0 h and every 3 h thereafter to determine growth, as measured by optical density at 600 nm (OD) and colony forming units (log CFU). Data were analyzed by ANOVA repeated measures using mixed procedures. Mean OD and log CFU values were not different between treatments at 0 h. There was an effect ($P < 0.05$) of treatment and treatment by time interaction on mean OD and log CFU. Overall mean OD values for $PGF_{2\alpha}$ treatments were different ($P < 0.05$) from control and decreased with increasing concentrations of $PGF_{2\alpha}$ in a dose dependent manner. Initial OD for treatments and control averaged 0.15 ± 0.11 at 0h, and the control reached 22.6 ± 0.27 at 24 h. In contrast, the 0.3, 0.6, 1.2 and 2.4 mg/mL treatments reached OD values of 15.6, 8.1, 5.47, and 1.1 ± 0.27, respectively at 24 h post-treatment. All $PGF_{2\alpha}$ treatments also differed ($P < 0.05$) in mean log CFU compared with control. Initial log CFU for treatments and control averaged 8.12 ± 0.02 at 0 h, and the control reached 10.5 ± 0.04 at 24 h. The 0.3, 0.6, 1.2 and 2.4 mg/mL treatments reached 9.4, 9.0, 8.1, and 1.8 ± 0.04 log CFU, respectively at 24 h post-treatment. The mean log CFU, over a 24 h period of time, for 0.3mg/mL and 0.6mg/mL were not different from each other. However, mean log CFU for 1.2mg/mL and 2.4mg/mL were different ($P < 0.05$) when compared with each other and also compared with 0.3mg/mL and 0.6mg/mL treatments. These results provide evidence for the first time, that $PGF_{2\alpha}$ has both bacteriostatic and bactericidal effects on the growth of in vitro.

Key Words: *S. aureus*, prostaglandin$F_{2\alpha}$, mastitis

483 Effects of partial replacement of corn grain with high fiber byproducts in calf starter on growth and ruminal pH in dairy calves during weaning transition. A. H. Laarman* and M. Oba, *University of Alberta*, *Edmonton, Alberta, Canada*.

This study evaluated the effects of partially replacing corn grain with high fiber byproducts in calf starter on growth and rumen pH in dairy calves during the weaning transition. Forty-two 2 wk old Holstein bull calves were blocked by BW and experiment start date, and offered one of 3 texturized calf starters. Control starter (CON) contained dry ground corn at 19% of dietary dry matter (DM) in the pellet. For a beet pulp starter (BP) and a triticale dried distillers' grains with solubles (DDGS) starter (DG), dry ground corn was replaced by beet pulp and triticale DDGS at 10% dietary DM. All calf starters contained steam flaked corn and steam rolled barley grain at 19 and 10% of dietary DM, and were formulated to contain 21.5% CP. Calf starter was provided ad libitum up to 2500 g/d. Calves were fed milk replacer (26% CP, 18% fat) at 1200 g/d until wk 5, and 900 g/d and 600 g/d for wk 6 and 7, respectively. Starting wk 8, when calves were completely weaned, hay was provided ad libitum. When a calf consumed at least 2450 g for 3 consecutive days, a small ruminant rumen pH-measuring device (20.6 mm diameter, 138 mm length, 245 g mass) was inserted orally to measure rumen pH continuously for 4 d. Statistical analysis was conducted using mixed procedure of SAS with fixed effects of block and treatment. Average daily gain (1.01 ± 0.02 kg/d) was unaffected by treatment. While mean rumen pH (5.78 ± 0.07) and acidosis duration (857.7 ± 38.7 min/d), time rumen pH was less than 5.8, were not affected by treatment, calves fed DG had more severe acidosis, indicated by a greater area under pH 5.8, than calves fed CON or BP (487.8 ± 57.8 vs 366.4 ± 57.8 and 325.1 ± 52.5 min × pH/d, respectively; $P < 0.05$). Mean rumen pH was positively correlated to hay intake ($r = 0.416$; $P < 0.05$) but not water intake, indicating that hay intake may play an important role in rumen pH regulation during the weaning transition in dairy calves. In conclusion, partially replacing corn grain with high fiber byproducts does not ameliorate, but may exacerbate, rumen acidosis during the weaning transition.

Key Words: rumen pH, calf starter, weaning transition

484 Effect of a pre-synchronization injection of prostaglandin $F_{2\alpha}$ during the voluntary waiting period on dairy cattle. K. D. Baldock*[1], M. E. Wilson[2], and D. L. Smith[1], [1]*Eastern New Mexico University*, *Portales,* [2]*West Virginia University*, *Morgantown*.

It is a common practice on United States dairies to use a prostaglandin $F_{2\alpha}$ ($PGF_{2\alpha}$) injection, during the voluntary waiting period to improve reproductive management. It has been hypothesized that $PGF_{2\alpha}$ will accelerate uterine involution which may decrease the number of days open, while improving first service conception rates. Our hypothesis is that $PGF_{2\alpha}$ given during the voluntary waiting period will improve the reproductive performance of the lactating dairy cow. The objective of this experiment was to administer $PGF_{2\alpha}$ to lactating Holstein dairy cattle during the voluntary waiting period and analyze the effects on first service conception rates, number of days open, services per conception, and days to first service. Lactating, Holstein dairy cows (n = 753) milked 3x per day, were randomly assigned either to the control group (n = 374; no injection of $PGF_{2\alpha}$ between d 30 and 36 postpartum) or treatment group (n = 379; injection of $PGF_{2\alpha}$ between d 30 and 36 postpartum). There were no significant differences ($P > 0.28$) between the treatment and control groups in first service conception rates, number of days open, services per conception and days to first service. Some earlier research suggested a benefit to a pre-synchronization injection of $PGF_{2\alpha}$. However, other researchers reported no benefit. In all cases, low animal numbers may have contributed to inconclusive results. Based on these findings in a large sample group, the common practice of $PGF_{2\alpha}$ administered during the voluntary waiting period of dairy cattle is not a beneficial reproductive management tool.

Key Words: dairy cow, prostaglandin $F_{2\alpha}$, volunteer waiting period

485 Effects of feeding brown midrib corn silage and dried distillers grains with solubles on performance of lactating dairy cows. H. A. Ramirez Ramirez*[1], P. J. Kononoff[1], and K. Nestor[2], [1]*University of Nebraska-Lincoln*, [2]*Dow AgroSciences LLC*, *Wooster, OH*.

Thirty-six Holstein cows (4 fitted with a rumen cannula), averaging 111 ± 35 DIM and 664 ± 76.5 kg BW were used in a replicated 4 × 4 Latin square. The objective was to investigate the effects of 2 corn hybrids, brown midrib (*bm3*) and conventional (DP) corn silages, and the inclusion of dried distillers grains and solubles (DDGS) on milk production and digestibility. In each 28 d period cows were assigned to one of 4 treatments that differed by corn silage hybrid and inclusion rate of DDGS; DP corn silage plus 0% DDGS (CON); *bm3* corn silage plus 0% DDGS (BMR); DP corn silage plus 30% DDGS (CONDG); and *bm3* corn silage plus 30% DDGS (BMRDG). Dry matter intake was affected by hybrid and DDGS ($P < 0.01$); and it was higher for cows consuming diets with *bm3* (25.8 and 24.4 ± 0.47 kg for *bm3* and DP), likewise for cows consuming DDGS (24.3 and 25.9 ± 0.47 kg/d for 0 and 30%). Hybrid and DDGS had an effect ($P < 0.01$) on total tract digestibility of NDF (NDFD). Compared with DP hybrid, NDFD was higher for *bm3* (32.5 vs. 38.1 ± 1.79%). In diets containing DDGS, NDFD was 37.8 and 42.2 ± 1.79% for CONDG and BMRDG. There was an interaction ($P < 0.01$) for total concentration of volatile fatty acids (VFA) and rumen pH as the highly digestible treatment BMRDG resulted in the highest concentration of VFA and the lowest pH. Milk yield was not affected by hybrid nor DDGS ($P > 0.05$) and averaged 30.6 ± 1.09 kg/d. Compared with DP, milk protein yield (MPY) was greater ($P < 0.01$) for *bm3* (0.97 vs. 0.93 ± 0.029 kg/d), similarly MPY was greater ($P < 0.01$) for diets containing DDGS (0.98 vs. 0.92 ± 0.029 kg/d). There was a hybrid by DDGS interaction ($P = 0.02$) for milk fat yield (MFY) resulting in 1.03, 1.08, 0.84 and 0.78 ± 0.045 kg/d for CON, BMR, CONDG and BMRDG. Fat corrected milk (FCM) was only affected by DDGS ($P < 0.01$) and averaged 30.0 and 26.4 ± 1.0kg/d for 0% and 30% inclusions; there was a trend ($P = 0.13$) to increase FCM when cows were fed *bm3* without DDGS. These results indicate that *bm3* corn silage and DDGS increase DMI, NDFD and MPY; however high inclusion of corn silage with 30% DDGS reduces FCM.

Key Words: corn silage, DDGS, nutrient digestibility

486 Effects of equine chorionic gonadotropin administration during the synchronization protocol on luteal volume, progesterone concentration and embryo survival in embryo recipient lactating Holstein cows. A. G. Kenyon*[1], G. Lopes Jr.[1], L. G. D. Mendonca[2], J. R. Lima[1], R. G. S. Bruno[1], and R. C. Chebel[1,2], [1]*Veterinary Medicine Teaching and Research Center, University of California Davis*, *Tulare,* [2]*Department of Veterinary Population Medicine, University of Minnesota*, *Saint Paul*.

Objectives were to determine the effects of treating embryo recipient lactating dairy cows with equine chorionic gonadotropin (eCG) during the synchronization protocol on luteal volume, progesterone concentration (P4) and pregnancy per embryo (P/ET). Cows not inseminated received the Presynch-Ovsynch (d −35 PGF, d −28 CIDR, d −21 PGF and CIDR removal, d −9 GnRH, d −2 PGF, d 0 GnRH) and cows inseminated started the resynchronization protocol (d −16 GnRH, d −9 GnRH, d −2 PGF, d 0 GnRH) 24 d after AI. Cows were randomly assigned to receive (eCG, n = 139) or not receive (control, n = 152) 800 IU of eCG on d −7. Blood was sampled on d −9, −2, 0, 7, and 14 and ovaries were examined by ultrasound on d −9, −2, and 7. Cows bearing a corpus luteum (CL) on d 7 received embryo transfer (ET). Pregnancy was diagnosed at 23 and 60 d after ET. Cows treated with eCG had more ($P = 0.03$) follicles >10 mm on d −2 than control cows (2.3 ± 0.1 vs. 1.9 ± 0.1) and there was ($P = 0.04$) an interaction between treatment and parity because eCG primiparous cows had more follicles >10 mm in diameter on d −2 than control primiparous cows (2.5 ± 0.1 vs. 1.7 ± 0.1), but there was no difference between multiparous cows (2.1 ± 0.1). Proportion of cows with estrous cycle synchronized from d −9 to d 0 was smaller ($P = 0.05$) for eCG treatment (61.0 vs. 71.7%) and fewer ($P = 0.03$) eCG cows received ET (79.1 vs. 87.5%). Among cows receiving ET, proportion with multiple CL on d 7 was not ($P = 0.35$) affected by treatment. Among cows receiving ET, eCG treatment increased ($P < 0.01$) total CL volume on d 7 (8.4 ± 0.4 vs. 6.6 ± 0.4 cm3) and tended ($P = 0.12$) to increase P4 between d 7 and 14 (4.1 ± 0.2 vs. 3.7 ± 0.2 ng/mL). Interaction between treatment and parity tended ($P = 0.07$) to affect P/ET at 60 d because eCG increased P/ET in multiparous cows (30.3 vs. 21.3%) and reduced P/ET in eCG primiparous (16.3 vs. 27.5%). Treatment with eCG reduced proportion of cows eligible to receive ET and only increased P/ET of multiparous cows.

Key Words: embryo transfer, equine chorionic gonadotropin, lactating Holstein cow

487 Adjusting milk replacer intake during heat stress and non-heat stress as a means of improving dairy calf performance. T. M. Chavez*, T. A. Wickersham, and G. A. Holub, *Texas A&M University*, *College Station*.

We evaluated the effects of varying planes of nutrition and heat stress on dairy calf performance. Holstein bull calves < 4 d of age were randomly assigned to 1 of 6 treatments arranged as a 2 × 3 factorial. The factorial consisted of 2 locations: inside (INS) or outside (OUT) and 3 feeding strategies: increasing amounts of milk replacer from 1.1% BW to 1.5% BW (INC), constant at 1.1% BW (CON), or decreasing from 1.6% BW to 1.2% BW (DEC). Provision of milk replacer was increased by 0.1% of BW weekly for INC and decreased by 0.1% of BW for DEC. Prior to initiating milk replacer treatments on d 9 all calves received 1.1% milk replacer per day. The BW used to determine the amount of

milk replacer fed was determined twice weekly. Calves had ad libitum access to commercial starter feed and water. Starter intake, water intake, and fecal score (1 to 4) were recorded daily. Respiration rates and rectal temperatures were collected twice daily at 0600h and 1800h. Temperatures averaged 23.0 ± 4.6 and 30.8 ± 8.5°C for INS and OUT, respectively; correspondingly, THI averaged 66.3 and 79.7 for INS and OUT, respectively. Over the 42 d study ADG was higher ($P < 0.01$) for INS calves compared with OUT (0.77 vs. 0.62 kg/d); however, no significant differences among feeding strategies were observed. Calves INS consumed more starter than those OUT (1.71 vs. 1.31 kg/d; $P < 0.01$). OUT calves had greater water intake than INS (3983 vs. 2228mL/d; $P < 0.01$). INS had greater AM rectal temperatures (101.74 vs. 101.52; $P < 0.01$) while OUT exhibited greater PM rectal temperatures (102.10 vs. 101.86; $P < 0.01$). Respiration rates for OUT were greater ($P < 0.01$) in the AM and PM than INS (35.78 vs. 33.27 and 46.82 vs. 34.65, AM and PM, respectively). Alternate milk replacer feeding strategies were not effective in ameliorating the negative effects of heat stress nor did feeding strategy impact calf performance in animals subject to a more favorable environment.

Key Words: heat stress, dairy calves, milk replacer

488 Comparison of postpartum health, uterine involution, and resumption of ovarian cycles of Holstein and crossbred dairy cows. L. G. D. Mendonca*, C. C. Abade, E. M. da Silva, and R. C. Chebel, *Department of Veterinary Population Medicine*, *Saint Paul, MN*.

Objectives were to evaluate whether Holstein (HO) and Montbeliarde sired crossbred dairy cows (MS) differ in regards to postpartum health, uterine involution, and resumption of ovarian cycles. Cows (HO = 46 and MS = 43) were enrolled in the study 45 d before expected calving date. Cows were examined daily from 0 to 14 DIM for diagnosis of pyrexia (>39.5°C), retained fetal membranes (RFM), puerperal metritis, ketosis, and displacement of the abomasum (DA). At 24 DIM cows were examined by vaginoscopy for diagnosis of clinical endometritis. Starting at 14 DIM cows were examined by ultrasound every third day until 42 DIM and volume of the previous gravid and non-gravid uterine horns were recorded as well as number and size of corpora lutea (CL) and follicles class II (5-9 mm) and class III (>9 mm). At 42 DIM cytology of the uterus was performed for diagnosis of sub-clinical endometritis. Incidences of RFM (HO = 6.5, MS = 7.0%; P = 0.89), metritis (HO = 13, MS = 4.7%; P = 0.12), DA (HO = 2.2, MS = 0%; P = 0.95) were not different between by breed, but HO cows tended (P = 0.07) to be more likely to have pyrexia (HO = 54.4, MS = 34.9%) and were (P = 0.03) more likely to have at least one of the diseases described above (HO = 56.5, MS = 34.9%). MS cows were (P = 0.01) less likely to have endometritis (HO = 47.8, MS = 22%), consequently MS cows tended (P = 0.07) to have smaller uterine discharge score (HO = 1.7±0.2, MS = 1.1 ± 0.3). There were no (P = 0.97) differences in incidence of sub-clinical endometritis (HO = 14.3, MS = 10%). Breed was not associated with volume of gravid (P = 0.70) and non-gravid (P = 0.27) uterine horns from 14 to 42 DIM. Although HO cows had (P = 0.01) more follicles class III from 14 to 42 DIM (1.6 ± 0.1 vs. 1.2 ± 0.1), MS cows tended (P = 0.07) to be more likely to ovulate by 42 DIM (75.6 vs. 90.2%). Holstein cows were at higher risk for puerperal disorders and tended to be less likely to ovulate by 42 DIM.

Key Words: postpartum health, Holstein, crossbred

Nonruminant Nutrition: Amino Acids 2

489 Impact of sulfur amino acid intake and immune system stimulation on pathways of sulfur amino acid metabolism at transcriptional level in growing pigs. A. Rakhshandeh*[1], A. Holliss[2], N. A. Karrow[1], and C. F. M. de Lange[1], [1]*University of Guelph, Department of Animal and Poultry Science*, [2]*University of Guelph, Advance Analysis Centre*, *Guelph, Ontario, Canada*.

Sulfur amino acid intake (SAA) and immune system stimulation (ISS) alter post-translational metabolism of SAA. In this study we investigated the impact of SAA intake and ISS on expression of key regulatory genes that control the pathways of SAA metabolism in different tissues of pigs. Restricted-fed barrows (BW 21.5 kg) were allotted to one of 2 levels of SAA intake (1.1 and 3.2, g/d) and injected with either saline (n = 8) or increasing amounts of *Escherichia coli* lipopolysaccharide (n = 16) every 48 h for 7 d. Pigs were then killed for the collection of liver, spleen and ileum tissues for total RNA extraction. Tissue and an internal standard (KANr) RNA were then reverse transcribed. Expression was simultaneously determined by multiplex PCR amplification of cDNA from tissues, the housekeeping gene (β-2-microglobulin) and the internal standard in the presence of their corresponding florescent labeled primers. The interactive effect (ISS × SAA) resulted in upregulation of adenosylhomocysteinase (AHCY) at higher level of SAA intake in liver of ISS pigs ($P < 0.01$). No interactive effect on other studied genes was observed. Increased SAA intake upregulated cysteine dioxygenase (CDO1), 3-mercaptopyruvate sulfurtransferase (MST) and cysteine sulfinic acid decarboxylase (CSAD) in liver ($P < 0.05$). Expression of CDO1, MST and cystathionine β-synthase (CBS) in liver was upregulated by ISS. However, ISS downregulated methionine adenosyltransferase 2 (MAT2) in liver ($P < 0.05$). Expression of methionine synthase (MTR) and cystathionine γ-lyase (CTH) was not affected by the treatments. Results of gene expression in spleen and ileum are forthcoming. This study suggests that the SAA metabolism pathways are changed at transcriptional level by ISS and SAA intake.

Key Words: sulfur amino acids, immune system stimulation, gene expression, multiplex PCR

490 The effect of feeding heavy and medium weight nursery pigs increased levels of amino acids on pig performance. J. L. Pietig* and C. E. Hostetler, *South Dakota State University*, *Brookings*

A study was conducted to determine the effect of feeding increased levels of amino acids to nursery pigs, which were heavy and medium weight at weaning. A total of 144 (n = 144) crossbred, mixed sex pigs (21.7 d of age) was used in the study. A 3 phase feeding program was used to mimic industry practice. Treatments consisted of nursery diets with increased levels of lysine, methionine, threonine and tryptophan. The control diet was designed to meet industry standards (IS; n = 36). Dietary concentrations of the aforementioned amino acids were increased above the control diet by 10% (+10; n = 36), 20% (+20; n = 36), and 30% (+30; n = 36) using synthetic amino acids. Pigs were blocked by body weight (Heavy; 7.87 kg BW and Medium; 5.88 kg BW) at weaning. Pigs were weighed at trial initiation and at each diet change; average daily feed disappearance (ADFD) was determined for each phase. All pigs were bled on d 4, 11, and 28 after initiation of the trial for determination of plasma urea nitrogen (PUN) levels. In phase 1 there was a significant effect of treatment on ADG (0.177 vs. 0.156, 0.150, 0.144 Kg; +10 vs. IS, +30, +20 respectively; $P < 0.05$) and feed to gain efficiency (F:G; 1.31 vs. 1.19, 1.18, 1.11; +20, +30, IS, +10 respectively; $P < 0.05$). In period 2 there was an effect of treatment on ADFD (0.367 vs. 0.412, 0.418, 0.448 Kg; +30, +20, +10, +IS respectively; $P < 0.05$) and PUN levels (13.23 vs. 8.55, 8.28, 7.741; IS, +20, +30, +10 respectively; $P < 0.05$). Also, PUN levels were affected by weight (10.83 vs. 8.07; Heavy vs. Medium respectively; $P < 0.05$). In phase 3 there was no significant effect of treatment on performance or PUN levels. Over the entire trial, there was a significant effect of treatment on F:G (1.38 vs. 1.42, 1.43, 1.464; +10, +30, +20, IS; respectively; $P < 0.05$) and PUN was effected by weight (12.707 vs. 10.328; heavy vs. medium; $P < 0.05$). These results indicate that there may be benefit to feeding higher levels of amino acids to nursery pigs and that medium weight pigs may benefit from increased amino acid levels compared with heavy weight pigs.

Key Words: swine, nutrition, amino acids

491 Amino acid digestibility in heated soybean meal fed to growing pigs. J. C. González*[1,2], B. G. Kim[2], A. Lemme[3], and H. H. Stein[2], [1]*National University of Colombia*, *Bogota, Condinamarca, Colombia*, [2]*University of Illinois*, *Urbana,* [3]*Evonik Degussa GmbH*, *Rodenbacher Chaussee, Hanau, Germany*.

Excessive heat treatment during processing may lead to destruction of AA and the formation of biologically unavailable AA-carbohydrate complexes (i.e., Maillard formation). The objective of the present experiment was to determine the effects of heat treatment of soybean meal (SBM) on standardized ileal digestibility (SID) of AA by growing pigs. Ten growing barrows (average initial BW: 25.3 ± 2.04 kg) were individually fitted with a T-cannula in the distal ileum and used in the experiment. Pigs were allotted to a replicated 5 × 5 balanced Latin square design with 5 diets and 5 periods. Four sources of SBM were prepared by 1) no heat treatment, 2) autoclaving at 125°C for 15 min, 3) autoclaving at 125°C for 30 min, or 4) oven drying at 125°C for 30 min. Four diets contained each of the 4 SBM sources as the sole source of AA. A N-free diet was used to estimate basal endogenous losses of AA. The SID of CP and all AA in SBM linearly decreased as the time of autoclaving increased from 0 to 30 min ($P < 0.01$; Table 1). Oven drying at 125°C for 30 min only tended to reduce the SID of CP and AA in this study. It is concluded that heat treatment in the form of autoclaving at 125°C impairs the digestibility of AA in SBM.

Table 1. Standardized ileal digestibility of CP and AA in soybean meal that has either not been heated, autoclaved (AC) or oven-dried (OD)[1]

	Soybean meal					
Item	Not heated	AC at 125°C for 15 min	AC at 125°C for 30 min	OD at 125°C for 30 min	SEM	P-value
CP, %	93.1[a]	88.8[a]	84.0[b]	91.4[a]	1.48	< 0.01
Lys, %	93.0[a]	89.3[b]	84.2[c]	91.3[ab]	1.21	< 0.01
Met, %	93.2[a]	91.1[a]	88.3[b]	92.4[a]	0.91	< 0.01
Thr, %	89.2[a]	87.1[ab]	83.5[b]	86.1[ab]	1.45	< 0.01
Trp, %	90.9[a]	88.0[ab]	83.8[b]	88.4[a]	1.37	< 0.01

[1]Each least squares means represents 10 observations.

Key Words: amino acid, digestibility, soybean meal

492 Effects of balanced protein level on growth performance and carcass composition of growing-finishing pigs. N. W. Shelton[1], R. D. Goodband[1], M. D. Tokach[1], S. S. Dritz[1], J. L. Nelssen[1], J. M. DeR-

ouchey[1], M. S. Redshaw[2], and J. K. Htoo*[2], [1]*Kansas State University, Manhattan,* [2]*Evonik Degussa GmbH, Hanau, Germany*.

A total of 1,003 barrows and gilts (PIC 337; initial BW of 51.5 kg) were used in a 88-d study to determine the effects of varied levels of balanced protein (BP) on growth performance and carcass characteristics. Balanced protein refers to balancing dietary AA according to the ideal protein ratio at least for the first 4 limiting AA. In a completely randomized design, 3 corn and soybean meal-based experimental diets were tested over 2 phases, including a growing phase (d 0–28; 51–79 kg BW) and a finishing phase (d 29–88; 79–130 kg BW) using 6 replicate gilt and 7 replicate barrow pens per treatment. Dietary treatments included a low BP diet which met the NRC (1998) requirements, a diet which met Evonik Degussa (ED) recommendations, and a diet which was formulated to be 10% above the ED recommendations. Diets were formulated to contain identical net energy content. No gender × BP interactions were observed ($P > 0.30$) for any of the growth performance and carcass responses. During the growing phase, G:F improved ($P = 0.001$) and ADG tended to increase ($P = 0.07$) as the BP level increased in the diet. The greatest improvements were achieved with the highest BP level containing 0.89% standardized ileal digestible Lys. Gilts had improved ($P < 0.001$) G:F from d 0 to 28 compared with barrows. During the finishing phase, BP levels did not affect ($P > 0.05$) growth performance which may have been confounded by a relatively long duration (60 d) of the finishing phase. Over the entire 88-d period, ADG and G:F improved ($P < 0.02$) as the dietary BP levels increased. Gilts had lower ADFI and improved G:F ($P < 0.01$) than barrows during the entire period. Carcass characteristics (yield, backfat depth, loin depth, lean percentage) and income over feed cost were not affected by feeding varied levels of BP. These results suggest that today′s pigs with high lean potential respond to a higher BP than current recommendations.

Key Words: balanced protein, lysine, pig

493 Effect of tryptophan level on growth performance in 10- to 50-kg pigs. D. Renaudeau*[1], M. Giorgi[1], C. Anais[1], and Y. Primot[2], [1]*Institut National de la Recherche Agronomique, UR143, Petit-Bourg, French West Indies, France*, [2]*Ajinomoto Eurolysine, Paris, France*.

The effect of dietary tryptophan (Trp) content and pig density were tested between 10 to 50 kg BW on a total of 80 Large White pigs (40 females and 40 barrows) as a complete randomized block design in a 2 × 2 factorial arrangement (2 replicates/treatment). Pigs were randomly assigned to one of 4 treatments in 8 similar pens (3 × 2 m) of 8 or 12 animals (0.75 or 0.50 pig/m^2). In each pen, females and barrows were equally mixed. Dietary treatments consisted of 2 diets with different standard ileal digestible (SID) Trp content (0.19 or 0.25%), where the SID lysine content (1.06%), energy level (10.2 MJ NE/kg) and ideal AA patterns (Lys, Thr, Met, Ile, Val) were kept constant. Data were subjected to an ANOVA including the effect of diet, pig density, replicate, sex, block and interactions (GLM procedure of SAS). There were no interaction between dietary Trp content and pig density ($P > 0.05$). The average daily feed intake (ADFI) was not influenced by pig density between 10 and 25 kg (827 g/d on average; $P > 0.05$). Between 25 and 50 kg, ADFI was reduced when pig density increased from 8 to 12 pig/pen (1600 vs. 1357 g/d; $P < 0.05$) which resulted in a non-significant reduction of the average daily gain (ADG) (715 to 646 g/d; $P = 0.07$). Between 10 to 25 kg, ADFI and ADG were significantly higher in high Trp diet (863 vs. 790 g/d and 500 vs. 454 g/d; $P < 0.05$). Feed conversion ratio (FCR) was not influenced by diet and averaged 1.7 kg/kg. Between 25 to 50 kg, ADG, ADFI and FCR were not affected by diet and averaged 681 g/d, 1480 g/d and 2.3 kg/kg, respectively. The lack of effect of high dietary Trp content from 25 to 50 kg could be explained by the fact that dietary lysine content was not limiting for growth for this BW range after 25 kg. For the whole experiment period, ADFI remained unaffected by diet ($P > 0.05$) and ADG tended to be higher in pigs fed high Trp diet (601 vs. 557 g/d; $P = 0.06$). These results suggested that a SID Trp content higher than 0.19 g/100 g or 0.18 g/100 g SID lysine is necessary to maximize growth performance in pigs especially between 10 to 25 kg BW.

Key Words: pig, amino acids, tryptophan

494 Estimation of optimum tryptophan to lysine ratio in wheat-barley or corn-soybean meal based diets for 15- to 35-kg pigs. J. K. Htoo*[1], M. Naatjes[2], K. H. Tölle[3], and A. Susenbeth[2], [1]*Evonik Degussa GmbH, Hanau, Germany*, [2]*Christian-Albrechts University, Kiel, Germany*, [3]*Training and Research Center Futterkamp, Bliekendorf, Germany*.

A 28-d dose-response assay was conducted with 880 mixed-sex pigs (Pietrain × dbNaima; initial BW of 14.4 kg) with 5 pen replicates per treatment to determine the optimum dietary standardized ileal digestible (SID) Trp:Lys ratio for 15 to 35 kg pigs fed corn-soybean meal (SBM) or wheat-barley based diets. Two Trp-deficient basal diets, based on wheat-barley or corn-SBM, were formulated, using analyzed ingredient AA contents and published SID AA values to meet requirements of AA other than Trp and Lys. The Lys level (1.05% SID Lys) was marginally limiting in all diets, which corresponds to 91% of requirement (1.15% SID Lys) recommended for the pigs used in the study. L-Trp was added to both basal diets at the expense of wheat or corn to create 7 SID Trp:Lys ratios (13.3, 14.8, 16.3, 17.8, 19.3, 20.8 and 22.3%), and a Lys-adequate diet (diet 8, equivalent to diet 7 with added L-Lys-HCl to contain 1.15% SID Lys) was also formulated as a control for both diet types. The SID Trp:Lys ratios (based on analyzed AA content) were 13.1, 14.2, 15.3, 16.4, 17.5, 18.6 and 19.7% in diets 1 to 7 of wheat-barley based diets, and 14.3, 15.4, 16.5, 17.6, 18.7, 19.8 and 20.9% in diets 1 to 7 of corn-soybean meal based diets, respectively. The ADG and FCR of pigs were improved ($P < 0.05$) with increasing Trp:Lys ratio for both wheat-barley and corn-SBM based diets. Feed intake was increased by graded level of Trp:Lys ratio in both wheat-barley ($P < 0.05$) and corn-SBM based diets ($P < 0.10$). The estimated SID Trp:Lys ratios to optimize ADG were > 19.7 and 15.9% in wheat-barley based diets, and > 20.9 and 17.8% in corn-SBM based diets based on the exponential (at 95% of plateau) and broken-line regression, respectively. The SID Trp:Lys ratios to optimize FCR were > 19.7 and 17.0% for wheat-barley based diets, and > 20.9 and 19.9% for corn-SBM based diets by using the respective exponential and broken-line models.

Key Words: lysine, ratio, tryptophan

495 Effect of lysine level and curve feeding on the performance and carcass characteristics of grow-finish pigs. K. L. Herkelman*[1], S. Kelley[2], S. Bailey[1], and E. Engle[3], [1]*Wenger's Feed Mill, Inc., Rheems, PA,* [2]*Country View Family Farms, Lancaster, PA*, [3]*Hatfield Quality Meats, Hatfield, PA*.

An experiment was conducted to evaluate the effect of lysine level and curve feeding on the performance and carcass characteristics of grow-finish pigs. Crossbred pigs (n = 1,012; initial BW: 28.4 kg) were blocked by BW and gender and allotted to 4 treatments with 10 replicate pens/treatment and 25 or 26 pigs/pen. Treatments were arranged in a 2 × 2 factorial design with 2 levels of lysine (Control or Control + 0.1% dietary lysine in each phase) and 2 types of feeding systems (Feed Budget or Curve Feeding). The Control treatment consisted of diets containing 1.21, 1.10, 1.00, 0.86, and 0.78% dietary lysine fed in 5 phases. Pigs fed

using a feed budget were fed 23, 34, 46, 57 and 16 kg/pig for phases 1 to 5, respectively. Pigs fed on the feed curve started each phase at the lysine level of pigs fed on the feed budget. Lysine level was decreased every 5 lb of feed disappearance/pig using a FeedPro feeding system by blending diets containing 1.31 and 0.78% lysine. All pigs were fed a Paylean (6.75 g/ton) diet from the end of phase 5 to market weight. Pigs were allowed ad libitum access to feed and water. Pigs were marketed by pen at an average slaughter weight of 129.4 kg and carcass AutoFom data was collected. No lysine level × feeding system interactions were observed for any parameter. An increase in dietary lysine improved ($P < 0.05$) growth rate (1.01 vs. 0.99 kg/day) and feed disappearance (2.40 vs. 2.36 kg/day) of pigs compared with pigs fed the Control. Efficiency of feed utilization was similar ($P > 0.10$) between pigs fed the Control and diets with increased lysine levels (2.38 kg feed/kg gain). Curve feeding improved ($P < 0.02$) the growth rate (1.01 vs. 0.99 kg/day) and efficiency of feed utilization (2.37 vs. 2.40 kg feed:kg gain) of pigs compared with pigs fed by feed budget. Carcass characteristic were not influenced ($P > 0.10$) by lysine level or feeding system. In conclusion, increasing dietary lysine increased feed disappearance and improved the growth rate of grow-finish pigs. Diets fed on a feed curve improved the growth rate and efficiency of feed utilization of pigs compared with using a feed budget.

Key Words: lysine, pigs, curve feeding

496 Effects of ileal sample collection strategies on ileal digestibility of CP and the concentration of chromium in ileal digesta. B. G. Kim*[1,2] and H. H. Stein[1], [1]*University of Illinois*, *Urbana*, [2]*Konkuk University*, *Seoul, Korea*.

An experiment was conducted to measure the effect of ileal sample collection time on the concentration and digestibility of CP by growing pigs. Eight barrows with an initial BW of 34.6 kg (SD = 2.1) were individually fitted with a T-cannula in the distal ileum and randomly allotted to a replicated 4 × 4 Latin square design with 4 diets and 4 periods per square. Three diets contained corn, soybean meal, or distillers dried grains with solubles as the sole source of CP. An N-free diet was also prepared. All diets contained 0.5% chromic oxide as an indigestible marker. Equal meals were provided at 0800 and 2000. Ileal digesta samples were collected in 2-h intervals from 0800 to 2000 during the last 3 d of each 7-d period. The concentrations of Cr (1.22, 1.39, 1.65, 1.61, 1.39, and 1.20%; SEM = 0.06) and CP (16.3, 19.0, 23.6, 22.1, 19.4, and 17.1%; SEM = 0.7) in ileal samples collected in each of the 6 2-h periods exhibited a quadratic effect ($P < 0.001$) that increased and then decreased in pigs fed the 3 CP-containing diets. However, apparent ileal digestibility of CP (62.2, 59.5, 59.2, 60.7, 61.7, and 59.6; SEM = 2.2) was unaffected ($P = 0.745$) by collection time, and the values were comparable to the 12-h digestibility (61.6%) calculated using the Cr and CP concentrations of 12-h collection periods. The endogenous loss of CP tended to decrease (27.4, 25.7, 29.5, 26.0, 22.3, 21.4 g/kg DMI; SEM = 4.5; $P = 0.099$) with collection time. Standardized ileal digestibility values of CP linearly decreased (81.0, 77.1, 79.4, 78.5, 76.9, and 74.3%; SEM = 2.2; $P = 0.008$), but values for the third and fourth 2-h periods were comparable to the 12-h standardized ileal digestibility (78.7%). In conclusion, diurnal variation of Cr and CP concentration were observed, but the digestibility of CP was largely unaffected by collection time. We suggest that 2 to 4 h of ileal sample collection from 4 h after feeding may provide samples that allow for calculation of a representative CP digestibility.

Key Words: diurnal variation, ileal digestibility, pigs

497 Ileal amino acids digestibility of raw and heat-processed pea protein concentrates in broilers. M. Frikha[1], D. G. Valencia*[2], M. P. Serrano[1], H. M. Safaa[3], R. Lázaro[1], and G. G. Mateos[1], [1]*Universidad Politécnica de Madrid*, *Madrid, Spain*, [2]*Nutral S.A.*, *Madrid, Spain*, [3]*Faculty of Agriculture, Cairo University*, *12613 Giza, Egypt*.

A trial was conducted to determine the apparent (AID) and standardized (SID) ileal digestibility of the AA of 2 different batches of pea protein concentrate (PPC) either raw or heat processed (HP, autoclaving at 108°C for 8 min at 0.6 bars) as compared with soy protein concentrate (SPC) in 21-d-old broilers. Each of the 5 treatments was replicated 6 times (6 cages with 6 chicks per replicate). The 2 PPC and the SPC batches contained 45.6, 44.6, and 52.4% CP, 3.48, 3.29, and 2.69% total Lys, and 9.4, 9.1, and 0.2 mg/g trypsin inhibitor activity (TIA), respectively. The diets were based on corn starch and sucrose and the ingredient tested was the only source of CP (20%). In addition, a N-free diet was used in 6 extra replicates to estimate the basal ileal endogenous losses. Chicks were fed their respective experimental diets ad libitum in mash form from 18 to 21 d of age. Chicks fed the HP PPC had higher ($P < 0.001$) AID of CP (87.61, 82.19, and 83.43%) and of most of indispensable AA (i.e, 92.14, 88.80, and 84.69% for Lys) than chicks fed the raw PPC with chicks fed the SPC being in general intermediate. The SID of most of indispensible AA was similar for the SPC and the HP PPC and higher for both ($P < 0.05$) than for the raw PPC. An interaction between type and HP of the PPC was observed; the beneficial effects of HP on AA digestibility were more pronounced in one of the 2 PPC samples studied ($P < 0.05$). The different response observed for the 2 PPC types with HP, was consistent with the higher reduction in TIA in one of the samples (9.4 to 2.8 mg/g vs. 9.1 to 5.8 mg/g, respectively). It is concluded that HP of PPC improves the ileal digestibility of CP and of the AA. Also, HP PPC had higher ileal digestibility of most AA than PPC. Thus, HP PPC is a good alternative to SPC in poultry diets.

Key Words: pea protein concentrate, heat processing, ileal amino acid digestibility broilers

498 Identification of lysine transport systems affiliated with differences in chick gain when fed a lysine limiting diet. M. A. Raymond* and B. D. Humphrey, *California Polytechnic State University*, *San Luis Obispo*.

Lysine (Lys) is the first or second limiting amino acid for growth in poultry feed, yet the mechanisms controlling Lys utilization within tissues are not well understood. Lys transporters facilitate the import and export of Lys within tissues. The objective of this study was to use a Lys limiting growth model to better understand the role of Lys transporters in Lys utilization within the pectoralis, liver, and duodenal mucosa. Male broiler chicks (3 d of age) were weighed, randomly assigned to pens and provided a Lys adequate (LA: 1.3% Lys) or Lys deficient diet (LD: 0.66% Lys). On d 14, chicks were sorted based upon d 3 to 14 gain. Chicks consuming the LD diet with the highest gain were designated as high gain (HG; n = 10) and chicks with the lowest gain were designated as low gain (LG; n = 10). LA chicks with average gain served as the control (C; n = 5). HG, LG and C chicks were housed in individual pens for 3 d. On a BW basis, HG chicks had 134% higher gain and 64% higher breast yield compared with LG chicks ($P < 0.05$) despite similar lysine intake ($P > 0.05$). Pectoralis, liver and duodenal mucosal scrapings were collected on d 17 for measurement of Lys transporter mRNA by real-time qPCR. Overall, HG and LG chicks had higher tissue Lys transporter mRNA abundance compared with C chicks. In the pectoralis, LG chicks had 1.6-fold higher CAT3 and 1.4-fold higher y^+LAT1 mRNA abundance compared with HG chicks ($P < 0.05$). In the liver, CAT3 mRNA abundance was 1.7-fold higher in LG chicks compared

with C chicks ($P < 0.05$). In duodenal mucosa, LG chicks had 1.45-fold higher y^+LAT2 mRNA abundance compared with HG chicks ($P < 0.05$). The difference in gain between LG and HG chicks was associated with increased mRNA abundance of LYS transporters within the pectoralis (CAT3, y^+LAT1), liver (CAT-3) and duodenum (CAT3, y^+LAT2). These data indicate that the respective tissue transporters may play an important role in the utilization of dietary Lys.

Key Words: lysine, transport, pectoralis

499 Valine and isoleucine as potential limiting amino acids in broiler diets based on corn, soybean meal, and meat and bone meal. L. Mejia*[1], W. A. Dozier III[2], R. E. Loar II[1], M. T. Kidd[3], P. B. Tillman[4], and A. Corzo[1], [1]*Mississippi State University*, *MS*, [2]*Auburn University*, *Auburn, AL*, [3]*University of Arkansas*, *Fayetteville, AR*, [4]*Ajinomoto Heartland LLC*, *Chicago, IL*.

A randomized complete block design study, using area of the house as a blocking factor, was designed to evaluate Ile and Val as potential fourth and fifth limiting amino acids in diets based on corn, soybean meal, and meat and bone meal. Eleven hundred and 52 Ross × Ross TP16 male broilers were randomly placed across 96 floor pens (12 birds/pen). Common diets were fed to all broilers from 0 to 28 d of age and formulated to satisfy all nutrient recommendations. An experimental diet was provided to the broilers from 28 to 42 d of age, served as negative control (NC), and was formulated to satisfy all nutrient recommendations with the exception of Ile and Val (0.57% dig Ile and 0.66% dig Val). The NC diet was supplemented with L-Ile and L-Val at either 0.05 or 0.10%, alone or in combination. A diet formulated to digestible Val and Ile of 0.76 and 0.67%, respectively, mimicking commercial practice served as a positive control (PC). Body weight gain was depressed ($P < 0.01$) with the NC, but was recovered to a weight similar to birds that were fed the PC when Val was added to the test-diet either alone or in combination with Ile. Feed conversion was improved ($P < 0.001$) when L-Val and L-Ile were simultaneously supplemented to the NC. Carcass weight and yield were unaffected ($P > 0.05$) by the dietary treatments. Abdominal fat percentage was reduced ($P < 0.05$) with the combined supplementation of L-Val and L-Ile to the NC. Breast meat yield seemed to be more responsive ($P < 0.01$) to L-Ile supplementation than L-Val. Results from this study suggest that Val needs may be more sensitive for live performance while breast meat yield was maximized with L-Ile supplementation. However, it seems that under these experimental circumstances, a combination of L-Val and L-Ile is required for optimum growth and meat yield of broilers.

Key Words: broiler, isoleucine, valine

500 Effect of different sorghum varieties on early chick growth. C. M. Rude*[1], M. A. Barrios[1], R. Rierson[1], S. Bean[2], and R. S. Beyer[1], [1]*Kansas State University*, *Manhattan,* [2]*ARS, USDA, Grain Marketing and Product Research Center*, *Manhattan, KS*.

Although corn is the predominant cereal grain used in commercial broiler rations in the US, price advantages sometimes allow the use of sorghum in least cost rations. Similar to corn and wheat, sorghum hybrids exist for human versus animal feed. Besides costs, geographical limitations, environmental impacts, grain yields and availability of sorghum by products could allow some of these products to be used in poultry rations. An experiment was designed to test the effect of grain sorghum varieties on broiler chick growth. Broiler starter rations were formulated to NRC recommendations, using sorghum as the cereal grain. Chicks were fed one of 4 different white sorghums: Macia, straight run sorghum grown almost exclusively in Africa; F 1000, popular commercial hybrid for food; Sp3303 new food hybrid; and MMR 315–10, relatively new food hybrid grown extensively in Russia. All sorghums were grown on the same farm in western Kansas. Diets were fed to 21 d of age, with feed and BW recorded on d 0 and 21, with FC calculated from this data. Each treatment had 8 replications, with 6 birds per pen housed in Petersime battery cages. Feed and water were provided ab libitum. Differences were observed between sorghums in BWG and FC ($P < 0.05$). Sorghum hybrid F1000 had the lowest BWG with 484 g, followed by Macia at 532 g. Highest BWG of 765 g was observed with the MMR 315–10 hybrid and which was statistically similar to Sp3303 with a BWG of 747 g. Two sorghums were statistically similar, F1000 and Macia, had lower feed consumption than the other 2 sorghums, Sp3303 and R315–10, who were also statistically similar. Feed conversion was 0.744, 0.752, 0.767, and 0.783 for the Macia, F1000, Sp3303 and MMR 315–10 varieties, respectively. Differences in growth are attributed to differences in the sorghums characteristics. Hybrid F1000 is widely used in the food industry for its high dough viscosity, an attribute that could reduce broiler performance. Macia is grown for its drought hardiness and disease resistance. These results indicate that caution is required when using varieties of sorghum that have been developed for other markets than animal feeding.

Key Words: sorghum, broiler, hybrid

501 Dietary hydrolyzed yeast extract enhances early innate immune function in broiler chicks. J. L. Saunders-Blades*, K. L. Nadeau, and D. R. Korver, *University of Alberta*, *Edmonton, Canada*.

The effects of dietary yeast on growth and immune function of broiler chicks were studied. A bioethanol process derived yeast product was fed as either intact (I) or hydrolyzed by a 1–3 β-glucanase (H), at 4 levels (250, 500, 1000 or 2000 g/t) plus a control diet (C) with no yeast for a total of 9 diets (n = 6 pens/treatment). BW and feed intake were measured for the starter (0 to 10 d) and grower (11 to 28 d) periods. Whole blood was obtained weekly from 10 chicks/treatment to make in vitro assessments on the number of cells able to engulf at least one *Escherichia coli* (% phagocytosis), average number of *E. coli*/cell (phagocytic capacity), and *E.coli* bactericidal capacity. There were no diet effects on broiler production traits during the starter period. During the grower phase, lower feed intake among birds fed 500 or 2000 g/t of H ($P < 0.05$) resulted in a marginally lower BW gain ($P = 0.056$) and overall BW ($P = 0.058$); feed efficiency was not affected. At 2 wk, cells from H birds had a greater % phagocytosis (11–13% increase) and phagocytic capacity (15–31% increase) than those in the I group ($P < 0.05$). There was no difference in % phagocytosis between the cells from birds in any H groups with the C treatment, however cells from birds in the H2000 group had a 13% greater phagocytic capacity than the C treatment. At 3 wk, H2000 resulted in a 10% lower % phagocytosis than the C chicks and all levels of I (from 5 to 15%; $P < 0.05$). At 4 wk, cells from I2000 and H250 birds had a greater % phagocytosis than those from C birds (14 and 17% increase, respectively; $P < 0.05$). Diet did not affect bactericidal capability at any age. Both the I and H yeast increased early innate immune function in broilers relative to C. The H yeast (>500g/t) was most effective at increasing innate immunity at 2 wk, as the broilers aged (>3wk) the difference between the I and H was less pronounced. This may be a function of changes in the development of the immune system and the components present in the different treatments to activate it as the bird ages.

Key Words: broiler, hydrolyzed yeast, innate immune function

502 Influence of pea hulls inclusion in the diet on digestive traits and nutrient retention in broilers. E. Jiménez-Moreno*[1], J. M. González-Alvarado[2], S. Chamorro[3], C. Centeno[3], R. Lázaro[1], and G. G. Mateos[1], [1]*Universidad Politecnica de Madrid*, *Madrid, Spain*, [2]*Universidad de Tlaxcala*, *México*, [3]*Consejo Superior de Investigaciones Científicas*, *Madrid, Spain*.

The effects of inclusion of pea hulls (PH; 47% neutral detergent fiber and 9% starch) in the diet on the digestive traits and total tract apparent of retention (TTAR) of nutrients were studied in broilers from 1 to 21 d of age. A control diet based on cooked rice, soy protein concentrate, and fish meal that contained 3,260 kcal AME_n/kg, and 1.25% digestible Lys was diluted with 0, 2.5, 5.0, and 7.5% PH (1.6, 2.6, 3.5, and 4.5% CF, respectively). Each treatment was replicated 6 times (a cage with 12 chicks). Digestive traits and nutrient retention were recorded at 7, 14, and 21 d of age, and jejunal histology was measured at 14 d of age. The relative weight (% BW) of proventriculus ($P \leq 0.01$), gizzard ($P \leq 0.001$), and ceca ($P \leq 0.05$) increased as the level of PH in the diet increased. Digesta content of the gizzard was increased ($P \leq 0.001$) and gizzard pH was reduced ($P \leq 0.001$) with 2.5% PH. No further changes were observed with 5% and 7.5% inclusion. Crypt depth decreased linearly ($P \leq 0.05$) with PH inclusion. However, villus height and villus height:crypt depth ratio were not affected. The TTAR of soluble ash and N increased with up to 5% PH inclusion ($P \leq 0.001$). Also, TTAR of DM and OM, as well as the AME_n of the diet ($P \leq 0.001$) were improved with 2.5% PH inclusion; however, a further increase to 5% reduced TTAR of these nutrients. We conclude that an increase in dietary PH increases proventriculus, gizzard, and ceca weight in broilers from 1 to 21 d of age. Also, the inclusion of 2.5% PH increases digesta content and reduces the pH of the gizzard. The inclusion of up to 5.0% PH in the diet (3.5% CF) improves N retention but reduces the AMEn of the diets. A further increase to 7.5% PH (4.5% CF in the diet) impairs digestibility of all nutrients studied. The optimal requirement of CF in diets for young chicks might be between 2.6% and 3.5%.

Key Words: pea hulls, nutrient digestibility, broiler

503 Dietary camelina meal for broiler chickens: 2. Thigh meat fatty acid profile and sensory evaluation. P. H. Patterson*[1], R. M. Hulet[1], T. L. Cravener[1], A. Y. Pekel[2], and J. E. Hayes[1], [1]*The Pennsylvania State University*, *University Park*, [2]*Istanbul University*, *Turkey*.

Camelina is an oilseed plant from the Brassicaceae family. It has recently been grown for biodiesel production with the meal utilized as a dietary protein supplement with a residual complement of omega-3 fatty acids. An experiment was conducted to examine the effect of dietary camelina meal (CM) supplementation on broiler live performance and meat quality. A total of 864 Ross x Cobb-500 straight run chicks were allocated to control (Con), 5% or 10% CM diet treatments with 8 pens per treatment from 1 to 35d. The CM utilized in this study contained 33.6% CP, 15.0% fat and 4.22% total omega-3 fatty acids. At the conclusion of the study, the birds were processed, cut up and meat frozen for further fatty acid analysis and sensory evaluation. Frozen thigh samples were thawed, skin was removed and then de-boned. The meat (270–280g portions) was placed in vacuum pouches, sealed under vacuum and held at 3.3C overnight before sensory evaluation. The meat was cooked sous-vide at 73.8C in a water bath for 50m. Cooked and cut meat (15–20g) was placed in insulated bowls and presented to 59 participants in a 2 triangle test sensory evaluation. Each participant received 6 bowls, 3 for test 1 and 3 for test 2. Two samples in each test were the same and participants were asked to choose the different sample. Dietary treatments significantly influenced thigh meat fatty acid profiles. Feeding the 10% CM diet increased thigh meat 18:3, 20:3, 20:5 (EPA), 22:5 (DPA), 22:6 (DHA) and total omega-3 fatty acids compared with meat from the Con and 5% CM fed birds which were not significantly different. Thigh muscle linoleic (18:3), EPA and DHA levels were increased 180, 100, and 128% by the 10% CM treatment respectively above the Con samples. Sensory evaluation showed participants were not able to distinguish between the Con and 5% CM thigh samples, yet 36 of 59 where able to identify the different sample when presented the Con and 10% CM meat ($P <$ 0.05). However, it should be noted that discrimination does not imply a preference by consumers and further acceptability trials would be required for preference determination.

Key Words: *Camelina sativa*, sensory evaluation, omega-3 fatty acids

504 Effect of feeding Mexican sunflower leaf *(Tithonia diversifolia*, Hemsley A Gray) on performance of broiler chicks. A. H. Ekeocha*[1], A. A. Mako[2], T. J. Williams[3], and A. Aderiye[1], [1]*Department of Animal Science University of Ibadan*, *Ibadan, Oyo State, Nigeria*, [2]*Department of Agricultural Production and Management Sciences, Tai Solarin University of Education*, *Ijagun Ijebu-Ode, Ogun State, Nigeria*, [3]*Department of Animal Physiology, University of Agriculture*, *Abeokuta, Ogun State, Nigeria.*

One hundred and fifty (150) day old Abor Acre broiler chicks were randomly allocated to 5 experimental diets of 30 birds each. The first diet was the standard (basal) starter and finisher diet and served as control. The other rations contained 2.5%, 5.0%, 7.5% and 10.0% Mexican sunflower leaf (MSL) respectively as graded replacement (w/w) for maize and Soya meal. The study investigated the performance and hematological responses of the birds to the diets. Mexican sunflower leaf meal supplementation did not improve performance characteristics over basal diets and significantly ($P < 0.05$) retarded feed intake, growth rate, feed conversion except for its inclusion at 5.0%, while hematological parameters were significantly ($P > 0.05$) enhanced except for eosinophil and lymphocytes concentration. Mexican sunflower leaf is therefore a promising feed ingredient that could be cheaply incorporated into poultry rations at 5.0% level when convectional feeds are inadequate.

Key Words: lesser known sunflower, feed intake, daily weight gain

505 Effect of feeding Mexican sunflower leaf *(Tithonia diversifolia*, Hemsley A Gray) on carcass characteristics of broilers. A. H. Ekeocha*[1], O. A. Adu[2], K. D Afolabi[1], and E. J Ubah[3], [1]*Department of Animal Science, University of Ibadan, Ibadan, Oyo State, Nigeria*, [2]*Department of Animal Production and Health, Federal University of Technology, Akure, Nigeria*, [3]*Department of Animal Science, Wageningen University, Wageningen, Netherlands*.

A study was conducted for 8 weeks to investigate the effect of feeding Mexican Sunflower Leaf *Tithonia diversifolia* on carcass characteristics of broilers. One hundred and fifty white day-old Abor Acre broiler chicks were used. The broiler chicks were randomly assigned to 5 treatments A, B, C, D and E. Treatment A served as control while birds in treatments B, C, D and E received Mexican Sunflower Leaf (MSL) at 2.5, 5.0, 7.5, and 10.0% respectively. Feeds and water were provided ad-libitum and the routine vaccination / medication followed the standard procedures. The results shows a significant ($P > 0.05$) decrease in all the parameters measured for carcass characteristics (shank, gizzard, head, crop, thigh, drumstick, wings, breast, back, neck, abdominal fat, spleen, heart, lung, liver, intestine and proventriculus) except for the neck weight where birds on treatment B (2.50 MSL) obtained the highest neck weight (182.31g) and the spleen with highest weight (3.60g) obtained in treatment C (5.0 MSL). The carcass quality were also significantly decreased ($P > 0.05$) except for the neck and spleen weights. The result of this study shows that inclusion of MSL at 2.5, 5.0, 7.5, and 10.0% has almost no effect on both the carcass characteristics and carcass quality of the broilers under study.

Key Words: sunflower, carcass characteristics, *Tithonia diversifolia*

506 A 42-day floor pen evaluation of broiler chickens fed standard energy and low energy diets supplemented with a blend of carvacrol, cinnamaldehyde and capsicum oleoresin with or without bacitracin. M. Sims*[1], D. Bravo[2], and A. Vikari[2], [1]*Virginia Diversified Research Corporation*, *Harrisonburg, VA*, [2]*Pancosma*, *Geneva, Switzerland*.

A 42-d, 30 bird/pen, 6 treatment, 8 rep. (48 pens) broiler study was conducted to compare the performance, carcass/breast yield, breast moisture loss and Salmonella shedding of broiler chickens fed standard (S) or low (L) ME feeds with either a blend of carvacrol, cinnamaldehyde and capsicum oleoresin (XT, Xtract 6930) 125 ppm in starter feeds, 100 ppm in grower feeds (S/XT, L/XT) or BMD 50 ppm (S/B, L/B) or a combination of BMD 25 ppm + XT 100 ppm (S/B+XT, L/B+XT). Pen and feed weights collected at 21d and 42d, Salmonella shedding at 20d and 41d and carcass/breast yield at 43d. Each paired treatments means were analyzed by use of a 2-tailed distribution basic *t*-test model with equal variances assumed and $P = 5\%$. At 21d, BW of S/XT (2.02 kg) and S/B+XT (2.01 kg) were higher than L/XT (1.92 kg), with other groups intermediate. The 42d BW of the S/XT group (2.34 kg) was greater than each of the Low ME groups (mean = 2.24 kg) and not different from S/B (2.31 kg). FCR at 42d was lower for S/XT (1.69) than for the S/B (1.79), L/B (1.77), or L/XT group (1.75). The 0-42 day mortality with culls removed of S/XT (2.5%) was lower than L/B+XT (5.4%). Salmonella shedding at 41d was lower for S/B+XT (0%) than S/B (16.7%), S/XT (12.5%), L/XT (12.5%) and L/B (25.0%). Carcass yields were not different by pens, males, or females. Pen breast yield of S/B group (33.7%) was greater than S/XT (32.6%) and S/B+XT groups (32.0%). Pen breast moisture loss of S/XT was lower (6.9%) than all other groups (mean = 9.6%) with S/B (10.0%) and L/BMD (10.4%) being the highest. Breast yields after moisture loss means were similar for S/XT and S/B (30.3%). These data show that broilers fed diets supplemented with XT have final BW, FCR, carcass

yield, breast yield, feed cost/bird and returns on investment similar to broilers fed standard diets supplemented with BMD 50 ppm.

Key Words: essential oils, broiler, carcass yield

507 Effects of mung bean waste inclusion on mash diet characteristic, growth performance and nutrient digestibility in pigs. P. Rungcharoen*, N. Amornthewaphat, Y. Ruangpanit, S. Rattanatabtimthong, and S. Attamangkune, *Kasetsart University*, *Bangkok, Thailand*.

Three experiments were conducted to evaluate the apparent metabolizable energy of mung bean waste in pigs and effects of mung bean waste inclusion in pig diets on growth performance and nutrient digestibility. In Exp 1, 2 consecutive trials were performed in starter (BW of 20 kg) and grower pigs (BW of 50 kg) in the determination of the apparent metabolizable energy of mung bean waste. Twenty 4 crossbred barrows (Large white × Duroc × Landrace) were enrolled in each trail (one pig in each cage; 12 metabolic cages per treatment). Treatments were corn soybean basal diet and 20% mung bean waste substituted basal diet. The apparent metabolizable energy of mung bean waste for a starter pig and a grower pig were 2,132.3 ± 137.83 and 2,557.1 ± 50.39 kcal/kg. In Exp 2, 2 trials were conducted in nursery phase (5 to 9 wk) and starter to finisher phase (11 to 24 wk) in a growth assay. A total of 192 pigs in each trial was allotted to a randomized completely block design (8 pigs per pen; 6 pens per treatment with 3 pens of gilts and 3 pens of barrows). Sex was a block factor. Treatments were mung bean waste inclusion of 0%, 2.5%, 5% and 7.5% in the experimental mash diets. Mung bean waste inclusion linearly decreased bulk density for all diets ($P \leq 0.001$) of both trials. There was no difference in growth performance of pigs in nursery phase and starter to grower phase. For finisher phase, however, there was decreased ADG from 712g to 597g in pigs fed mung bean waste diets ($P \leq 0.05$). In Exp 3, 24 barrows (BW of 7.5 kg) were used in the determination of nutrient digestibility (one pig in each cage; 6 metabolic cages per treatment). Treatments used were the same as in Exp. 2. Mung bean waste inclusion in the diet did not affect the digestibility of protein, fat and fiber. In conclusion, incorporation of 7.5% mung bean waste in the nursery to grower pig diets did not showed negative responses to growth performance and nutrient digestibility. However, low bulk density of mung bean waste mash diet needed to be concerned.

Key Words: pig, mung bean waste, growth performance

508 Short-term feeding of genetically modified Bt maize (MON810) to weanling pigs: Effects on gut microbiota, intestinal morphology and immune status. M. C. Walsh*[1], S. G. Buzoianu[1,3], G. E. Gardiner[3], M. C. Rea[2], R. P. Ross[2], and P. G. Lawlor[1], [1]*Teagasc, Pig Production Development Unit, Moorepark Research Centre*, *Fermoy, Co. Cork, Ireland*, [2]*Teagasc, Moorepark Food Research Centre*, *Fermoy, Co. Cork, Ireland*, [3]*Waterford Institute of Technology*, *Waterford, Ireland*.

The objective of this study was to identify any effects short-term (31 d) feeding of genetically modified (GM) Bt (MON810) maize may have on gut microbiota, intestinal morphology and immune status of weanling pigs. Male pigs (n = 32) were weaned at ~28 d of age, blocked by weight and ancestry and randomly assigned to 1 of 2 treatments; non-GM isogenic maize or transgenic MON810 maize. Fecal samples were collected for microbiological analysis on d −1 and 30. Ileal and cecal digesta and small intestinal tissue were sampled at slaughter (d 31) for microbiological and histological analysis, respectively. Cytokine production from stimulated peripheral blood mononuclear cells (PBMCs) was measured on d 0 and 29. All data were analyzed as a randomized complete block design using the GLM procedures of SAS. Feeding GM maize had no observed effect on fecal *Lactobacillus* or total culturable anaerobe counts or ileal and cecal counts of *Lactobacillus*, *Enterobacteriaceae* or total anaerobes. Fecal *Enterobacteriaceae* counts in GM maize-fed pigs tended to be reduced on d 30 ($P = 0.10$) compared with control pigs. Feeding GM maize had no effect on duodenal, jejunal, ileal villus height or crypt depth. However, non-GM fed pigs tended ($P = 0.10$) to have more goblet cells/μm of duodenal villus compared with GM fed pigs. Phorbol myristate acetate stimulated PBMCs isolated from pigs fed GM maize tended ($P = 0.10$) to produce less IL-12 than control PBMCs on d 30. There was no effect of treatment on IL-10, IL-6, IL-4, TNFα or IFNγ production from resting or stimulated PBMCs. In conclusion, short-term feeding of GM maize to weanling pigs has demonstrated no observed adverse effects on intestinal morphology or systemic immunity while it was associated with a reduction in potential pathogens in the feces.

Key Words: pigs, MON810 maize, microbiota

509 Effects of dietary oat hulls and sugar beet pulp on productive performance and nutrient digestibility of broilers from 1 to 42 d of age. J. M. Gonzalez-Alvarado[1], E. Jiménez-Moreno[2], F. D. Royón[2], R. Lázaro[2], and G. G. Mateos*[2], [1]*Universidad de Tlaxcala*, *México*, [2]*Universidad Politecnica de Madrid*, *Madrid, Spain*.

The effects of the inclusion of additional fiber in the diet on growth performance and digestive traits were studied in broilers from 1 to 42 d of age. The control diet was based on rice and contained 3,120 kcal AMEn/kg, 1.12% digestible Lys, and 1.5% crude fiber content. The 2 experimental diets included 3% of either oat hulls (OH) or sugar beet pulp (SBP). Growth performance was measured from 1 to 42 d, total-tract apparent retention (TTAR) of nutrients were determined at 32 d, and the relative weight (RW; g/kg BW) of the GIT and the gizzard was measured at 42 d of age. Cumulatively, broilers fed OH had higher ($P \leq 0.001$) ADG and better ($P \leq 0.01$) FCR than broilers fed SBP or the control diet. From 1 to 10 d of age, OH inclusion improved ($P \leq 0.01$) ADG (19.5 vs. 16.8 g/d) and FCR (1.215 vs. 1.333) as compared with the control diet. Also, SBP improved FCR in this period but the effects disappeared with age. In fact, from 25 to 42 d of age, SBP inclusion reduced ($P \leq 0.05$) feed intake with respect to the control diet and feed intake ($P \leq 0.05$) and BWG ($P \leq 0.001$) with respect to the OH diet. The RW of the GIT was higher ($P \leq 0.05$) with the SBP than with the control diet with the OH diet being intermediate. Also, the RW of the gizzard increased ($P \leq 0.001$) with fiber inclusion and the effects were more pronounced ($P \leq 0.05$) with OH than with SBP. Fiber inclusion increased ($P \leq 0.01$) TTAR of all nutrients and AMEn of the diet. The improvement in TTAR observed for DM was more pronounced ($P \leq 0.01$) for OH than for SBP. We conclude that OH inclusion improves growth performance at all ages in broilers fed low fiber diets. Also, SBP inclusion improves growth performance from 1 to 10 d of age but not thereafter. The TTAR of nutrients are improved by fiber inclusion and the benefits are more pronounced with OH than with SBP.

Key Words: fiber sources, digestive organ size, broiler performance

510 Influence of origin on nutritional and quality parameters of soybean meal. G. G. Mateos*[1], M. P. Serrano[1], S. Sueiro[2], M. González[2], M. Hermida[2], P. G. Rebollar[1], and R. Lázaro[1], [1]*Universidad Politécnica de Madrid*, *Madrid, Spain*, [2]*Laboratorio de Mouriscade*, *Pontevedra, Spain*.

Soybean meal (SBM) is the main source of protein in non-ruminant diets. Most published tables of ingredient composition for feed formulation

differentiate 2 types of SBM based on its CP content (regular with 44% CP and high protein with 47 to 48% CP) and do not have into consideration the origin or processing method of the beans. However, available information indicates that processing and origin of the beans might have an effect on the nutritional value of SBM. The present research (n = 345) was conducted to determine the influence of origin (USA; Brazil, BRA; Argentine, ARG) on protein quality and nutrient value of SBM. On DM bases, USA meals (n = 139) had more CP (53.8 vs. 52.8 vs. 51.5%; $P < 0.001$) and less NDF (8.8 vs. 10.7 vs. 12.0%; $P < 0.001$) than ARG (n = 121) and BRA meals (n = 85). Sucrose and stachyose content was higher for USA than for BRA with ARG meals being intermediate (8.1 vs. 6.7 vs. 7.5% and 6.4 vs. 5.3 vs. 5.5%, respectively; $P < 0.001$). The USA meals had more phosphorus (0.79 vs. 0.68 vs. 0.74%; $P < 0.001$) than the BRA meals with ARG meals being intermediate. Also, BRA meals had more Fe (189 vs. 128 and 133 mg/kg; $P < 0.001$) but less K (2.3 vs. 2.6 and 2.5%; $P < 0.001$) than ARG and USA SBM. The USA meals had higher KOH solubility (87.6 vs. 82.3 and 84.3%; $P < 0.001$), protein dispersibility index (19.8 vs. 17.1 and 15.5%; $P < 0.001$), and trypsin inhibitor activity (3.9 vs. 3.0 and 3.0 mg/g; $P < 0.001$) than the ARG or BRA meals. The amino acid profile (% CP) varied with the source of SBM. The content of Lys (6.15 and 6.09 vs. 5.96%; $P < 0.001$), Met + Cys (2.86 and 2.86 vs. 2.75%; $P < 0.001$), Thr (3.91 and 3.92 vs. 3.83%; $P < 0.001$), and of 5 key amino acids (Lys, Met + Cys, Thr, Trp; $P < 0.01$) were higher for USA and ARG than for BRA SBM. It is concluded that the nutrient composition and protein quality parameters favor the utilization of USA meal over the South American meals in poultry diets.

Key Words: soybean meal survey, protein quality, nutritional value

511 Lactose in diet influences the degradation of mixed linked β(1-3;1-4)-D-glucan in the small intestine of pigs. K. E. Bach Knudsen*, *Aarhus University, Faculty of Agricultural Sciences*, *Department of Animal Health and Bioscience, Tjele, Denmark*.

The objective of the current study was to investigate if lactose in diet would influence the degradation of mixed linked β(1–3;1–4)-D-glucan (β-glucan) in the small intestine. B-glucan is an important cell wall (dietary fiber, DF) component of the endosperm of barley and oats. The digestibility of β-glucan in the small intestine from both cereals is among the highest of all DF components, but in one particular study with oat-based diets it was significantly lower than what was found in other studies. In this study whey protein containing lactose was used as protein supplement. Lactose is slowly digestible in the small intestine. To investigate if lactose could be causative for the lower digestibility of β-glucan in the study with whey protein, it was decided to quantify the content of lactose in the diets and to analyze for lactose in digesta samples from the small intestine (the small intestine was divided in 3 by length equal segments: SI1, SI2, SI3) and ileal digesta along with parameters for organic acids (lactic acids and short-chain fatty acids). Diets containing lactose were based on oat goats, oat flour, and oat bran (lactose 1.2–3.8% of DM), whereas the reference diets were based on rolled oats, rolled oats and oat bran, wheat flour with added oat bran and wheat flour with added β-glucan (lactose 0–0.1% of DM). Lactose was identified in digesta up to SI2, but disappeared in digesta from SI3 and the ileum. There was no difference in the digestibility of β-glucan among diets up to SI3, whereas the digestibility in ileum was significantly higher in diets without lactose compared with diets containing lactose. With all diets, β-glucan was virtually completely digested in the cecum. No difference was found in the concentration of organic acids between diets either in SI3, ileum or cecum. In conclusion slowly digestible lactose was the most likely cause of the reduced digestibility of β-glucan in oat diets containing lactose.

Key Words: β-glucan, digestion, pigs

512 Effects of dietary calcium formate inclusion on broiler growth performance, bone ash, and tibia breaking strength. S. Pohl*, D. Caldwell, J. Lee, J. Coppedge, K. Stringfellow, S. Dunn-Horrocks, K. Jessen, and M. Farnell, *Texas A&M University*, *College Station*.

Calcium formate (CaFo; Rovelan–Lanxess Corporation, Germany) is a commonly used source of calcium in poultry and swine feed in the EU. Due to increased cost, US interest in alternate feedstuffs has grown. The objective of this study was to evaluate CaFo in broiler diets as an alternate calcium source during a 49d pen trial. A total of 2,160 male Cobb 500 broilers were randomized and placed in 40 floor pens with 50% used litter and 50% fresh pine shavings. Four experimental groups (0.0, 0.5, 1.0, and 1.5% CaFo) were evaluated with 10 replicate pens per treatment. Bulk pen weights were determined at the conclusion of each feeding phase (d15, 28, 42, and 49). Additionally, at d15, 28, and 42, one bird was removed from each pen and tibia removed for determination of bone strength and ash. At termination (d49) an additional 3 birds were removed from each pen for tibia sampling. Parameters evaluated for each phase included average BW, FCR, bone strength, bone ash content, and mortality. With regard to BW, significant differences ($P \leq 0.05$) were seen at d15 with 1.0% CaFo showing decreased BW. At d28 the 0.5% CaFo diet showed increased BW with respect to the 1.0 and 1.5% CaFo diets. At d42 and 49 all diets yielded statistically equivalent BW. For the duration of the trial, no differences were observed with regard to FCR among diets. No significant differences were seen among treatment groups with regard to mortality, tibia weight, or bone ash percentage. With respect to tibia breaking strength, a significant increase in breaking force was observed in the 1.0% CaFo treatment group in comparison to the control and 1.5% CaFo groups. These data suggest that CaFo may be used as a calcium alternative in broiler diets and may potentially increase bone strength in larger broilers when included at the appropriate concentration.

Key Words: broiler, calcium formate, bone ash

513 Broiler breeder age and dietary Cu, Zn and Mn source affect chick bone development at hatch. C. A. Torres* and D. R. Korver, *University of Alberta*, *Edmonton, AB Canada*.

Organic sources of dietary trace minerals (OTM) can have higher bioavailability than inorganic sources (ITM). OTM in the hen's diet might positively impact bone development in the embryo as Cu, Zn and Mn are involved in bone development. We investigated the effects of maternal dietary Cu, Zn and Mn source and level on chick bone traits at hatch from early (EEP; 33 wk), mid (MEP; 46 wk) and late (LEP; 60 wk) hen age. Broiler breeders (n = 18/diet), were housed in individual cages, and fed a basal ration low in Cu, Zn and Mn. Trace minerals were added as: 1) Control: ITM; mineral sulfates at industrial levels (100 ppm Zn, 120 Mn, 10 Cu); 2) OTM: Zn, Mn and Cu chelated by 2-hydroxy-4-(methylthio) butanoic acid (HMTBA) at NRC (1994) levels (50 ppm Zn, 60 Mn, 10 Cu); 3) OTM+ITM: Trt 1 plus an additional 40 ppm Zn, 40 Mn and 20 Cu as OTM; 4) High ITM: Trt 1 plus 40 ppm Zn, 40 Mn and 20 Cu as ITM. Weekly egg production, and chick bone weight, thickness and length data were analyzed using repeated measures analysis (PROC MIXED). Total and settable eggs, egg weight and hatchability were analyzed as a 1-way ANOVA (PROC MIXED). Significance was set at $P \leq 0.05$. Total and settable egg production, egg weight and hatchability to 60 wk of hen age were not affected by diet. Femur weight (with chick weight as a covariate) decreased 12% from EEP to LEP. At EEP, chicks from the OTM hens had femurs and tibias that were thicker than chicks from Control (both by 5%) and High ITM (both by 6%) hens. At MEP, chicks from the OTM and High ITM hens had thicker femurs (by 4 and 7%, respectively) than chicks from the OTM+ITM group; none of the treatment chicks were different from the Control chicks. At LEP there was no diet effect on femur and tibia thickness. Dietary TM affected chick bone thickness at early and mid hatches even though bone development appeared to decrease with hen age. Despite a lower level of supplemental TM, tibia development at hatch was increased in the OTM group relative to all other treatments at EEP; OTM resulted in greater femur development relative to the ITM and High ITM at EEP, and relative to OTM + ITM at MEP.

Key Words: broiler breeder age, organic trace mineral, chick bone development

514 Use of the broiler (*Gallus gallus*) as an in vivo screening tool for Fe bioavailability in maize-based diets. E. Tako*[1], M. Lung'aho[1], L. V. Kochian[2], O. A. Hoekenga[2], and R. P. Glahn[2], [1]*Cornell University*, *Ithaca, NY,* [2]*Robert W. Holley Center for Agriculture and Health*, *Ithaca, NY*.

Iron biofortification of staple food crops such as maize (*Zea mays*), is a strategy that alleviates Fe deficiency. By using in vitro cell culture model, 2 maize varieties were developed for high and low Fe bioavailability. In vitro observations should be tested in animals before human efficacy studies. Therefore, the maize varieties were tested for Fe bioavailability by using the broiler chicken as a model. Diets were made with 75% w/w maize of either the low (Low) or high (High) Fe bioavailability maize; Fe content did not differ between varieties (both 24 µg/g). In vitro analysis showed lower cellular ferritin formation (ie. Fe uptake, $P \leq 0.05$) in cells exposed to the Low (20 ng/mg) vs. High (37 ng/mg) diets. One-week-old broiler chicks (n = 6) were fed the maize based diets for 4 weeks. Hemoglobin (Hb), body weight, feed consumption, liver ferritin and gene expression were measured. Duodenal DMT1, Dcytb and ferroportin were higher ($P < 0.05$) in the Low group vs. the High group, indicating a response to lower dietary Fe availability. Hb concentrations, hemoglobin maintenance efficiency, Hb-Fe and liver ferritin were higher in the High group vs. the Low group ($P \leq 0.05$), indicating greater Fe absorption from the High diet and improved Fe status. We conclude that the in vivo results support the in vitro observations, i.e., the High variety contains more bioavailable Fe than the Low and that maize shows promise for Fe biofortification. In addition, the results indicate that, the broiler model can serve as an intermediate screening tool for Fe bioavailability before human efficacy trials.

Key Words: broiler, bioavailability, maize

515 Relationship between expression of sodium-dependent phosphate transporter type II-b gene and phosphorus utilization in broilers. O. A. Olukosi*, S. A. Adedokun, K. M. Ajuwon, and O. Adeola, *Purdue University*, *West Lafayette, IN*.

Broiler chicks at 21 d old were used to study the relationship between the level of expression of sodium-dependent phosphate transporter type IIb gene (NaPi-IIb) in 3 sections of the small intestine (duodenum, jejunum or ileum) and P utilization. Birds were allocated at 1-d old to 4 treatments in a randomized complete block design, each treatment had 7 replicate cages with 8 birds per replicate cage. Corn-soybean meal diets formulated to meet all nutrients requirements except for P were fed throughout the study. The ratio of Ca to total P was kept constant in all

diets. Non-phytate P levels in the diets were 2.5, 3.5, 4.5 and 5.5 g/kg. Twenty-eight birds, one bird from each cage, with weight closest to the average weight of the cage, were killed at d 21. Mucosa scraping was collected from the duodenum, jejunum and ileum of the selected birds and the expression level of NaPi-IIb relative to GAPDH was determined by RT-PCR. Ileal digesta was collected on d 21 from the remaining birds in the cage. Expression level of NaPi-IIb was negatively correlated with P level and total P intake but positively correlated with P digestibility ($P < 0.05$) at the jejunum. Correlation of expression level of NaPi-IIb at duodenum and ileum were mostly opposite to that at jejunum. Expression level of NaPi-IIb was similar in duodenum and jejunum but lowest ($P < 0.05$) at the ileum. Dietary P level had no influence on NaPi-IIb expression at any section of the small intestine. Ileal P digestibility was not affected by P supply but both total and digestible P intake were increased ($P < 0.01$) with increasing level of P in the diets. The data indicate that all the sections of the small intestine contribute to prececal P disappearance but duodenum and jejunum contribute the most. In addition, the data indicate that manipulation of NaPi-IIb expression level especially at the jejunum will strongly influence P utilization and excretion in broilers.

Key Words: broilers, phosphate transporter, small intestine

516 Effects of HMTBA chelated zinc, manganese and copper on performance, mineral status and immunity of broilers. Y. Ruangpanit*, S. Attamangkune, S. Rattanatubtimthong, and C. Khomkamon, *Kasetsart University*, *Nakhon-Pathom, Thailand*.

Two studies were conducted to investigate the effects of HMTBA chelated Zn, Mn and Cu on performance, mineral status and immunity of broilers. In Exp. 1, the effects of HMTBA Zn, Mn and Cu on performance and mineral status of broiler were evaluated. Two thousand, day-old, Ross 308 were divided into 2 dietary treatments including, 1) Corn-soy basal diet containing inorganic Zn, Mn and Cu at the recommended levels of the Thai standards (ITM) and 2) Corn-soy basal diet containing HMTBA Zn, Mn and Cu (Mintrex) at 25% of the inorganic levels used in ITM diet (CTM). Both diets were calculated to be isonitrogenous and isocaloric and were offered in pellet form. Each treatment consisted of 20 replications with 50 broilers per replication (25 males and 25 females). All birds were raised in environmental controlled house for 42 d. At the end of the experiment, carcass trail was evaluated. Liver and bone were collected for mineral analysis. Birds received CTM diet had significantly lower feed intake during 1–17 and18–35 d, and lower body weight gain during 1-17 d ($P < 0.05$). However, no significant difference in overall broiler performance and carcass trait were observed. The Zn, Mn and Cu concentrations in serum at d 20 were similar, but serum Zn and Cu concentrations of birds fed CTM diet were lower at d 42 ($P < 0.05$). Liver Zn, Mn and Cu concentrations and Zn and Cu concentrations in bone were not significant different. However, birds received CTM diet had lower bone Mn concentrations ($P < 0.05$). In Exp. 2, the effects of HMTBA Zn, Mn and Cu on immunity, oxidative stress status and mineral excretion were evaluated. One hundred and twenty, 12 d old, male Ross 308 were assigned into 2 dietary treatments as in Exp. 1. Each treatment consisted of 6 replications with 10 birds per replication. All birds were raised in metabolic cages. Birds fed CTM diet had higher secondary IgG responses against 7% SRBC antigen ($P < 0.05$). Both ITM and CTM birds had similar serum MDA concentration. Expectedly, broiler fed CTM diet had lower Zn, Mn and Cu excretion ($P < 0.05$). From this study, it can be concluded that chelated trace minerals have higher bioavailability and lower levels can be fed in the diet.

Key Words: broiler, organic mineral, mineral excretion

517 Effect of organic zinc supplementation on growth performance and carcass quality of broilers. H. M. Salim*, H. R. Lee, C. Jo, S. K. Lee, and B. D. Lee, *Chungnam National University*, *Yuseong, Daejeon, South Korea*.

The effect of supplementing diets with organic zinc on growth performance and carcass quality of female broiler chickens was investigated. A total of 3,200 1-d-old female broiler chicks were randomly assigned to 4 floor pens, 800 birds per pen, with 4 replicates (200 birds/replicate). A corn-wheat-soybean meal basal diet (Control) was formulated, and 20 ppm organic zinc (20 OZ), 40 ppm organic zinc (40 OZ), and 80 ppm organic zinc (80 OZ) were added to the basal diet to form 4 dietary treatments. During the 5-wk experimental period, feed and water were provided ad libitum. Body weight, feed intake, feed conversion and mortality were measured. At the end of the feeding trial, 2 birds per replicate pen were selected according to average body weight, slaughtered, defeathered and carcass evaluation was performed. For histology analysis, about 1 cm2 of skin samples from the thigh and back region of each bird were collected, embedded, sectioned, stained, and thickness of skin layers were examined under light microscope. Results showed no significant difference between the treatments in growth performance. A significant increase ($P < 0.05$) of thigh skin epidermis and dermis thickness were shown in the organic zinc supplementation groups; however, no effect of the zinc on the thickness of back skin epidermis and dermis was found. Collagen content in breast and thigh muscles was not influenced by organic zinc supplementation but a significant increase of collagen content was found in the back and thigh skin ($P < 0.05$). This increase of collagen content was significantly higher in the back and thigh skin of OZ 80 compare with OZ 20. Shear force of back skin and muscles was not significantly influenced by the dietary supplementation of zinc. Water holding capacity in breast muscle increased significantly ($P < 0.05$) when birds were fed OZ 40 and OZ 80; however, organic zinc supplementation had no adverse effect on over all consumer acceptability of broiler meat. It has been concluded that dietary organic zinc does not affect growth performance of broilers but increases collagen content in skin, thereby improving carcass quality of broilers.

Key Words: organic zinc, skin quality, broilers

518 Effect of dietary copper source and level on GI copper levels and ileal *E. coli* survival in broiler chicks. K. C. Klasing* and A. Naziripour, *University of California*, *Davis*.

Pentahydrate copper sulfate (CS) and tribasic copper chloride (TBCC) are the primary Cu sources fed at high levels to improve the health and growth of animals. TBCC is less soluble in water than CS but is more bioavailable so our goal was to examine their biological properties along the GI tract. These 2 Cu sources were fed at 150 ppm to 6 pens per trt of 3 broiler chicks per pen from d 3 to 14 of age. Intestinal luminal content was collected to determine total Cu, water extractable Cu, Cu that could be extracted using the strong complexing agent, ethylenebis-hydroxyphenylglycine (EHPG), and Cu that could not be extracted (presumed to be unavailable for nutritional and microbicidal purposes). Bacteriostatic activity to *E. coli* spiked into ileal intestinal contents was greater for TBCC than for CS ($P < 0.05$). Total Cu in luminal contents was not affected by Cu source. CS increased duodenal luminal soluble Cu and epithelial metallothionein more than TBCC ($P < 0.05$), indicating that it was taken up by epithelial cells at a greater rate in the upper small intestine, but this effect did not occur in the lower intestines. TBCC resulted in more EHGP-extractable Cu in all regions of the intestines ($P < 0.05$) and less unremovable Cu ($P = 0.05$), which may be related to its greater bioavailability and anti-coli activity.

Key Words: copper, intestines, broilers

519 Effects of dietary iron and age on cellular copper metabolism in liver of weanling pigs. R. S. Fry*, J. W. Spears, S. L. Hansen, H. C. Liu, and M. S. Ashwell, *North Carolina State University*, *Raleigh*.

Thirty-six weanling, male pigs were used in a 2 × 3 design to determine the effect of dietary iron (Fe) and age on hepatic cellular copper (Cu) metabolism. Pigs received diets containing 97 mg/kg Fe (control) or 797 mg/kg Fe (H-Fe) for either 21, 42, or 63 d. On each of these d 6 pigs per treatment were harvested and liver and bile were collected for Cu analysis and mRNA analysis of hepatic Cu transporters and chaperones. On the day before harvest jugular blood was obtained for plasma Cu and ceruloplasmin (Cp). Liver Cu was not affected by diet, but was affected by age. Pigs harvested on d 21 had higher ($P < 0.01$) liver Cu than pigs harvested on d 42 and 63. Plasma Cu and Cp were not affected by diet but both increased ($P < 0.01$) with age. Bile Cu was affected by a treatment × day interaction ($P < 0.05$). On d 21, bile Cu tended to be higher ($P < 0.10$) in H-Fe vs. control pigs, but did not differ on d 42. However, by d 63, bile Cu tended to be lower ($P < 0.10$) in H-Fe vs. control pigs. Messenger RNA of Ctr1, Atox1, and Atp7b were affected ($P < 0.05$) by a treatment × day interaction, and Cp mRNA tended ($P < 0.10$) to be affected by a treatment × day interaction. On d 21 and 63, Ctr1 was not affected by diet, but on d 42 mRNA of this Cu-importer was lower ($P < 0.01$) in H-Fe vs. control pigs. On d 21, Atox1, a chaperone that delivers Cu to the Cu-exporter, Atp7b, was markedly higher ($P < 0.01$) in H-Fe vs. control pigs, but did not differ on d 42 and 63. On d 21, Atp7b tended ($P < 0.10$) to be higher in H-Fe vs. control pigs. By d 42, Atp7b was lower ($P < 0.01$) in H-Fe vs. control pigs and was numerically ($P = 0.11$) lower in H-Fe pigs on d 63. On d 21 and 42, Cp, a Cu-dependent ferroxidase, was not affected by diet, but by d 63 it was lower ($P < 0.05$) in H-Fe vs. control pigs. In conclusion, age did not affect mRNA of Cu transporters and chaperones. However, high dietary Fe affected bile Cu and Cu transporters and chaperones involved in the secretory pathway of Cu metabolism. These data provide a better understanding of how Fe antagonistically affects Cu metabolism.

Key Words: pigs, copper, iron

520 Effect of level and source of dietary copper on copper metabolism in the small intestine of weanling pigs. R. S. Fry*, M. S. Ashwell, W. L. Flowers, K. R. Stewart, and J. W. Spears, *North Carolina State University*, *Raleigh*.

Thirty weanling pigs were used to determine the effect of level and source of dietary copper (Cu) on performance and Cu metabolism in the duodenum, proximal jejunum, and ileum. Dietary treatments consisted of 1) control (no added Cu), 2) 225 mg supplemental Cu/kg from Cu sulfate ($CuSO_4$) or 3) 225 mg supplemental Cu/kg from tribasic Cu chloride (TBCC). Feeding regimen consisted of 3 phase diets. Phase 1 diets were fed from d 0 to 6, phase 2 diets were fed from d 7 to 21, and phase 3 diets were fed for the remainder of the study. Prior to harvest on d 35 and 36, pigs were fasted for 8 h then re-fed for 8 h. Digesta and mucosal scrapings were collected from each section of the intestine for determination of soluble Cu and mucosal Cu concentrations. Digesta pH was obtained upon collection. During phase 1, TBCC pigs had higher ($P < 0.05$) average daily gain and gain:feed than $CuSO_4$ and control pigs. However, overall performance for the 35 d study was not affected by Cu level or source. Digesta pH increased ($P < 0.01$) as digesta descended down the small intestine, but did not differ by Cu level or source. Soluble Cu in the digesta and mucosal Cu in duodenum, proximal jejunum, and ileum were higher ($P < 0.05$) in Cu supplemented vs. control pigs. In the duodenum, soluble Cu in digesta tended ($P < 0.10$) to be lower while mucosal Cu was lower ($P < 0.05$) in TBCC vs. $CuSO_4$ pigs (104.3 vs. 130.3 mg/kg Cu). Soluble Cu in digesta from proximal jejunum and ileum was not different between Cu sources. However, pigs fed TBCC had higher ($P < 0.01$) Cu concentrations in mucosa of the proximal jejunum than $CuSO_4$ fed pigs (44.7 vs. 22.1 mg/kg Cu). In the ileum, mucosal Cu tended ($P < 0.10$) to be higher in TBCC vs. $CuSO_4$ pigs. In conclusion, pigs supplemented with Cu had much higher concentrations of soluble Cu in the digesta and intestinal mucosa than control pigs. Furthermore, Cu source affected Cu uptake differently throughout the small intestine. Markedly lower water solubility of TBCC compared with $CuSO_4$ may explain these differences.

Key Words: pigs, copper, metabolism

521 Dietary calcium and phosphorous and organic and inorganic trace minerals on nursery pig growth performance. J. S. Jolliff* and D. C. Mahan, *The Ohio State University*, *Columbus*.

Dietary Ca and P levels were evaluated for their effect on trace mineral usage as measured by postweaning growth performance and plasma minerals. Two levels of Ca and P (Ca:P) and 5 trace mineral (TM) treatments (2 × 5 factorial) were analyzed as an RCB over 6 blocks with 240 total nursery pigs (6.43 kg BW) for 35 d. The 2 Ca:P levels were 0.80% Ca and 0.65% P (Low) and 1.10% Ca and 0.91% P (High). Of the 5 TM treatments, 4 comprised a 2 × 2 factorial between 2 TM sources (organic or inorganic) and 2 TM levels. The first TM level (1x) provided 15 ppm Cu, 15 ppm Fe, 10 ppm Mn, and 140 pp Zn while the second level (2x) provided twice the amount of TM of the first level. The fifth TM treatment was no TM supplemented to the diet, i.e., all minerals were considered indigenous (basal). Pigs were weighed and feed disappearance recorded once per week postweaning. On d 35, all pigs were bled and hemoglobin, hematocrit, and plasma minerals were analyzed. TM treatment affected pig BW ($P < 0.05$) from d 21 onwards with the Basal TM treatment resulting in lighter weight pigs. Furthermore, pigs fed the Basal TM treatment had lower ($P < 0.05$) ADG, ADFI, and G:F by 21 d postweaning. Inorganic TM resulted in greater ADFI for the entire 35 d trial. There were Ca:P x TM interactions ($P < 0.05$) for BW, ADG, ADFI, and G:F in the later half of the nursery period. TM treatment affected ($P < 0.05$) pig hemoglobin with Basal having the lowest concentrations, inorganic TM having greater concentrations than organic, and the 2x TM level having greater concentrations than the 1x level. Pig hematocrit showed a similar pattern to hemoglobin, although TM level had no effect ($P > 0.05$). Low Ca:P resulted in greater ($P < 0.05$) plasma P and Zn than High Ca:P. Pigs in the Basal treatment had lower ($P < 0.05$) plasma P, Fe, and Zn than pigs receiving supplemental TM. There were no Ca:P interactions for any blood constituents. In summary, pigs fed inorganic TM had greater feed intake, hemoglobin concentrations, and hematocrit while High Ca:P reduced plasma P and Zn.

Key Words: pig, calcium, minerals

522 Effect of organic and inorganic trace mineral source and preslaughter deletion on tissue mineral content of pigs. Y. L. Ma*, M. D. Lindemann, G. L. Cromwell, and G. Rentfrow, *University of Kentucky*, *Lexington*.

Crossbred pigs weaned at 21 ± 3 d (n = 144; BW = 7.4 kg) were used to assess an organic form (ORG) of several trace minerals to standard inorganic forms (IN) on tissue mineral content when those minerals were deleted for various times preslaughter. Pigs were allotted to 24 pens (6 pigs/pen) based on gender and BW and fed a diet containing either IN ($CuSO_4 \cdot 5H_2O$, ZnO, $FeSO_4 \cdot H_2O$, MnO) or ORG (Bioplexes; Alltech Inc., Nicholasville KY) trace minerals (Cu, Zn, Fe, Mn) at the NRC (1998) requirement for each of 5 dietary phases of BW (equivalent to

14, 14, 42, 28, 42–d periods). Two pigs were removed from each pen at the end of phase 4 (BW = 82.6 kg), and at the end of phase 5 (BW = 126.6 kg) for the collection of tissue samples. After phase 4, 3 pens from each treatment were switched to a common diet without trace mineral supplementation in 2–wk intervals. This resulted in 4 groups within the IN and ORG source in which supplementation was deleted for 0, 2, 4, and 6 wk preslaughter. All data are reported on an mg/kg tissue DM basis. At the end of phase 4, ORG Mn content was greater ($P < 0.03$) in heart (0.77 vs. 0.68), liver (9.46 vs. 8.30), and longissimus dorsi (LD; 0.30 vs. 0.23). ORG Cu was greater ($P < 0.03$) in LD (2.12 vs. 1.89). ORG Fe was greater ($P < 0.03$) in LD (21.8 vs. 19.4) but lower in liver (466.1 vs. 564.4). Zn source did not affect tissue content. At the end of phase 5, increased length of deletion period (from 0 to 6 wk) resulted in a decrease (linear and quadratic, $P < 0.01$) in liver Zn (ORG – 209.2 to 118.8; IN – 183.8 to 124.8) and an increase (linear, $P < 0.01$) in heart Mn (ORG – 0.76 to 1.12; IN – 0.64 to 1.03) and liver Mn (ORG – 8.21 to 12.68; IN – 7.27 to 13.23). The only mineral source by deletion period interaction ($P < 0.04$) was in LD Zn where increasing deletion was associated with less Zn in IN–fed pigs (63.9, 55.7, 56.8, and 49.8) but not in ORG–fed pigs (56.4, 59.5, 56.7, and 62.0). The results demonstrate differential effects of mineral deletion on tissue mineral content depending on both mineral assessed and source of the mineral.

Key Words: trace minerals, pigs

523 The "immunocrit," a simple measure of passive transfer, is a useful predictor of nursing ability and preweaning mortality of piglets. J. L. Vallet*, J. R. Miles, L. A. Rempel, and L. A. Kuehn, *USDA, ARS, U.S. Meat Animal Research Center*, *Clay Center, NE*.

Initiation of lactation and newborn piglet nursing ability are 2 factors that can influence preweaning mortality. We have developed the "immunocrit" that can assess both lactation initiation and neonatal piglet nursing ability based on the transfer of immunoglobulin G (IgG) from the sow to the piglet. To perform an immunocrit, 50 μL serum was mixed with 50 μL 40% ammonium sulfate, the mixture was loaded into a hematocrit capillary tube and centrifuged for 5 min. The result was the ratio of the mm precipitate to mm solution in the tube. To test the immunocrit, the smallest piglet in 205 litters was sacrificed, blood was collected and full and emptied stomachs were weighed to obtain the weight of stomach contents. Blood was analyzed for IgG by precipitation of serum samples with protein A-Sepharose followed by SDS-PAGE. Densitometry of the heavy chain of IgG was used to quantify IgG. To test use in cattle, blood samples from 96 calves were obtained 24 h after birth and IgG was measured (Bovine IgG radial immunodiffusion kit; VMRD, Inc.). Piglet and calf blood samples were also analyzed by immunocrit. For piglets, the correlation between densitometry and immunocrit values was 0.83. For calves, the correlation between kit IgG and immunocrit values was 0.90. Piglet immunocrit values were also correlated ($r = 0.44$; $P < 0.01$) with stomach contents at 24 h, indicating that immunocrits could be used to screen for piglet nursing ability. To assess the influence of immunocrit values on piglet preweaning survival, immunocrits were performed on every piglet in 48 1st and 68 2nd parity litters and survival to weaning was recorded. Preweaning survival was independently associated ($P < 0.01$) with birth weight of the piglet and immunocrit values. Second parity sows had greater litter average immunocrit values compared with 1st parity sows (0.133 ± 0.003 and 0.123 ± 0.004, respectively; $P < 0.05$). These results indicate that the immunocrit is a useful tool to monitor colostrum intake in piglets and calves.

Key Words: colostrum, immunoglobulin, lactation

524 Influence of temperament on stress hormone and IgG concentrations in Brahman calves. N. C. Burdick*[1], D. A. Neuendorff[2], R. C. Vann[3], J. G. Lyons[1], T. H. Welsh Jr.[1], and R. D. Randel[2], [1]*Texas AgriLife Research*, *College Station,* [2]*Texas AgriLife Research*, *Overton,* [3]*MAFES, Mississippi State University*, *Raymond*.

This study was designed to determine the influence of temperament on cortisol, epinephrine (EPI), norepinephrine (NE), and IgG concentrations in Brahman calves. Calves from crops in 2006 and 2007 were selected based on temperament score measured 28 d before and at weaning. Based on temperament score the 10 calm, intermediate, and temperamental calves from each sex (bulls and heifers) were selected from each calf crop (n = 120). Blood was collected 28 d before weaning, at weaning, and 28 and 56 d post-weaning to determine serum cortisol and IgG, and plasma EPI and NE concentrations. Data were analyzed using the MIXED procedure of SAS specific for repeated measures. Sources of variation included temperament, sex, day, and year. Cortisol ($P < 0.01$) was, and EPI tended ($P = 0.08$) to be, greater in 2006 than 2007. Cortisol was affected by temperament with calm calves having lower cortisol (14.4 ± 0.7 ng/mL; $P < 0.01$) than intermediate (18.6 ± 0.7 ng/mL) and temperamental (30.8 ± 0.7 ng/mL) calves. Heifers had greater cortisol than bulls ($P < 0.01$; 22.9 ± 0.6 and 19.6 ± 0.6 ng/mL, respectively). Cortisol increased from d0 (18.5 ± 0.8 ng/mL) through d+56 ($P < 0.01$; 25.2 ± 0.8 ng/mL). Calm calves had lower EPI (149 ± 18 pg/mL) than intermediate (203 ± 18 pg/mL) and temperamental calves ($P < 0.01$; 381 ± 18 pg/mL). Heifers had greater EPI ($P < 0.01$; 278 ± 14 pg/mL) than bulls (212 ± 15 pg/mL). Concentrations of EPI decreased from d-28 (326 ± 20 pg/mL) through d+56 ($P < 0.01$; 169 ± 22 pg/mL). Calm calves had lower concentrations of NE than intermediate and temperamental calves ($P < 0.04$; 510 ± 72, 732 ± 74, and 719 ± 72 pg/mL, respectively). Concentrations of NE changed over time ($P = 0.01$) and were not affected by sex ($P = 0.98$). Concentrations of IgG were not affected by temperament ($P = 0.43$) or time ($P = 0.22$) but tended to be affected by sex with heifers (26.7 ± 2.2 mg/mL) having greater IgG than bulls (21.6 ± 2.2 mg/mL; $P = 0.11$). In summary, temperamental calves have greater stress hormone concentrations. Additionally, cortisol, EPI, and IgG concentrations can vary depending on sex of the calf.

Key Words: cattle, temperament, stress

525 Effect of cytochrome P450 and aldo-keto reductase inhibitors on progesterone decay in primary bovine hepatic cell cultures. C. O. Lemley* and M. E. Wilson, *West Virginia University*, *Morgantown*.

Progesterone is required for maintenance of pregnancy and peripheral concentrations of progesterone are affected by both production and inactivation. Hepatic cytochrome P450 (CYP) and aldo-keto reductases (AKR) play a pivotal role in the first step of steroid inactivation. The current objectives were to discern the proportional involvement of hepatic progesterone catabolic enzymes on progesterone decay using specific enzyme inhibitors. Liver biopsies were taken from 6 lactating dairy cows and dissociated using a non-perfusion technique. Confluent wells (n = 12/treatment) were preincubated for 4 h with enzyme inhibitor and then challenged with progesterone for one hour. Cell viability was unaffected ($P > 0.50$) by inhibitor treatment and averaged 84 ± 1%. In control wells 50% of the progesterone had been inactivated after a one hour challenge with 5 ng/ml progesterone. Preincubation with curcumin (CYP and AKR inhibitor), ticlopidine (CYP2C inhibitor) or naproxen (AKR inhibitor) caused the greatest reduction ($P < 0.001$) in progesterone decay compared with controls and averaged 77, 39 or 37%, respectively. Hydroxylation of 4-nitrophenol to 4-nitrocatechol in intact cells was inhibited by 65% ($P < 0.001$) after treatment with curcumin or ticlopidine. However, phase II glucuronidation of phenol red or 4-nitrocatechol in intact cells was inhibited ($P < 0.01$) by treatment with curcumin, dicumarol or naproxen, showing a lack of specificity in phase I enzyme inhibition (CYP and AKR). The contribution of CYP2C and CYP3A enzymes to progesterone decay in bovine hepatic cell cultures appeared to be 40 and 15%, respectively. Depending on the inhibitor used it would appear that the AKR enzymes contributed 40% to the observed progesterone decay; however, a portion of this loss may be due to glucuronosyltransferase (phase II enzyme) inhibition. A greater understanding of these steroid biotransformation pathways in the dairy cow could help researchers modify the bioavailability of progesterone.

Key Words: cytochrome P450, aldo-keto reductase, progesterone decay

526 Residual feed intake selection and its effects upon pre- and postpartum changes in NEFA concentrations and body weight and condition in Brahman females. A. K. Poovey*[1,2], A. N. Loyd[1,2], A. W. Lewis[1], D. A. Neuendorff[1], S. L. Morgan[1,2], L. C. Caldwell[2],

T. D. A. Forbes[3], T. H. Welsh Jr.[2], and R. D. Randel[1], [1]*Texas AgriLife Research*, *Overton,* [2]*Texas AgriLife Research*, *College Station,* [3]*Texas AgriLife Research*, *Uvalde*.

Residual feed intake (RFI) is one method to identify efficient animals based upon the relationship of predicted to actual individual feed intake. Nonesterified fatty acid (NEFA) concentrations are the products of catabolism of triglycerides and are negatively correlated with energy balance and body weight in females. The objective of this study was to examine the relationship among RFI status with pre- and postpartum NEFA concentrations in beef females. Based upon prior post-weaning RFI evaluations, Brahman females (n = 93) were classified as having either a negative RFI (efficient) or a positive RFI (inefficient). Body condition score (BCS), body weight (BW), and serum samples were collected at weekly intervals beginning 5 wk before and continuing through 5 wk after calving. Pre-calving, NEFA concentrations did not differ between low and high RFI groups ($P > 0.3$). There was an interaction between NEFA concentrations and prepartum time period ($P = 0.02$). However, during this time, RFI ($P = 0.8961$) and age group ($P = 0.11$) did not affect change in BW although there tended to be differences in BW between 2 year old (YO) heifers and cows 4 years and older ($P = 0.05$). Similarly, change in BCS was not affected by RFI ($P = 0.88$); however, age group tended to differ ($P = 0.06$). Specifically, 2 YO cows lost more BCS than 3 YO ($P = 0.02$) and 3 YO tended to lose more BCS than cows 4+ YO ($P = 0.07$). Postpartum NEFA concentrations changed over time ($P = 0.02$) and were affected by sampling week ($P = 0.02$). Neither age nor RFI influenced changes in BW ($P = 0.75$; $P = 0.98$, respectively) or BCS ($P = 0.29$; $P = 0.79$, respectively). Circulating concentration of NEFA in pre- and postpartum females was not related to RFI previously evaluated when the females were heifers. Changes in BW and BCS did not differ due to previous evaluation for RFI as heifers during the same peri-partum periods. Age of cow was the only factor found to be related to serum NEFA concentrations or changes in BW and BCS.

Key Words: feed efficiency, nonesterified fatty acids, peri-partum cows

527 Ruminal degradability and intestinal release of different vitamin A formulations. D. P. Preveraud* and P. A. Geraert, *Adisseo France SAS*, *Antony, France*.

The most convenient way to provide vitamin A (VA) to ruminants is to include it with concentrate mixtures. Feed industry usually formulates a VA ester emulsified into a gelatin beadlet to ensure good stability and biological availability. The aim of this study was to evaluate the rumen degradability and intestinal release of different VA formulations, including the double emulsion (Microvit A1000 Supra, Adisseo), by using a Mobile Nylon Bag (MNB) methodology. Two dairy cows equipped with ruminal and duodenal cannulas were used in a 2-period crossover experimental design. The 9 tested formulations were incubated in the rumen in nylon bags (6 replicates) for 6, 10 or 18h and residues from these bags were then incubated in a pepsin HCl solution (38.5°C, pH 2) for 2.5h to simulate abomasal digestion, and finally inserted through the duodenal cannula to be recovered from feces after 24h. Nylon bags were then analyzed for their VA content and results were expressed as a percentage of residual VA compared with initial content of non-incubated product (see table). Microscopic photographs were also taken to follow the degradation of the different formulations. The overall results of this experiment indicated that these VA sources could be divided into 3 groups according to their rumen stability and in relation with their formulation: stable (double emulsion, Microvit), intermediate (products A, B, C, G and H) and sensitive (products D, E and F). Despite a low (14%) but significant loss of the double emulsion formulation after 18h incubation in rumen, 81% of the initial amount finally reaches the intestine where VA is totally released. Among the sources of vitamin A being studied, the double emulsion formulation seems to be more bioavailable to cattle. This should be confirmed later on by a greater tissue concentration of VA.

Table 1. VA residues[1] at each step of the MNB technique (% of initial content)

	6-h rumen	10-h rumen	18-h rumen	abomasum	feces
Microvit A1000 Supra	102^{l}	97^{l}	86^{ijk}	81^{hi}	ND
product A	76^{ghi}	57^{f}	23^{d}	2^{a}	ND
product B	82^{hij}	72^{gh}	20^{cd}	ND	ND
product C	70^{g}	45^{e}	10^{abc}	ND	ND
product D	26^{d}	6^{a}	ND	ND	ND
product E	24^{d}	4^{a}	ND	ND	ND
product F	18^{bcd}	18^{bcd}	19^{cd}	7^{ab}	3
product G	51^{ef}	20^{cd}	ND	ND	ND
product H	76^{ghi}	70^{g}	53^{ef}	24^{d}	ND

[1]Values are LS means; ND: Non Detectable; letters indicate statistical difference within columns (Fisher Test: $P < 0.05$; $\alpha = 5\%$)

Key Words: vitamin A formulation, rumen stability, intestinal release

528 Poisson analysis of number of services per conception for Iranian Holstein cows. H. Farhangfar*[1] and F. Bahri[2], [1]*Birjand University*, *Birjand, Iran*,

[2]*Ferdowsi University of Mashhad*, *Mashhad, Iran*.

To evaluate the effects of some environmental factors on the number of services per conception (NSC) in Iranian Holstein cows, a total of 38,074 records obtained from 10,726 cows at different parities (1985–2009) was utilized. All records were collected from a very large dairy herd comprising of 2 separate units. The units were different from each other from dairy farm management point of view. Average number of services per conception was 2.29 in the whole data set. A generalized statistical linear model was applied to analyze NSC. Poisson distribution was assumed for NSC and a log link function was applied for the response variable. In the model, fixed effects of period of years (in 3 levels), month of insemination, technician, parity and unit were included. Based upon the year of insemination, 3 year periods were defined as follows: 1985–1990, 1991–2000 and 2001–2009. The statistical model was run with the use of GLMMIX procedure add in program implemented in SAS software. The results indicated that year period and unit were the only significant factors that influenced NSC ($P < 0.01$). Least squares means of NSC (in original scales) were 2.1776, 2.2807 and 2.2805 for year periods of 1985–1990, 1991–2000 and 2001–2009, respectively. The least squares means of NSC (in original scales) of farms units were obtained to be 2.1707 and 2.3234 for units 1 and 2, respectively revealing slightly different reproductive efficiency between 2 units of the dairy herd. Among different parities, the largest and lowest NSC least squares means were found for parity 7 and 10, respectively. However, no significant differences were revealed among the parities. From the results of this research it could be concluded that the reproductive efficiency of Iranian Holstein cows has been deteriorating over the past decades suggesting that a sophisticated genetic selection program

should be considered for improving the traits associated with reproduction performance.

Key Words: Iranian Holstein, Poisson analysis, reproduction performance

529 Effects of continuous infusion of tumor necrosis factor-alpha (TNFα) into adipose tissue on glucose and fatty acid metabolism in lactating dairy cattle. C. A. Martel*[1], L. K. Mamedova[1], E. J. Minton[1], M. L. Jones[2], J. A. Carroll[3], and B. J. Bradford[1], [1]*Department of Animal Sciences and Industry*, *Kansas State University*, *Manhattan*, [2]*Veterinary Medical Teaching Hospital, Kansas State University*, *Manhattan*, [3]*Livestock Issues Research Unit, ARS-USDA*, *Lubbock, TX*.

Late-lactation Holstein cows (n = 9/treatment) were used to evaluate effects of TNFα administration on glucose and fatty acid (FA) metabolism. Cows were blocked by feed intake and milk yield and randomly assigned within block to 1 of 3 treatments: control, TNFα, and pair-fed control. Treatments (4 mL saline or 14 μg/kg TNFα in 4 mL saline) were infused continuously over 7 d via 2 osmotic pumps in the adipose layer in the tailhead region. Plasma, milk samples, milk yield, and DMI data were collected daily. On d 7, pumps were removed and liver and contralateral tailhead adipose samples were collected. Results were modeled with fixed effect of treatment and random effect of block; *P* values >0.10 were considered non-significant. TNFα did not alter adipose or liver TNFα mRNA abundance, plasma TNFα, IL-4, IL-6, or interferon-γ concentrations, DMI, or rectal temperature. Milk fat and lactose concentrations decreased with TNFα ($P < 0.05$), but milk yield was unchanged and treatments did not alter the proportion of short vs. long-chain FA in milk on d 7. Treatments did not alter plasma NEFA concentration, liver triglyceride content, or adipose mRNA abundance for hormone-sensitive lipase or perilipin. Plasma glucose turnover rate, as measured by disappearance of U-^{13}C-glucose bolus, was not altered by treatment, nor was liver mRNA abundance for phosphoenolpyruvate carboxykinase or pyruvate carboxylase. However, TNFα tended to decrease adipose TNFα mRNA abundance ($P = 0.09$) and increase liver IL-10 mRNA abundance ($P = 0.05$) compared with controls. This TNFα delivery protocol may have allowed for an adaptive anti-inflammatory response to suppress systemic inflammation, which may account for the lack of metabolic responses, in contrast with previous responses to daily subcutaneous TNFα injections.

Key Words: dairy, TNFα, gluconeogenesis

530 Reproductive rate of semi-free ranging Bison (*Bison bison*) at the National Bison Range. M. J. Borgreen*[1,2], T. J. Roffe[2], E. M. Berry[1], R. B. McCosh[1], and J. G. Berardinelli[1], [1]*Montana State University*, *Bozeman,* [2]*US Fish and Wildlife Service*, *Bozeman, MT*.

Recruitment of calves at the National Bison Range (NBR) near Moiese, Montana, has dropped from the historic average of 87 to 33 calves per 100 breeding-age cows in 2008. The purpose of monitoring the NBR bison pregnancy rate (PR) and calf recruitment is to determine where in the reproductive cycle NBR female bison fail to recruit calves. The reproductive cycle was divided into 3 stages: conception to early embryonic development; maintenance of pregnancy during the second and third trimesters; and, calving to recruitment. In 2008, transrectal ultrasonography was used to determine PR in cows (ages 4 to 12 yr) in October; 28 of 41 cows (68%) were pregnant. Pregnant cows were painted with a unique bleach number. Fecal samples were collected in Oct., Jan., Mar. and Apr. until the bleach number was illegible. Fecal samples were analyzed for progesterone (P4). Pregnancy rates estimated by fecal P4 concentration decreased ($P < 0.01$) from 100% (n = 28) in Oct. to 53% (n = 15) in Apr. The percentage lost continuously decreased throughout the second stage, with the largest percent decrease between first and second trimester (17%). Of the original 28 pregnant cows the PR in April was 53%; a reduction of 47%. This closely matched calf recruitment of the herd at the 2009 roundup (71 calves for 126 cows; 56%): indicating that the accuracy for estimating pregnancy using fecal P4 was 94.7%. In 2009, PR was determined by ultrasonography of 89 cows, including 38 of the 41 cows from 2008. Pregnancy rate for 2009 was 63%, which was similar to PR in 2008 (68%). Radio collars were secured to 27 pregnant and 10 non-pregnant cows. These animals will be monitored throughout the rest of the reproductive cycle to determine calf production using fecal P4 assay. Fecal P4 assays appear to give an accurate estimate of PR in semi-free ranging bison. In conclusion, it appears that the decrease in calf recruitment at the NBR can be, at least in part, due to fetal losses during gestation.

Key Words: bison, fecal progesterone, pregnancy rate

Physiology and Endocrinology: Sperm-Oviduct Interactions in Livestock and Poultry

531 Evidence that oviduct secretions influence sperm function: a retrospective view for livestock. G. J. Killian*, *The Pennsylvania State University*, *University Park*.

The mammalian oviduct has long been recognized as an organ essential to the success of reproduction. Bovine, ovine, porcine and equine animal models have offered clear advantages for oviduct study related to gamete physiology, fertilization and early embryo development. Livestock species are amenable to surgical alteration of the reproductive tract, estrous cycle manipulation, gamete cryopreservation, artificial insemination as well as in vitro fertilization and embryo production. Although most reproductive technology developed for livestock was intended to benefit production animal agriculture, these techniques are a treasure trove of tools for researchers to better understand how the oviduct influences gamete function. Oviduct secretions obtained from in vitro tissue cultures or via indwelling oviduct catheters have been used for analyses to define the protein, lipid, carbohydrate, enzyme and electrolyte compositions of the secretions during the estrous cycle or in response to hormone treatment. Oviduct secretions or components purified there from have also been used in in vitro assays to assess their ability to bind to sperm and/or influence on sperm viability, motility, sperm capacitation, the acrosome reaction, sperm-egg binding, egg penetration as well as subsequent embryo development. Compelling data have emerged which show that the composition of secretions differs during the estrous cycle and that their composition differs whether they originate from the ampullar or isthmic regions of the oviduct. These differences in composition are functionally relevant and associated with different responses by sperm. Evidence suggests that oviduct -specific glycoproteins, glycosaminoglycans, carbohydrates, norepinepherine, catecholamines, heat-shock protein and osteopontin are components of the oviductal milieu which have the capacity to modulate sperm function. Continued research on the livestock oviduct will likely unravel the role that specific oviduct secretions have in modulating sperm function and how these modifications ultimately affect fertilization and embryo development.

Key Words: sperm, oviduct, secretions

532 Role of the oviduct in maintaining sustained fertility in hens. M. R. Bakst*[1] and J. P. Brillard[2], [1]*ARS, USDA*, *Beltsville, MD*, [2]*INRA*, *Tours, France*.

In poultry, sperm transferred by natural mating or artificial insemination (AI) into the distal end of the vagina immediately begin their ascent to the utero-vaginal junction (UVJ) located at the anterior end of the vagina. During their transport there is an intense sperm selection process that may reduce the number of sperm initially transferred by as much as 99.5%. Those "select" sperm reaching the UVJ enter the thousands of tubular invaginations of the vagina's surface epithelium located in the UVJ mucosa, collectively referred to as the sperm-storage tubules (SST). Sperm residing in the SST lumen are capable of surviving for several weeks while retaining their fertilizing capacity. Resident sperm are released gradually from the SSTs while the hen is in egg production, ascend to the site of fertilization, and interact with the next ovulated ovum. In this manner, given the absence of an estrus to synchronize ovulation with copulation, poultry, and birds in general, are assured a population of sperm at the site of fertilization during a daily succession of ovulated ova. Over the past decade several new and diverse observations have been published addressing the microanatomy of the UVJ and SST, and the cellular and molecular mechanisms orchestrating oviductal sperm selection and storage. These include: the SST numbers in different poultry species and lines of high and low fertility; roles of the immune system and possibly neuroendocrine-like cells in the vagina in sperm selection and storage; the roles of aquaporins and a fluid exchange mechanisms contributing sperm release from the SSTs; and, gene expression of the SST epithelial cells with or without resident sperm. The objective of this presentation is to integrate these observations into a comprehensive understanding of the cellular and molecular events influencing the fate of sperm in the hen's oviduct, particularly in the area of oviductal sperm selection and storage.

Key Words: poultry, reproduction, oviduct

533 Effect of sperm mobility phenotype on fertility, sperm competition, and in vivo sperm storage in the domestic fowl. D. P. Froman*, *Oregon State University*, *Corvallis.*

Sperm mobility is a quantitative trait. Phenotype is determined by the extent to which sperm move against resistance at body temperature. This ability is measured in vitro by sperm penetration of 6% (wt/vol) Accudenz from an overlaid sperm suspension. The study of sperm mobility has provided: 1) an estimate of heritability, 2) an explanation for phenotypic variation based upon properties of individual motile sperm, 3) a plausible model that explains why a portion of sperm ejaculated by any given male are immobile in addition to why this proportion varies among males, and 4) loci of interest within the fowl genome. The distinction between sperm motility and mobility is critical. Whereas all mobile sperm are motile, not all motile sperm are mobile; for a motile cell must have a velocity >30 μm per second to be mobile in vitro. This distinction is biologically significant because sperm mobility phenotype predicts male fertility when hens are inseminated with a fixed number of viable sperm. Immobile sperm contain dysfunctional mitochondria, and the time course for mitochondrial failure begins before ejaculation. Percentages of affected sperm appear to range between 10 and nearly 100%. This variation is attributed to a genetic predisposition that puts sperm cells at risk as they pass through the deferent ducts of the testis. Sperm mobility is heritable ($h^2 = 0.30$), and phenotype is influenced by a maternal additive genetic effect, attributed to the Z chromosome based upon genome-wide SNPlotype analysis. To date, experiments have been reductionist in nature. Nonetheless, synthesis of experimental outcomes has afforded 4 new insights. These include: 1) how fitness varies among normal, fertile males within a population, 2) a likely mechanism enabling in vivo sperm storage, 3) a quantitative, gene-based definition of semen quality, and 4) a new approach to semen preservation based upon bioenergetic theory. In essence, sperm are self-propelled DNA delivery vehicles. This presentation will explain how the self-propulsive nature of sperm varies among males and how such variation affects male fitness.

Key Words: domestic fowl, fertility, sperm

534 Bovine oviduct-sperm interactions preceding fertilization. S. S. Suarez*, *Cornell University*, *Ithaca, NY*.

The bovine oviduct is not a simple conduit for sperm. The epithelium and luminal fluids of the oviduct affect the physiological state of sperm and movement of sperm into and through the oviduct. There is evidence that the oviduct is open to sperm for only a limited time after insemina-

tion; furthermore, sperm may require certain cell surface proteins to gain access. After entering the oviduct, bull sperm bind to the oviductal epithelium using 3 proteins in the BSP family (PDC109 or BSPA1/A2, BSPA3, and BSP30K), which are the major secreted proteins of the seminal vesicles. The BSP proteins coat the heads of sperm when they come into contact with vesicular secretions at ejaculation. Putative oviductal receptors for the BSP proteins are 4 proteins in the annexin family (ANXA1,2,4,5). Sperm binding to oviductal epithelium results in the development of a storage reservoir of sperm in the lower oviduct. There is evidence that binding prolongs the fertility of sperm; that is, when sperm coated with BSP proteins are incubated with apical plasma membranes of oviductal epithelium, their motile lives are extended. Release of sperm is likely a gradual process, with sperm breaking loose and then reattaching several times. The gradual release of sperm would reduce the numbers that arrive at the oocyte at any one time, thereby preventing polyspermy, and would also prolong the arrival of sperm in the upper oviduct to ensure that fertilization takes place. Capacitation may play a role in sperm release, because the process involves shedding of BSP protein and reduces bull sperm binding to oviductal epithelium. Capacitation of bull sperm is enhanced in vitro by heparin and heparin-like glycosaminoglycans have been detected in bovine oviduct fluid. Considering the role of heparin in capacitation, it is interesting that both BSP and annexin proteins bind heparin. Differential shedding of the BSP proteins and their differing affinities for the 4 annexin proteins may result in a gradual and directed release of sperm toward the site of fertilization.

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Key Words: sperm, oviduct, seminal vesicles

535 In vivo imaging of in situ motility of fresh and liquid-stored ram spermatozoa in the ewe genital tract. X. Druart*[1], J. Cognié[1], G. Baril[1], F. Clément[2], J.-L. Dacheux[1], and J.-L. Gatti[1], [1]*UMR 6175 INRA, CNRS-Université de Tours-Haras Nationaux*, *Nouzilly, France*, [2]*INRIA Paris-Rocquencourt*, *Le Chesnay Cedex, France*.

The fertility of ram semen after cervical insemination is substantially reduced by 24 h of storage in liquid form. The effects of liquid storage on the transit of ram spermatozoa in the ewe genital tract was investigated using a new procedure allowing direct observation of the spermatozoa in the genital tract. Ejaculated ram spermatozoa were fluorescently labeled and used to inseminate ewes in estrus either cervically through the vagina or laparoscopically into the base of the uterine horns. Four hours after insemination, the spermatozoa were directly observed in situ using fibered confocal fluorescence microscopy. The high resolution video images obtained with this technique allowed determination of the distribution of spermatozoa and individual motility in the lumen of the ewe's genital tract. The results showed a gradient of increasing concentration of spermatozoa from the base of the uterus to the UTJ 4 h after intrauterine insemination into the base of the horns. The in vitro storage of spermatozoa in liquid form decreased their migration through the cervix and reduced the proportion of motile spermatozoa and their straight line velocity at the UTJ and their transit into the oviduct.

536 Comparison of timed AI pregnancy rates in Santa Gertrudis (SG) and SG crossbred heifers following the 7-d or 5-d CO-Synch+CIDR protocol. R. L. Stanko*[1,3], K. D. Arnold[1], J. R. Ramirez[2], S. Moore[2], and R. Silguero[2], [1]*Texas A&M University-Kingsville*, *Kingsville,* [2]*King Ranch, Inc.*, *Kingsville, TX,* [3]*Texas AgriLife Research*, *Beeville*.

Our objective was to evaluate the effectiveness of CO-Synch + CIDR protocols and timed AI (TAI) in beef heifers typical to the gulf coast states. Heifers (n = 239) of 2 breed types were used: Santa Gertrudis (SG, n = 145) and SG x Red Angus, F1 (SGX, n = 94). Heifers (n = 6, 2.5%) were removed from data set due to lost CIDR or absence at TAI or pregnancy determination. Age was determined from recorded birth date, and BCS and BW was recorded at CIDR insertion. All heifers were administered GnRH (100 µg, i.m.) and either a new (n = 121) or an autoclaved, once-used (n = 118) CIDR insert (1.38 g progesterone) at random on d 0. CIDR inserts were removed and prostaglandin F2α (PG, 25 mg, i.m.) was administered on d 7 (n = 160) with TAI performed 55 to 58 h after PG or CIDR inserts were removed and PG administered twice on d 5 (n = 73) with TAI at 72 to 75 h after PG. All heifers were administered GnRH (100 mg, i.m.) following TAI. Pregnancy was diagnosed by transrectal ultrasonography at 34, 35 or 36 d after TAI. Heifer age, BW, BCS, and TAI pregnancy rate (PR) was 372.0 ± 2.0 d, 331.0 ± 3.1 kg, 5.6 ± 0.04, and 43.8%, respectively. Chi-squared analysis was used to determine differences in PR. Overall, PR was greater ($P < 0.01$) in SGX (51/92, 55.4%) than in SG (51/141, 36.2%) heifers. Similar ($P > 0.1$) PR was observed between heifers receiving the once-used or new CIDR (56/115, 48.7% vs. 46/118, 39%), and between heifers on the 7-d or 5-d CIDR insert (68/160, 42.5% vs. 34/73, 46.6%). SG heifers receiving the 7-d CO-Synch + CIDR protocol had lower ($P < 0.01$) pregnancy rate (30/91, 33.0%) than SGX (38/69, 55.0%) receiving the same protocol. However, SG and SGX heifers receiving the 5-d CO-Synch + CIDR protocol had similar ($P > 0.1$) PR (21/50, 42.0% vs. 13/23, 56.5%, respectively). Heifers with less than 1/4 Brahman influence had acceptable PR with the CO-Synch + CIDR protocol, regardless of duration or CIDR type. The 5-d CO-Synch + CIDR protocol may prove to be an acceptable TAI protocol for SG heifers. Other synchronization of estrus and ovulation protocols are needed to enhance success rate of TAI in cattle adapted to the gulf coast region.

Key Words: heifer, CIDR, synchronization

537 Neither temperament or residual feed intake affect sexual maturity in Brahman heifers. A. N. Loyd*[1], D. A. Neuendorff[1], A. W. Lewis[1], T. D. A. Forbes[2], and R. D. Randel[1], [1]*Texas AgriLife Research*, *Overton*, [2]*Texas AgriLife Research*, *Uvalde*.

Selection of calm and feed efficient cattle based on temperament and residual feed intake (RFI), respectively may improve the overall profitability of beef cattle operations. While studies have investigated the relationships of temperament and RFI with growth parameters, only limited data are available concerning reproductive traits. The objective of this study was to evaluate the effects of temperament and RFI on sexual maturity of Brahman heifers. Brahman heifers born in 2005 (n = 48) and 2006 (n = 54) were evaluated at weaning for temperament using pen score (PS) and exit velocity (EV). Temperament score was calculated for each heifer as the average of PS and EV. Heifers (n = 38 in 2005; n = 41 in 2006) were fed a balanced ration at 2.5% BW twice daily at 0800 and 1600 h in Calan gates. Residual feed intake was calculated from weekly feed intake and BW data collected for 70 d. Following the feeding trial, heifers were allowed to graze coastal bermudagrass pasture and were exposed to a mature Brahman bull for natural breeding. Age at calving was recorded and age at sexual maturity was defined as 292 d before calving. Weight at sexual maturity was determined from BW and ADG data collected every 28 d. For statistical analysis, heifers were categorized as calm, intermediate or temperamental based on ± 0.5 standard deviation (SD) of both the mean EV and mean temperament score. RFI sign was used to categorize heifers as efficient (negative RFI) or inefficient (positive RFI). Heifers were also classified as efficient,

intermediate or inefficient based on ± 0.5 SD of the mean RFI. Using EV, temperament score, RFI sign, and RFI category as class variables, age and weight at sexual maturity were analyzed by PROC GLM. No differences ($P > 0.05$) were detected among these parameters comparing all temperament and RFI classifications. These data suggest that selection for RFI or temperament should not affect age or weight at sexual maturity in Brahman heifers.

Key Words: heifer, residual feed intake, temperament

538 Evaluation of a reproducible model for necrotic enteritis in broilers and analysis of NetB toxin profiles of different field isolates of *Clostridium perfringens*. S Shivaramaiah*[1], J. R. Barta[2], S. L. Layton[1], M. J. Morgan[1], R. E. Wolfenden[1], B. M. Hargis[1], and G Téllez[1], [1]*University of Arkansas*, *Fayetteville,* [2]*University of Guelph*, *Guelph, ON, Canada*.

Necrotic enteritis (NE) caused by Type A strains of *Clostridium perfringens* (CP) is an economically important disease in commercial poultry production. *Eimeria* infection is considered an absolute prerequisite to cause NE by disrupting intestinal integrity. Several reproducible NE models have used either immunosuppression or dietary modifications as common predisposing factors in conjunction with *Eimeria* infection. Preliminary data from our studies indicated that *Salmonella* infection early in the age followed by *Eimeria* and CP challenge accentuated NE-associated morbidity and mortality. In 2 replicate experiments, day-of-hatch chicks (n = 25/trt) were randomly assigned as Negative control (G1), *Eimeria* + CP (G2) or *Salmonella* + *Eimeria* + CP (G3). Challenge organisms included wild type *Salmonella typhimurium* (ST; ~2 × 10^8 cfu/chick) at day-of-hatch, sporulated oocysts of *E. maxima* (4 × 10^4/chick), at either D18 or D21, and 2 field strains of CP (1 × 10^8 cfu/chick), at either D22–23 or D25–26. Body weight (BW) was recorded before *Eimeria* challenge and at termination (D25 or D28) to determine weight gain. In addition, total mortality and lesion scores were evaluated. BW and lesion score data were analyzed using JMP7 while mortality was analyzed using the chi-squared test of independence. In both experiments, chicks in G3 suffered reduced ($P < 0.05$) weight gain as compared with either G1 or G2. In addition, total mortality and lesion scores were higher ($P < 0.05$) in G3 as compared with G2. Toxin profiling for challenge strains were evaluated to check for the presence of NetB, a toxin which is apparently obligatory for disease. Future studies are directed toward confirmation of the obligatory role of NetB in the pathogenesis of NE and the potential of NetB negative isolates to cause NE. The ability of selected probiotics to ameliorate NE is also currently under investigation.

Key Words: *Salmonella*, necrotic enteritis, NetB

539 Effects of a microbial litter amendment on litter quality and broiler performance. M. J. Hinkle*[1], S. M. Gottselig[1], J. L. McReynolds[2], J. T. Lee[1], and C. D. Coufal[1], [1]*Texas A&M University*, *College Station*, [2]*USDA-ARS*, *College Station, Texas*.

The reuse of litter in broiler production can lead to litter pathogen buildup and high levels of ammonia in broiler housing, thus resulting in poor broiler performance. This study evaluated the effects of a commercially available microbial culture litter amendment product on litter characteristics, ammonia production and broiler performance. Eight pens approximately 3 × 3 m each were used to rear broilers to 49 d of age at a density of 743 cm^2 (0.8 ft^2) per bird. Four pens were treated with the amendment according to the manufacturer's specification, and the remaining 4 pens served as untreated controls. Litter that had been used for 14 flocks was obtained from a commercial broiler farm and placed into the pens at an average depth of 11 cm. Feed consumption and mortality were recorded for each pen throughout the experiment. Ammonia production was measured by placing an enclosed chamber over the litter and sampling the headspace after 20 min with a Drager CMS unit. Ammonia measurements were taken one week before chick placement, at the time of chick placement, and once per week for the remainder of the grow-out. Litter samples were collected at the same time and location as ammonia measurement. On d 49, all caked litter was removed from each pen, weighed and sampled. Litter and cake samples were analyzed for total aerobic and anaerobic microbial counts. Paw scores were also recorded on d 49 for all birds using a 3-point scale (0, 1 or 2). Data were subjected to ANOVA using the GLM procedure with means deemed significantly different at $P < 0.05$. Percent mortality was significantly lower for treated pens (2.1%) than control (3.65%), but no statistical differences were observed for any other parameters measured. Average ending BW, feed:gain, paw score and cake weight per pen were 3.24 kg, 1.74, 0.75 and 128 kg for control pens and 3.19 kg, 1.70, 0.69 and 104 kg for treated pens, respectively. Average chamber ammonia concentrations decreased from 193 ppm at chick placement to 70 ppm at d 21, then increased to 131 ppm on d 49. Based on this experiment, the microbial amendment had a positive effect on broiler performance.

Key Words: broiler, litter, amendment

540 Bacterial content following simulated rainfall on poultry waste. J. H. Metcalf*[1], P. A. Moore Jr.[2], A. M. Donoghue[2], I. Reyes-Herrera[1], K. Arsi[1], P. J. Blore[1], and D. J. Donoghue[1], [1]*Poultry Science Department, University of Arkansas*, *Fayetteville,* [2]*Poultry Production and Product Safety Research Unit, USDA-ARS*, *Fayetteville, AR*.

To evaluate potential bacterial runoff from poultry litter, litter was applied to test plots and exposed to simulated rainfall. The experiment consisted of 21 small (100 sq. ft) plots which were subjected to simulated rainfall after litter was applied to the plots. Water runoff samples were tested for *Salmonella* and *Campylobacter*, 2 bacterial pathogens associated with poultry. Each trial consisted of 7 treatments; 1) controls (no litter) or the equivalent of 2) one ton/acre of normal litter, 3) 2 ton/acre of normal litter, 4) 4 ton/acre of normal litter, 5) 2 ton/acre of alum-treated litter, 6) 2 ton/acre deep stacked litter, and 7) 2 ton/acre composted litter. Rainfall was applied at the rate of 5 cm/h until the first runoff was observed from each plot (mean 37 min) and then continued for an additional 30 min. Rainfall was applied at one, 8 and 15 d after litter application and the trials were replicated 3 times. Data were analyzed by ANOVA using the GLM procedure of SAS and a probability of $P < 0.05$ was required for statistical significance. No *Campylobacter* was isolated from any of the runoff samples, and most samples tested negative for *Salmonella* as well. While most samples were negative, *Salmonella* was recovered from some plots, including the untreated control plots (no litter). Because *Salmonella* was recovered from untreated controls, the *Salmonella* detected may originate from sources other than the applied litter (e.g., wild birds, rodents, deer).

Key Words: Water runoff, *Salmonella*, *Campylobacter*

541 Effect of a low sulfur diet on air emissions, nutrient excretion, and performance of laying hens. W. Wu-Haan*[1], W. Powers[1], R. Angel[2], D. Karcher[1], and T. Applegate[3], [1]*Michigan State University*, *East Lansing,* [2]*University of Maryland*, *College Park,* [3]*Purdue University*, *West Lafayette, IN.*

The objectives of the current study were to evaluate the effect of feeding commercial diet (C), reduced S (RedS) diet, and a low S (LowS) diet on air emissions, nutrient excretion, and performance of Hy-line W36 laying hens from 47 to 50 wk of age (4 environmental rooms/diet; 56 hens/room). The C, RedS, and LowS diets were formulated to contain 0.19%, 0.11%, and no supplemental DL-Met. Methionine intake of 274.7, 361.6, or 406.7 mg/hen/d resulted in increasing egg weights

of 61.1, 63.9, and 65.1 g ($P < 0.01$) for the LowS, RedS and C diets. Analyzed S contents (2,602; 2,540; and 2,460 ppm) corresponded to S intakes of 244.6, 236.6, and 217.0 mg/bird/d in hens fed C, RedS and LowS diets ($P < 0.01$). Egg production (89%) and BW change (18.4 g) were unaffected by diet ($P > 0.05$) over the study period. A decrease in daily H2S emission was observed ($P < 0.01$) as S content in the diet decreased. Daily H2S emissions from hens fed C, RedS, and LowS diets were 0.83, 0.62, and 0.44 mg/bird ($P < 0.01$). Overall, hens fed LowS diet decreased daily H2S emissions by 46.4% (mg/kg BW basis), 45.6% (mg/kg FI basis), 46.7% (mg/g egg mass basis), 22.9% (mg/kg excreta DM basis) and 44.1% (mg/g S intake basis), respectively ($P < 0.01$) compared with hens fed the C diet. Emission factors that resulted from feeding the RedS diet were intermediate to those for the C and the LowS diets. No significant diet effects on daily emissions of SO2 (0.35 mg/kg BW), NH3 (480 mg/kg BW), NO2 (3.0 mg/kg BW), CH4 (32.4 mg/kg BW), non-CH4 (4.6 mg/kg BW), CO2 (48.8 g/kg BW), and O2 utilization (−122 g/kg BW) were observed during the trial period. In addition, total DM excretion (20.8 g/bird/d) was unaffected by diet. However, S excretion decreased ($P < 0.01$) from hens fed LowS diet (98.6 mg/bird/d) and RedS diet (105.3 mg/bird/d) compared with those fed the C diet (137.6 mg/bird/d). The results of this study demonstrate that feeding less DL-Met has great potential to reduce H2S emissions and S excretion from laying hens and reducing DL-Met up to 40% had no negative impact on hen performance; however, completely eliminating DL-Met supplementation resulted in less cumulative egg mass.

Key Words: air emission, egg, sulfur

542 Comparison of nutrient balance and performance of laying hens, housed in either enriched or conventional cage systems, over an entire production. M. Neijat*[1], J. D. House[1], W. Guenter[1], and E. Kebreab[2], [1]*University of Manitoba*, *Winnipeg, Canada*, [2]*University of California*, *Davis*.

The move to alternative cage designs for laying hens has the potential to lead to differences in hen behaviors, with a resultant effect on manure characteristics and estimates of nutrient flow. To this end, an experiment was conducted to assess nitrogen (N), calcium (Ca) and phosphorus (P) balances, manure weight and composition, and indices of performance of laying hens housed under 2 distinct caging systems. A total of 4,836 commercial Shaver White hens were caged in either enriched (EC) or conventional (CC) (average floor space per hen of 642.6 and 468.4 cm^2 respectively) under a semi-controlled environment. Enriched cages provided hens with a curtained nesting area, scratch pad and perches. All birds were fed the same standard layer diet for 11 periods in 4 week intervals. Data, expressed on a hen basis, were analyzed as repeated measures using the MIXED model procedure of SAS. Egg production, feed conversion ratio, body weight, egg weight and egg mass were not significantly different between the 2 systems. Lower feed intake ($P < 0.01$) (92.5 vs. 95.0 g/d DM basis) and manure output ($P < 0.01$) (79.8 vs. 91.3 g/d as is basis and 27.0 vs. 28.1 g/d DM basis) were observed in birds housed in EC compared with CC. Manure DM% were 31.0 and 34.1 for CC and EC respectively. Overall mean Ca and P excretions in manure were significantly ($P < 0.01$) lower in EC birds (2.11 ± 0.04 and 0.619 ± 0.005 g/d respectively) than their counterparts in CC (2.29 and 0.643 g/d respectively). There were no significant differences in the amount of manure N excreted by birds in both cage systems (1.94 and 1.96 ± 0.02 g/d for EC and CC respectively). Taking into account the increasing intensity of poultry production, welfare and environmental concerns, enriched caging systems may help in reducing Ca and P excretions, and the total weight of manure.

Key Words: caging, manure, nutrient excretion

543 Effects of the removable chicken house on the growth performance of broilers and indoor environment parameters. A. G. Chen*, Z. Wang, X. M. Wang, Q. H. Hong, and C. M. Yang, *Zhejiang University*, *Hangzhou, China*.

A total of 880 one-day-old Ling-nan broilers were selected to study the effects of the removable chicken house on the growth performance and indoor environment parameters. All broilers were raised in the removable house during 0–21d period and then were randomly divided equally into 2 groups, each with 4 replications, and respectively raised in the removable chicken house (the trial) and in the general fixed one (the control) from 22d to 70d. Both groups of chickens received the same diets include a starter for 0–21d, a grower for 22–49d and a finisher for 50–70d period, respectively. The growth performance of broilers was determined every period and the indoor environment parameters, average temperature (AT), average relative humidity (ARH) were measured daily and average ammonia concentration (NH_3) was detected at 0800, 1400 and 2000 h every other day. During the entire test period, the average daily gain (ADG) in the trial group was 28.05 ± 7.04g and was 0.75% ($P > 0.05$) higher than that in the control, and the feed to gain ratio (F/G) 3.10 ± 0.82 was 0.96% ($P > 0.05$) lower than that of the control, respectively. The survive rate of the trial group was 94.38%, a little higher than the control′s (93.75%). The incidence of diseases in the removable group was 5.00 ± 0.68% and in the fixed group was 8.25 ± 1.71%. When the average outdoor temperature was 6.12°C, AT, ARH and NH_3 in the removable chicken house were 11.22°C, 64.67% and 2.98ppm, respectively, while in the general fixed one, the data were 9.96°C, 67.60% and 2.70ppm, respectively. The results showed that there were similar indoor environment parameters and growth performance of broilers in 2 types of chicken houses, but the removable chicken house resulted in lowered incidence of diseases.

Key Words: removable chicken house, fixed chicken house, environment parameters

544 Effect of DDGS and mineral sources on air emissions from laying hens. W. Li*[1], W. Powers[1], D. Karcher[1], R. Angel[2], and T. J. Applegate[3], [1]*Michigan State University*, *East Lansing*, [2]*University of Maryland*, *College Park*, [3]*Purdue University*, *West Lafayette, IN*.

The objectives of the current study were to evaluate the dietary effects of distillers dried grains with solubles (DDGS) and the sources of mineral supplement on air emissions from Hy-line W-36 hens from 50 to 53 wk of age (3 environmental rooms/diet; 56 hens/room). Diets were arranged in a 2 × 2 factorial design. Factors were dietary concentration of DDGS (0 or 20% of diet dry matter) and source of minerals (common inorganic sources; In or organic mineral sources from Pancosma, Geneva, Switzerland; Org). Analyzed diets contained 18.31% CP, 0.68% P and 4.20 Ca. Analyzed S content was 0.25%, 0.26%, 0.30% and 0.31% for the 0In, 0Org, 20In and 20Org diets. Concentration and airflow of ammonia (NH_3), hydrogen sulfide (H_2S), nitrous oxide (N_2O), methane (CH_4) and non-methane total hydrocarbons (NMTHC) were measured in exhaust air from each room. Egg weight (65.12g) and egg production (88%) were not affected by diet ($P > 0.05$). Feed intake in hens fed the 0Org (106.88 g/d/hen) was greater than for hens fed any of the other treatments (104.29, 104.93 and 103.92 g/d/hen in 0In, 20In and 20Org). Feeding DDGS decreased mass of NH3 emitted daily (592 vs. 512 mg/hen/d for 0% and 20% DDGS) and the following emission factors: mg/kg BW (by 16%), mg/g N consumed (by 17%), mg/g egg (by 14%). No mineral source effects were observed for NH_3 emission variables. Feeding DDGS increased daily CH_4 emissions by 13 to 15% (39.3 vs. 45.4 mg/hen/d; and 0.70 vs. 0.82 mg/g egg/d; $P < 0.05$). Daily H_2S emitted (0.78 mg/hen/d), N_2O emitted (58.6 mg/hen/d), non-methane total

hydrocarbon (24.4 mg/hen/d) ($P > 0.05$) were not changed as a result of diet fed. Mass of excreta (27.3 vs. 31.5 kg DM) and mass of N excreted (1.25 vs. 1.52 kg N) from 56 hens over a 3-wk period were increased as a result of feeding DDGS. Diet inclusion of DDGS or organic trace minerals did not change short-term performance of laying hens. Feeding 20% DDGS reduced NH_3 emissions, increased CH_4 emissions and had no effect on emissions of other gases. Substitution of inorganic trace mineral sources with organic sources did not alter air emissions.

Key Words: laying hen, DDGS, organic trace mineral

545 Effect of amino acid formulation and supplementation on nutrient mass balance and air emissions from turkeys. Z. Liu[1], W. Powers*[1], D. Karcher[1], R. Angel[2], and T. J. Applegate[3], [1]*Michigan State University*, *East Lansing*, [2]*University of Maryland*, *College Park*, [3]*Purdue University*, *West Lafayette, IN*.

Nutrient mass balance and air emissions were determined for turkeys fed 4 diets in a 2 × 2 factorial design to determine the effects of diets with 100 or 110% of NRC (1994) recommended amino acid (AA) formulation and diets containing 2 (Lys and Met) or 3 (Lys, Met, and Thr) supplemental AA. Hybrid tom turkeys were raised and monitored in 12 rooms (3 reps/diet; 20 toms/room at hatch culled to 16 toms/room at 4 wk then 12 toms/room at 8 wk of age). All feed and litter entering and leaving the rooms were quantified and analyzed for nutrient content. Air emissions were measured throughout the 20-wk study. Data were analyzed statistically by ANOVA using the MIXED model procedure of SAS. The 100% NRC diets contained less N compared with the 110% NRC (2.64% vs. 2.73% during wk 16 to 20). Diets containing 3 vs. 2 supplemental AA had less N content (2.61% vs. 2.76% during wk 16 to 20). Cumulative feed intake (55.67 kg/tom) and BW (19.85 kg/tom) were not affected by diet. Feeding 3 supplemental AA resulted in lower N content in excretion (3.21% vs. 3.50%, $P < 0.05$) as compared with feeding 2 supplemental AA and an interaction between the main effects was observed ($P < 0.05$). The 100% NRC diets resulted in lower emission rates of NH_3 (1.52 vs. 1.77 g/tom-d), non-methane hydrocarbon (0.10 vs. 0.12 g/tom-d) and H_2S (3.78 vs. 4.69 mg/tom-d) compared with the 110% NRC diets ($P < 0.05$). Feeding 3 supplemental AA resulted in lower NH_3 emission rates (1.23 vs. 1.68 g/tom-d, $P < 0.05$) as compared with feeding 2 supplemental AA and a significant interaction was observed ($P < 0.05$). The 100% NRC diets reduced cumulative NH_3 emission by 14% compared with the 110% NRC (187 vs. 218 gN/tom, $P < 0.05$). The 3 supplemental AA diets reduced cumulative NH_3 emission by 23% compared with the 2 supplemental AA (176 vs. 230 gN/tom, $P < 0.05$). Total N emission averaged 217 gN/tom. Across all 4 diets, N partitioning, as a percentage of inputs, averaged 32%, 58%, 12%, and −2% for retention, excretion, air emission, and unaccounted losses respectively. The results demonstrated the potential of reducing nutrient excretion and air emissions from turkeys through diet modification of AA, and illustrated fate of N, P and S in a turkey production system.

Key Words: diets, retention, excretion

546 Magnitude and variability of distillers grains greenhouse gas credits in the corn-ethanol-livestock life cycle. V. R. Bremer*, A. J. Liska, H. S. Yang, T. J. Klopfenstein, G. E. Erickson, D. T. Walters, and K. G. Cassman, *University of Nebraska*, *Lincoln*.

Feeding distillers grains (DGS) to livestock is an important part of the greenhouse gas (GHG) mitigation benefit due to ethanol production. Three scenarios were used to evaluate the magnitude and variability of DGS GHG emissions credit and GHG balance of ethanol relative to gasoline in the corn-ethanol-livestock life cycle with the Biofuel Energy Systems Simulator (BESS; www.bess.unl.edu). The BESS model accounts for GHG emissions associated with corn production for ethanol and livestock feed, ethanol plant operation based on type of DGS produced, corn, urea, and soybean meal displaced when DGS is added to livestock diets, differences in feedlot cattle enteric fermentation, and feedlot fuel use change due to DGS feeding. Scenario 1evaluated feeding Nebraska wet, modified, or dry DGS to feedlot steers, Scenario 2 evaluated feeding Midwest dry DGS to beef, dairy, or swine, and Scenario 3 evaluated Iowa, Nebraska, and Texas corn-ethanol-livestock production systems by types of DGS fed to different livestock classes. The DGS GHG emissions credit from the analyzed scenarios varied by more than 2-fold, from 11.5 to 28.3 g CO2e per MJ of ethanol produced, depending on the fraction of DGS used without drying, the proportion of DGS used to feed feedlot cattle vs. dairy or swine, and the location of corn production. Quadratic improvements in DMI ($P = 0.01$), ADG ($P < 0.01$), and G:F ($P = 0.09$) of feedlot cattle fed increasing levels of wet DGS are an important part of maximizing DGS GHG credits. Regional variability in GHG intensity of crop production and future livestock feeding trends will determine the magnitude of DGS GHG offset against GHG emissions elsewhere in the corn-ethanol-livestock life cycle. The DGS GHG credit represents a 19 to 38% offset of total corn-ethanol-livestock life cycle positive emissions and a 41 to 60% reduction in GHG emissions of ethanol motor fuel relative to gasoline. The DGS GHG credit was optimized when wet DGS was fed to beef cattle.

Key Words: distillers grains, environment, greenhouse gases

547 Methane production, fermentation patterns and protozoa numbers In Vitro as related to sources of rumen fluid from different cattle feeding systems and animal waste substrate digestion. C. L. Ross*, M. A. Froetschel, S. Buaphan, S. Chinnasamy, and K. C. Das, *The University of Georgia*, *Athens*.

Rumen fluid, collected by stomach tube, from beef cattle grazing pasture, lactating dairy cattle fed a total mixed ration, and beef cattle fed a feedlot ration were used to determine the influence of different rumen microbial inoculations on In Vitro methane production and fermentation of animal wastes, in a 3x3 factorial designed experiment. Broiler litter, dairy and swine manure were used as substrates. A modified Tilley and Terry procedure was used and fermentation gas was collected in sampling bags with septum valves. Dry matter and gross energy digestion and volatile fatty acids and ammonia production and protozoa counts were measured using standard techniques after 24 h incubations. All parameters were corrected with measurements from rumen fluid blank incubations without substrate. The source of rumen fluid did not affect the volume of methane produced ($P > 0.3$), but the volume of methane produced in vitro tended to increase by 75% with broiler litter as a substrate ($P < 0.08$). Ammonia production increased with rumen fluid from dairy and feedlot compared with grazing cattle, several fold especially with broiler litter as substrate (rumen fluid by substrate interaction $P < 0.02$). Total VFA produced were 40 to 90% higher with broiler litter and swine manure as compared with dairy manure ($P < 0.01$) and IVDMD was almost 2 fold greater with broiler litter as compared with the other wastes as substrate ($P < 0.01$). The moles of methane produced per digestible energy fermented was 2-fold greater with rumen fluid from feedlot cattle ($P < 0.08$) but there was no difference in efficiency of methane produced as related to type of animal waste used as substrate. The methane produced per energy fermented was positively correlated to protozoa counts ($r = 0.58$, $P < 0.03$) and negatively correlated to VFA production ($r = 0.70$, $P < 0.01$). Mixed cultures of rumen fluid especially from feedlot cattle, have potential to enhance animal waste remediation and methane generation for bio-fuel production.

Key Words: animal waste, bio-fuel production, methane

548 Trace mineral metabolism in ruminants. T. E. Engle*, *Colorado State University*, *Fort Collins*.

Trace minerals have long been identified as essential dietary components for domestic livestock species. Included in the category of essential trace minerals (or microminerals) are chromium, cobalt, copper, iodine, iron, manganese, molybdenum, nickel, selenium, and zinc. Numerous biochemical reactions require trace minerals for proper function. It has been well documented that deficiencies of various trace minerals can result in metabolic diseases. The interactions between trace minerals and metabolic processes are extremely complex. Trace minerals have been identified as essential components for carbohydrate, lipid, protein, and vitamin metabolism, and have been shown to be involved in hormone production, immunity, and cellular homeostasis. Past and current research would suggest that copper (Cu) is involved in lipid metabolism in ruminants. Copper supplemented at physiological concentrations to beef cattle has been reported to be involved in cholesterol metabolism, ruminal biohydrogenation, catecholamine production, and lipid metabolism of subcutaneous adipose tissue. Additional impacts of Cu on lipid metabolism and homeostatic mechanisms related to Cu metabolism are currently being investigated. Recently, we have reported that genes involved in bovine liver Cu homeostasis, ATP7A, ATP7B and Cox17, are correlated with CTR1 gene expression in the bovine liver, similar to those reported for non-ruminants. Despite the apparent involvement of certain trace minerals in animal production and disease resistance, deficiencies of trace minerals have not always increased the susceptibility of domesticated livestock species to natural or experimentally induced infections or decreased performance. There are many factors that could affect an animal's response to trace mineral supplementation such as the duration, concentration, and source of trace mineral supplementation, physiological status of an animal (i.e., pregnant vs. non pregnant), the absence or presence of dietary antagonists, environmental factors, and the influence of stress on trace mineral metabolism.

Key Words: trace mineral, beef cattle, copper

549 Effects of copper supplementation on performance and carcass characteristics of cattle fed diets containing 60% DDGS. T. L. Felix* and S. C. Loerch, *The Ohio State University*, *Wooster*.

Dried distillers grains with solubles (DDGS) are an excellent source of energy and protein for feedlot cattle and their dietary inclusion may improve performance and reduce cost of gain. Because of the high S levels, DDGS have not typically made up the majority of the diet even when it would be economically advantageous to do so. Dietary S above 0.4% may reduce cattle performance and increase incidence of polioencephalomalacia. Copper binds with S in the rumen to form insoluble copper sulfides. The hypothesis was that including Cu in high DDGS diets would bind S, thereby reducing potential toxic effects and improving animal performance. The objective of this research was to determine effects of 3 supplemental Cu levels on performance and carcass characteristics of cattle fed diets containing 60% DDGS (S = 0.46%). Angus-cross yearling steers and heifers (n = 87; initial BW = 238 ± 36 kg) were blocked by sex and allocated to 12 pens. Treatments were: 1) 60% DDGS with 0 ppm Cu supplementation, 2) 60% DDGS with 100 ppm Cu supplementation, 3) 60% DDGS with 200 ppm Cu supplementation. The remainder of the diet was grass hay (10%) and a vitamin-mineral supplement (15%). Diets were offered ad-libitum throughout the finishing phase (168 d). Three randomly selected cattle from each pen (n = 36) were slaughtered on d 168. Carcass data and liver samples were collected. Copper supplementation did not affect ADG ($P > 0.35$). However, cattle that were supplemented with Cu had numerically lower DMI than those not supplemented, resulting in improved feed efficiency ($P = 0.03$) in cattle supplemented with Cu (G:F = 0.167, 0.177, and 0.177 for 0, 100, and 200 ppm Cu, respectively). There were no treatment effects ($P > 0.05$) on measured carcass characteristics. Cattle supplemented with 100 and 200 ppm Cu had higher liver Cu concentrations ($P < 0.0001$; mean = 708.24 and 933.32 ug/g, respectively) than cattle that were not supplemented with Cu (mean = 86.29 ug/g). These data suggest that cattle consuming diets with S above the maximum tolerable limit may be supplemented with Cu to improve Cu absorption and feed efficiency. Effects on S absorption are being pursued.

Key Words: DDGS, feedlot cattle, copper

550 Vitamin A restriction does not improve marbling in Holstein bulls at the same extent as in Holstein steers. S. Marti*[1], C. Realini[2], A. Bach[3,1], and M. Devant[1], [1]*Department of Ruminant Production, IRTA*, *Barcelona, Spain*, [2]*Carcass Quality Subprogram, IRTA*, *Girona, Spain*, [3]*ICREA*, *Barcelona, Spain*.

The aim of the current study was to evaluate if a temporal vitamin A restriction could increase marbling and thus could be an alternative method to castration in Holstein bulls to improve fattening. Forty-seven Holstein calves, 24 steers and 23 bulls (initial BW = 252 ± 3.5 kg and age = 187 ± 7.5 d), were randomly allocated to 4 treatments. Treatments followed a 2x2 factorial design with gender (bulls vs steers) and vitamin A level (restricted at 1.3 × 1,000 IU/kg, VAR, vs control at 4.6 × 1,000 IU/kg, CTR). Animals were fed concentrate and straw ad libitum. Feed consumption and BW were recorded every 28 d. Animals were slaughtered at 331 ± 7.3 d of life. The LM was removed from each carcass from the 7th to the 13th rib and pH, LM area, instrumental color, i.m. fat content, instrumental tenderness, oxidative and color stability, and purchase decisions were evaluated. Data were analyzed using a mixed-effects model with repeated measures that included initial BW, level of vitamin A, gender, time (month or aging), and the interactions between these factors, as fixed effects, and animal as a random effect. Steers had a lesser ($P < 0.01$) final BW, ADG, and HCW compared with bulls. The i.m. fat was lesser ($P < 0.01$) in bulls (2.8 ± 0.30%) than in steers (4.2 ± 0.30%), and greater ($P = 0.05$) in VAR (3.9 ± 0.31%) than in CTR (3.0 ± 0.31%) animals. Vitamin A restriction increased i.m. fat from 2.7 to 2.9% (7%) in bulls and from 3.4 to 4.9% (44%) in steers. Vitamin A did not affect tenderness, but oxidative stability tended ($P = 0.09$) to be greater in meat from VAR than from CTR at 21 d of aging. Purchase decision scores were greater ($P = 0.05$) in VAR (3.35 ± 0.07) than in CTR meat (3.16 ± 0.07). Vitamin A restriction does not affect animal performance, improves meat oxidative stability, and increases i.m. fat; however vitamin A restriction does not achieve the marbling levels obtained with castration in Holstein bulls.

Key Words: beef, marbling, vitamin A

551 Effect of added sulfur on in vitro fermentative activity of ruminal contents from steers fed corn-based diet. S. Uwituze*, L. C. Hollis, and J. S. Drouillard, *Kansas State University*, *Manhattan*

We previously reported that elevated sulfur (S) levels in finishing diets containing dried distiller′s grains with solubles (DDGS) decreased DMI and ADG of cattle, but were associated with increased diet digestibility

in vivo. An in vitro titration study was conducted to investigate effects of added sulfur (S) on IVDMD, VFA profiles, and NH_3 production from different substrates by mixed ruminal organisms. The study was a randomized complete block design with a 2 × 7 factorial treatment arrangement. Factor 1 consisted of substrate (a 94:4.5:1.5 mixture of ground corn, soybean meal, and urea [GC-SBM] or a 69.4:30.6 mixture of ground corn and DDGS [GC-DDGS]), and factor 2 consisted of the level of added S (0; 0.1; 0.2; 0.3; 0.4; 0.5; or 0.6% of substrate, DM basis) using sodium sulfate as the S source. Basal S levels were 0.18 and 0.28% of DM for GC-SBM and GC-DDGS, respectively. Isonitrogenous substrates (0.5 g DM) with varying levels of S were combined with a 2:1 mixture of McDougall′s buffer and strained ruminal fluid from a single donor animal (fed 40% alfalfa and dry-rolled corn) and incubated in triplicate for 24 h at 39C. The study was repeated for 3 d. Concentrations of VFA, NH_3, and IVDMD were analyzed using Proc Mixed of SAS with fixed effects of substrate, S, and substrate × S, and random effects of day, day × substrate, day × S, and day × substrate × S. Concentrations of NH_3, total VFA, individual VFA, A:P ratio, and IVDMD were unaffected by S ($P > 0.05$) or by the S × substrate interaction ($P > 0.05$). Cultures with GC-DDGS yielded lower concentrations of NH_3, propionate, butyrate, and valerate, and had lower IVDMD than GC-SBM cultures ($P < 0.05$). Substrates yielded marked differences in fermentative end products, but elevated sulfur did not alter in vitro fermentation of these substrates by mixed ruminal microorganisms. These data suggest that previous in vivo changes in digestibility associated with high sulfur are likely attributable to host factors, such as feed intake level.

Key Words: sulfur, distillers grains, fermentation

552 Dietary sulfur negatively affects gain and mineral status in beef steers. E. L. Richter*, M. E. Drewnoski, and S. L. Hansen, *Iowa State University*, *Ames*.

Crossbred yearling steers (n = 96; 321 ± 29 kg BW) were used in a trial to examine the effects of feeding a high sulfur (S) distillers grains (DDGS) supplement to steers on pasture before moving into the feedlot. Steers were blocked by weight and were supplemented with either a low S DDGS (0.3% S; LS; n = 48) or LS DDGS plus 0.3% S from sodium sulfate (high S; HS; n = 48). During the 35 d backgrounding period steers were supplemented daily at 1% BW and were stripgrazed weekly on 2 ha smooth bromegrass pastures (4 pastures per treatment; n = 12 steers per pasture). Mean daily supplement intake was 3.6 kg DM per head for both treatments. Daily S intake was greater ($P < 0.01$) for HS steers compared with LS steers (23.7 and 14.2 g S, respectively). Forage mass offered and grazing residual mass did not differ among treatments ($P = 0.6$ and 0.4, respectively). In vitro dry matter digestibility was not different between treatments ($P = 0.9$). Blood samples were collected on d 0 and 35 for plasma mineral analysis. On d 35 HS steers exhibited lower ($P = 0.05$) plasma magnesium (Mg) concentrations (18.4 mg/L) compared with LS steers (19.3 mg/L). Average daily gains for the 35 d period were not different ($P = 0.5$) due to treatment. On d 35 steers were moved into feedlot pens and housed in groups of 4 by treatment. Half of the steers remained on their original S treatment and half were switched to the opposite treatment, resulting in 4 treatments in total (LS-LS, LS-HS, HS-LS, HS-HS; n = 24 per treatment). Steer weights were collected on d 89 of the finishing period (d 124 of the study). HS steers tended ($P = 0.06$) to have lower ADG compared with steers receiving the LS diet during the finishing period (1.4 and 1.6 kg, respectively). In summary, plasma Mg was lower in HS steers and high dietary S negatively impacted gain during the finishing period, but did not affect steer gains while on pasture. Microbial population analysis of rumen fluid samples collected during the backgrounding and finishing periods may clarify these differences.

Key Words: cattle, magnesium, sulfur

553 Inclusion of molybdenum and copper with high distiller's grain diets as a strategy to mitigate hydrogen sulfide emissions. L. D. Cross*, S. R. Rust, and W. J. Powers, *Michigan State University*, *East Lansing*.

A rising concern with feeding high levels of distiller's grain with solubles (DGS) is its high sulfur content and the effects it might have on hydrogen sulfide emissions from gas produced in the rumen and/or from emissions from excreted feces. A study was conducted with 12 Holstein steers housed in individual environment-controlled rooms to monitor gas production of ammonia, hydrogen sulfide, and methane. Steers (3 treatments, 4 steers/treatment) were assigned to either a control diet (Trt1): 81% high moisture corn (HMC), 10% corn silage, 4% mineral supplement, and 5% soybean meal; 40% DGS diet (Trt2): 40% DGS, 46% HMC, 10% corn silage, and 4% mineral supplement; or Trt3 which was comprised of Trt2 with an added mineral supplement of 6 ppm molybdenum (Mo) and 60 ppm copper (Cu). The Cu-Mo mineral supplement served as a potential strategy to mitigate hydrogen sulfide emissions. Gaseous emissions were monitored for 4 weeks and fecal bags were placed on steers the last 6 d to determine what effects separating urine and feces would have on air emissions. Results demonstrated that 40% DGS diets increased ammonia emission (5.44 g/d vs. 11.73 g/d for the control diet compared with the DGS diets ($P = 0.01$) and hydrogen sulfide (16.41 mg/d vs. 183.45 mg/d for the control diet compared with the DGS diets ($P = 0.03$). The use of 6 ppm Mo and 60 ppm Cu did not reduce hydrogen sulfide emissions when 40% DGS diets were fed. No diet effect was observed for methane emissions (25.04 g/d). Separating feces from urine reduced ammonia and hydrogen sulfide emissions from exhausted room air. Most hydrogen sulfide (>99%) and ammonia (88.2%) emissions were from the manure and not eructated by the animal. Most methane emissions were due to eructation (>99%). Dietary addition of Cu and Mo did not mitigate hydrogen sulfide emissions.

Key Words: DGS, hydrogen sulfide, molybdenum and copper

554 The effect of supplemental molybdenum and copper on the concentrations of hydrogen sulfide in the rumen gas cap and copper in the liver of yearling steers consuming high sulfate water. R. K. Peterson*[1], J. J. Wagner[1], T. E. Engle[1], and T. C. Bryant[2], [1]*Colorado State University*, *Fort Collins,* [2]*JBS Five Rivers Cattle Feeding*, *Greeley, CO*.

Seventy-two crossbred yearling steers (323 kg) were utilized in an experiment to evaluate the effect of supplemental molybdenum (Mo) and copper (Cu) on the concentrations of hydrogen sulfide (HS) in the rumen gas cap and Cu in the liver of feedyard steers. Four dietary treatments were utilized: control - 90 mg/kg Cu from copper carbonate; organic Cu - 45 mg/kg Cu from copper proteinate and 45 mg/kg Cu from copper carbonate (OCu); molybdenum - 90 mg/kg Cu from copper carbonate and 100 mg/kg Mo from sodium molybdate (M); and molybdenum plus organic Cu - 90 mg/kg Cu from copper carbonate, 45 mg/kg Cu from copper proteinate, and 100 mg/kg Mo from sodium molybdate (MCu). The average HS concentration in the rumen gas cap was reduced ($P < 0.05$) from 1200 ± 78 to 951 ± 94 mg/L for steers fed MCu as compared with control. The number of steers with HS concentrations of 500 mg/L and greater was reduced ($P < 0.01$) from 76.5% for control to 53.1% for the MCu treatment. The number of steers with HS concentrations of 1000 mg/L and greater was reduced ($P < 0.01$)

from 50.6% for control to 30.2% for MCu. A 19.6 fold increase ($P < 0.0001$) in fecal Mo and a 13.5% increase ($P < 0.10$) in fecal sulfur were observed for MCu steers as compared with control. From May 6 through June 17, liver Cu concentration, on a dry weight basis, increased ($P < 0.06$) for control steers from 373 to 472 mg/kg but declined ($P < 0.05$) for M steers from 401 to 276 mg/kg. Average daily gain appeared higher ($P < 0.06$) for MCu steers as compared with other treatments. These data indicate that the concentration of HS in the rumen gas cap can be reduced without adversely affecting performance by feeding supplemental Mo; however, it is not known whether reductions in HS of this magnitude are physiologically important in reducing the incidence of polioencephalomalacia.

Key Words: molybdenum, copper, hydrogen sulfide

555 Effects of supplemental manganese on ruminal pH and hydrogen sulfide concentration in beef steers fed high-sulfur diets containing distillers grains plus solubles. J. M. Kelzer*[1], T. D. Maddock[2], M. Ruiz-Moreno[1], A. DiCostanzo[1], G. I. Crawford[3], and G. C. Lamb[2], [1]*University of Minnesota*, *St. Paul*, [2]*North Florida Research and Education Center, University of Florida Extension Regional Center*, *Marianna*, [3]*Extension Regional Office, University of Minnesota*, *Hutchinson*.

Effects of including 1000 ppm manganese (Mn; supplied as manganese oxide) in high dietary sulfur (S) feedlot diets containing distillers grains plus solubles on ruminal pH and hydrogen sulfide (H_2S) concentration were examined. Seven ruminally cannulated beef steers (437 ± 61 kg initial BW) were assigned randomly to treatments in a switchback design (2, 14-d periods). Treatments included a base finishing diet (65% rolled corn, 21% dried distillers grains plus solubles, 8% bahia hay, 15% CP, 1.31 Mcal NEg/kg DM, 0.46% S) containing either 0 ppm Mn (CON) or 1000 ppm Mn (MNO). Wireless sensors programmed to record pH every 5 min were inserted into the rumen on d 10. Steers were allowed access to treatments from 0730 to 1630 daily. Rumen gas samples were collected at −1, 1, 2, 3, 4, and 6 h post-feeding on d 11–12 and analyzed for H_2S concentration. Daily DMI was similar ($P = 0.61$) across treatments (8.61 vs. 8.91 ± 0.53 kg/d for MNO and CON, respectively). Ruminal pH was higher ($P = 0.02$) at 1 h before feeding with MNO (6.29) vs. CON (6.01). However, no pH differences were observed ($P > 0.17$) between treatments at other time points (5.90 vs. 5.77, 5.81 vs. 5.66, 5.74 vs. 5.62, 5.70 vs. 5.62, and 5.62 vs. 5.61 ± 0.08 for MNO vs. CON at 1, 2, 3, 4, and 6 h post-feeding, respectively). Ruminal H_2S concentration was similar ($P = 0.24$) between treatments at all time points (0.35 vs. 0.36, 1.55 vs. 1.76, 2.42 vs. 3.16, 2.77 vs. 3.74, 3.59 vs. 3.63, and 3.98 vs. 4.18 ± 0.31 µg/mL for MNO vs. CON at −1, 1, 2, 3, 4, and 6 h post-feeding, respectively). Cumulative ruminal H_2S concentration tended to be lower ($P = 0.09$) with MNO compared with CON (6.47 vs. 7.74 ± 0.53 µg/mL). Results suggest including 1000 ppm Mn in high S finishing diets may initially maintain higher ruminal pH to reduce cumulative ruminal hydrogen sulfide gas concentration in feedlot cattle.

Key Words: feedlot cattle, hydrogen sulfide, manganese oxide

556 Effects of supplemental manganese on performance and stress responses in beef cattle fed low- and high-sulfur finishing diets containing distillers grains plus solubles. J. M. Kelzer*[1], T. D. Maddock[2], T. N. Holt[3], A. DiCostanzo[1], G. I. Crawford[4], and G. C. Lamb[2], [1]*University of Minnesota*, *St. Paul*, [2]*North Florida Research and Education Center, University of Florida Extension Regional Center*, *Marianna*, [3]*Colorado State University*, *Fort Collins*, [4]*Extension Regional Office, University of Minnesota*, *Hutchinson*.

To investigate the effects of including 400 ppm manganese (Mn) in low- and high-sulfur (S) finishing diets on performance, pulmonary arterial pressure (PAP), and plasma acute phase protein (APP) response, 40 crossbred beef cattle (274 ± 51 kg initial BW; 27 steers, 13 heifers) were assigned in a 2 × 2 factorial design. Treatments were fed for 56-d and included base diets containing either 0.25 (LS) or 0.43% dietary S (HS) and 0 (NOMN) or 400 ppm Mn (MN). Base diets contained 65% rolled corn, 15.5% dried distillers grains plus solubles, 10.5% soy hulls, 14.4% CP, and 1.40 Mcal NEg/kg DM. To achieve targeted levels of S and Mn, calcium sulfate and Mn oxide were added. Plasma blood samples and PAP were collected on all cattle on d 0, 7, 14, 28, and 56. On d 22, 4 randomly selected steers from each treatment were subjected to a stress challenge by subcutaneous injection of 2 mL of *Mannheimia hemolytica* (One-Shot, Pfizer, Inc.). Blood samples were collected at −1, 0, 1, 2, 3, 4, 5, 6, 10, and 22-h post-challenge to determine APP response. There was a tendency ($P = 0.08$) for a MN*S interaction for DMI. Supplemental MN reduced ($P < 0.01$) DMI in HS diets (6.46 vs. 7.10 kg/d) but not in LS diets ($P = 0.62$). Compared with LS, HS diets decreased ($P < 0.01$) ADG (0.95 vs. 1.40 kg) and reduced ($P < 0.01$) G:F (0.138 vs. 0.176). Supplemental MN tended to reduce ($P = 0.07$) PAP (32.0 vs. 33.7 mmHg), but S had no effect ($P = 0.63$). Haptoglobin was similar ($P > 0.10$) among treatments and averaged 6.6 mg Hbβ/100 mL. Ceruloplasmin (CER) was increased ($P < 0.01$) with LS vs. HS diets (15.0 vs. 10.3 mg/dL). A MN × S interaction occurred ($P = 0.01$) for CER area under curve (AUC) in steers subjected to the stress challenge. Steers fed MN-HS had lower ($P < 0.01$) CER AUC than NOMN-HS. Low-S treatments were similar ($P = 0.50$) for CER AUC, and both were higher ($P < 0.01$) than either HS treatment. Supplemental Mn tended to decrease PAP and in HS diets, reduced DMI and CER AUC following a stress challenge, while high-S concentration in finishing diets reduced performance and CER levels in cattle.

Key Words: beef cattle, manganese, sulfur

557 Effects of sulfur content of wet or dry distillers grains in beef cattle finishing diets on intake, ruminal pH, and hydrogen sulfide. J. O. Sarturi*, G. E. Erickson, T. J. Klopfenstein, J. T. Vasconcelos, K. Rolfe, and M. G. Dib, *University of Nebraska*, *Lincoln*

A metabolism study was conducted to evaluate dietary sulfur (S) in beef cattle finishing diets formulated with wet and dry distillers grains with solubles (DGS) containing low (0.82%) and high (1.16%) S concentration. Six steers with rumen cannulas (BW = 381 ± 31kg) were assigned to 1 of 5 treatments in an unbalanced Latin square design (6 steers and 5 diets) and fed for 5, 14 d periods. Steers were fed once daily ad libitum. Treatments were arranged as a 2x2+1 factorial with factors being moisture (wet or dry DGS included at 40% of diet DM), S concentration (high or low), and a diet containing wet DGS from high S provided at 32% of diet DM to match the low S wet DGS. All diets contained 15% corn silage, 5% supplement, and a blend (60:40) of high-moisture and dry-rolled corn. Intake and pH (wireless pH probes) were collected on the last 7 d of each period. Ruminal gas samples were collected 8h post feeding on the last 3d of each period, and H2S analyzed. Chromium oxide (7.5g) was added into the rumen twice a day, every day, and spot fecal samples were collected twice daily on the last 5 d of each period for DM digestibility (DMD). Data were analyzed using the GLIMMIX procedures of SAS. No interaction ($P > 0.16$) was observed between moisture and S for DMI, DMD, or H2S. Steers fed dry DGS had greater DMI ($P < 0.01$) than steers fed wet DGS (10.6 vs. 9.1 kg/d). Likewise, steers fed low S DGS consumed more ($P < 0.01$) than steers fed high S

DGS (10.4 vs. 9.3kg/d). Greater ($P = 0.06$) H2S was observed for wet DGS (9.33 vs. 2.87 µmol/L gas, SEM = 2.80) compared with dry DGS. High S DGS tended ($P = 0.13$) to increase H2S compared with low S DGS. An interaction between moisture and S was observed for average pH ($P < 0.01$). Steers fed high S wet and low S dry DGS had greater ($P < 0.01$) average pH compared with low S wet and high S dry DGS, but these differences were subtle. Greater ($P < 0.01$) DMI and H2S were observed when low S DGS at 40% was fed compared with high S at 32% inclusion (10.0 vs 8.8 kg/d; 1.87 vs. 7.09 µmol/L gas). Sulfur of DGS impacts DMI and ruminal H2S production and wet DGS may be more prone to conversion of S to H2S in the rumen.

Key Words: byproduct, metabolism, sulfur

558 Days on feed and dietary sulfur content affect rumen hydrogen sulfide concentrations in feedlot steers. M. E. Drewnoski*, E. L. Richter, and S. L. Hansen, *Iowa State University*, *Ames*.

For feedlot cattle on high sulfur (S) diets, low rumen pH during the transition period may cause more sulfide in the rumen to be in the gaseous form of hydrogen sulfide (H_2S), increasing the risk of S induced polioencephalomalacia (PEM). To investigate the effects of transition diet on rumen H_2S concentrations, 96 yearling steers were blocked by weight (321 ± 29 kg) and assigned to receive either a low S (LS) distiller's grains (DDGS) or LS plus 0.3% S (high S; HS) supplement while grazing bromegrass pastures for 35 d. Concentrations of H_2S did not differ on d 35 due to treatment (trt; $P = 0.9$). Steers were then moved into the feedlot (4 steers per pen) and received ad libitum hay plus 1% BW DDGS for 10 d, followed by 3 7 d step-up diets. When steers were moved into the feedlot, half of the steers remained on their original S trt and half were switched to the opposite trt. Previous S diet did not affect DM intake or H_2S concentrations ($P > 0.1$) during the feedlot period, therefore only dietary feedlot trt means are presented. Intake (DM) did not differ among trt ($P = 0.5$). One steer per pen was sampled for rumen H_2S concentrations on the last d of each transition diet, and on d 25 of the finishing period. Concentrations of H_2S did not differ due to dietary S trt until corn composed 28% or more of the diet. Interestingly, daily S intakes within trt did not differ between TMR3 and TMR4 ($P > 0.4$), yet H_2S levels for both trt were greater on TMR4 vs. TMR3 ($P < 0.01$), suggesting that extra-dietary factors such as rumen microbial population shifts may be occurring during this time.

Table 1. Diet, S intake and rumen gas H_2S concentrations

	d on	% of diet DM			S intake, g/d		Rumen gas H_2S, mg/L	
Diet	diet	Hay	DDGS	Corn	LS	HS	LS	HS
Hay + DDGS	10	57	43	0	29.0d	41.1c	1400bc	1733b
TMR 1	7	47	40	13	17.3fg	43.0c	605cd	1283bc
TMR 2	7	32	40	28	18.1f	45.4b	280d	1091bc
TMR 3	7	17	40	43	19.4ef	50.8a	644cd	1849b
TMR 4	25	10	40	50	20.4e	51.8a	1316b	4964a

[a-g]Means lacking common letters differ ($P < 0.05$).

Key Words: cattle, hydrogen sulfide, sulfur

559 Selenium fed in inorganic and organic forms differentially and commonly alters liver gene expression profile of growing beef heifers. S. F. Liao*[1], K. R. Brown[1], A. J. Stromberg[2], W. R. Burris[1], J. A. Boling[1], and J. C. Matthews[1], [1]*Department of Animal & Food Sciences*, *University of Kentucky*, *Lexington,* [2]*Department of Statistics*, *University of Kentucky*, *Lexington*.

To determine if source of dietary selenium (Se) supplements differentially affects liver gene expression profile of beef cattle, after 75 d-feeding without Se supplementation, 30 Angus heifers (age 336 ± 6 d, BW 393 ± 9 kg) were randomly assigned to 3 dietary treatments (n = 10) and individually fed 7.8 to 8.2 kg/d of a corn and cottonseed hull-based diet to achieve an ADG of 0.5 kg/d. For each animal, the basal diet supplied 0.4 mg Se/d, whereas the mineral premixes provided no additional Se (Control), 3 mg inorganic Se/d as sodium selenite (ISe treatment), or 3 mg organic Se/d as Sel-Plex (Alltech; OSe treatment). After 105 or 106 d on the treatments, liver samples were collected by aspiration biopsy and total RNA extracted. The mRNA from 6 randomly-selected animals/treatment were individually subjected to microarray analysis (Affymetrix Bovine GeneChip). Raw microarray data were corrected and normalized with gcRMA-Medianpolish algorithms, and then statistically analyzed with 1-way ANOVA and means separation contrasts (Partek Genomics Suite software). ISe treatment altered ($P \leq 0.01$) 56 gene transcripts (30 upregulated, 26 downregulated), whereas OSe treatment altered ($P \leq 0.01$) 53 gene transcripts (31 upregulated, 22 downregulated). Bioinformatics analysis (Ingenuity Pathways Analysis) of these gene transcripts found that the affected genes were associated with nutrient metabolism (e.g., GCLM, CANT1); cellular growth, proliferation, and immune response (e.g., KNG1, CL-43, TLN1); cell communication or signaling (e.g., IGF2, IGFBP3); and tissue/organ development and function (e.g., BHLHB2, KLF10, KLF11). We conclude that source of supplemental Se affected liver gene expression: 26 genes were solely affected by ISe treatment, 23 solely affected by OSe treatment, and 30 commonly affected by both ISe and OSe treatments.

Key Words: cattle, liver, dietary selenium supplementation, nutrient-gene interaction

560 Meta analysis of dairy cow responses to dietary forage NDF. D. Sauvant*[1] and D. R. Mertens[2], [1]*Agroparistech-INRA*, *Paris, France*, [2]*US Dairy Forage Center*, *Madison, WI.*

Dietary forage NDF (fNDF) offers the potential of combining fiber and its particle size influences in a common index. For this reason, it may be more precise than dietary NDF or proportion of concentrate to predict dairy cow responses. To evaluate this hypothesis a database was compiled from 116 published experiments (n = 289 treatments) where dietary NDF or concentrate varied. Forages were long or coarsely chopped. Dietary NDF averaged 34.4 ± 8.2% of DM while fNDF was 26.2 ± 10.2% (from 11.0 to 59.6). Meta analyses with GLM allowed to focuse on within experiment regressions. Chewing index (CI; 38.2 ± 11.8 min chewing/kg DM Intake) was linearly related to fNDF (CI = 19.8 + 0.70 fNDF, n = 195, nexp = 80, rmse = 2.9). Mastication time also increased with fNDF, but obtained a plateau of 865 min/d at fNDF around 52%. Dry matter intake (20.4 ± 3.5 kg/d) was related negatively and curvilinearly to fNDF (= 22.6 - 0.003 fNDF2, rmse = 1.1), and milk yield (28.3 ± 7.1 kg/d) presented a similar shape (= 22.6 - 0.005 fNDF2, rmse = 1.4). Opposite responses were observed for milk percentages of fat (= 2.5 + 0.07 fNDF - 0.00008 fNDF2, rmse = 0.17) and protein (= 3.3 + 0.001 fNDF - 0.00001 fNDF2, rmse = 0.08). Ruminal pH was positively related to fNDF (= 5.62 + 0.023 fNDF - 0.00014 fNDF2, n = 145, nexp = 56, rmse = 0.08). Acetate/propionate ratio increased with fNDF (= 1.05 + 0.10 fNDF - 0.001 fNDF2, n = 163, nexp = 66, rmse = 0.24). Values of pH = 6.1 and A/*P* = 3.0 corresponded to fNDF = 24%. An increase in fNDF significantly increased the rumen liquid load (RLL = 73 ± 11.1 kg, = 53.6 + 1.14 fNDF - 0.014 fNDF2, n = 76, nexp = 32, rmse = 5.0) and rumen liquid outflow rate. In contrast, fNDF decreased the organic matter digestibility (= 74.1 - 0.139 fNDF, n = 186, nexp = 73, rmse = 2.3) and the energy balance became negative when fNDF > 31.5%. In conclusion, most predictions were curvilinear and fairly accurate. As a measure of fill effect, the minimization of fNDF enhances the milk performance, however when fNDF is < 20–25% DM the risk of acidosis increases.

Key Words: forage NDF, dairy cow, meta analysis

561 Effect of forage type on passage rate estimated from rumen evacuation studies. S. J. Krizsan*[1], S. Ahvenjärvi[2], and P. Huhtanen[1], [1]*Department of Agricultural Research for Northern Sweden, Swedish University of Agricultural Sciences*, *Umeå, Sweden*, [2]*MTT-Agrifood Research Finland, Animal Production Research*, *Jokioinen, Finland*.

A meta-analysis of studies using the flux/compartmental pool method with indigestible NDF (iNDF) as internal marker was conducted to study the effect of forage type on particle passage rate (k_p) in cattle. Data were comprised of 172 treatment means from 49 studies conducted in Europe and in the USA. A total of 145 diets were fed to dairy cows and 27 to growing cattle. Prerequisite for inclusion of an experiment was that DMI, intake of NDF (NDFI), proportion of concentrate (CProp) in the diets, live weight (LW), and diet chemical composition (concentrations of CP, NDF, NFC and iNDF) were determined or could be estimated. Mixed model regression analysis including a random study effect was used to generate prediction equations of k_p. Initially 13 different forage types were classified, but when not different ($P > 0.10$) from grass silage the groups were pooled. The best fit model when forage type was not included was: k_p (%) = 1.19 + 0.0879 × NDFI (g/kg LW) + 0.792 × CProp (on NDF basis) + 1.21 × iNDF/NDF (RMSE = 0.231%, Akaike's information criterion = 199 and $R^2 = 0.66$). The best general equation correcting for the effect of forage type was: k_p (%) = 1.54 + 0.0866 × NDFI (g/kg LW) (RMSE = 0.207% and $R^2 = 0.80$). The effect on k_p of fresh grass (FG), mixes of alfalfa and corn silage(AS/CS) and dry or ensiled alfalfa as sole forage component (AH/AS) were estimated by adjusting the intercept in the general equation accounting for forage. The adjustment factor on the intercept for FG, AS/CS and AH/AS were −0.914, +0.831 and +0.237, respectively. The results from this meta-analysis suggested that consistency of ruminal digesta is affected by intrinsic forage characteristics that influence particle passage rate. Further, including an effect of forage type on k_p could not be explained by any of the chemical composition parameters of the diets.

Key Words: cattle, forage type, passage rate

562 Abrupt changes in forage dry matter of one to three days affect intake and milk yield in early lactation dairy cows. J. Boyd* and D. R. Mertens, *US Dairy Forage Research Center*, *Madison, WI.*

Our objective was to determine the effects of 1, 2, and 3 d changes in forage dry matter on lactating cow performance and yield. Forty-four Holstein cows (22 primiparous and 22 multiparous) averaging 65 DIM, 43.3 kg/d of milk, and 574 kg body weight were used in study conducted from October through December 2009. Within each parity, cows were assigned to 1 of 11 blocks based on production and days in lactation and one cow of each parity-block was randomly assigned to 1 of 2 groups. Study design was replicated 2 × 2 Latin squares for each set 1, 2, or 3 d treatments. Each period consisted of a 3d pre-treatment, 1 to 3d treatment, and a 3d post-treatment phase. Diets contained about 18% alfalfa and 36% corn silage (DM basis) and were control (Ctrl) with no water added and treatment (Trt) with water added to decrease forage DM by 8%-units, which mimicked rainfall events on a bunker silo and feeding an imprecise ration based on as-fed ratios of ingredients. Ctrl ration was adjusted daily to maintain DM ratios of ingredients during the study. Milk yield was recorded daily and component samples were taken 2x daily. Forages, TMR, and refusals were sampled daily and concentrates sampled 2x weekly. Chemical composition (DM, CP, NDF) of samples were determined by NIR. Data was analyzed using Proc MIXED of SAS with cow within parity-block as a random variable. On day1, DMI was reduced 2.4 ($P < 0.0001$), 1.2 ($P = 0.0001$), and 0.8 kg ($P = 0.003$), for the 1, 2, and 3d treatments, respectively, but DMI recovered during the following 1 to 3 d even during Trt phases. Although daily milk decreased slightly on day1 of each Trt, the decrease was largest on day2: −1.4 ($P = 0.02$), −2.6 ($P = 0.002$) and −1.9 kg ($P = 0.006$), for the 1, 2, and 3d treatments, respectively. Smaller reductions in daily milk occurred on the remaining days of Trt and for 4% fat-corrected milk. We conclude that abrupt changes in forage DM cause economically significant reductions in daily milk yield, but the duration of the change does not worsen the losses if adequate ration amounts are provided.

Key Words: dry matter changes, precision feeding, milk yield

563 Effects of corn silage harvested with or without ears on rumen fermentation and milk performance of dairy cows. M. Boivin*, R. Gervais, and P. Y. Chouinard, *Université Laval*, *Québec, QC, Canada*.

The objective of this study was to evaluate the effects of grain fraction in corn silage (CS) on rumen fermentation and milk performance of dairy cows. To reach this objective corn ears were manually removed from half of the plants in the same field. Whole CS and earless CS were

harvested the day after. Eight multiparous (4 rumen fistulated) Holstein cows (84 ± 31 DIM) were fed TMR in a double 4x4 Latin square design with 21-d periods. Treatments were WCS: 23% whole CS (DM basis), RCS: reconstituted CS with 12.4% earless CS and 10.6% high moisture corn, ECS: 23% earless CS, and GS: 23% grass silage. All TMR contained alfalfa silage, grass hay, ground corn, soybean meal, corn gluten meal, soy hulls, and corn oil. Contrasts were made to compare WCS vs. RCS, WCS vs. ECS, and ECS vs. GS. Statistical difference was declared at $P < 0.05$, and tendency at $0.05 \leq P \leq 0.10$. DMI did not differ between WCS and RCS or between ECS and GS, but was higher for WCS compared with ECS (27.5 vs. 25.2 kg/d). Milk yield was higher with WCS than ECS and RCS (42.8, 39.0 and 39.5 kg/d, respectively), and tended to be higher with GS (40.7 kg/d) than ECS. Milk fat content and yield were unaffected by treatments. Milk protein content of ECS was lower than WCS (2.94 vs. 3.04%) and tended to be lower than GS (2.99%). Milk protein contents of WCS and RCS were similar. Milk protein yield was higher for WCS than RCS and ECS, and was lower for ECS than GS (1.30, 1.20, 1.14, 1.21 kg/d, respectively). Rumen pH recorded at 0, 1, 2, 4 and 6 h post feeding decreased linearly with time, but was not affected by treatments. Mean rumen NH3-N concentrations recorded at the same sampling times were lower with GS than ECS (10.8 vs. 12.6 mg/dl). Mean proportions of acetate were lower and those of propionate were higher for WCS than for ECS (59.9 vs. 61.9% and 22.1 vs. 19.8%, respectively). Acetate to propionate ratio was greater with ECS compared with WCS (3.14 vs. 2.74). Under the condition of this experiment removing the grain fraction from CS reduced milk production and modified ruminal fermentation without affecting milk fat content and yield.

Key Words: corn silage, corn stalklage, forage-to-concentrate ratio

564 Comparison of alfalfa and orchardgrass hay as replacements for grain in lactating dairy cow diets. M. L. Raeth-Knight*[1], H. G. Jung[1,2], P. R. Peterson[1], N. B. Litherland[1], and J. G. Linn[1], [1]*University of Minnesota*, *St. Paul*, [2]*USDA-Agricultural Research Service*, *St. Paul, MN*.

A study was conducted to compare lactating dairy cow performance when alfalfa (40% NDF) or orchardgrass (60% NDF) hay replaced corn grain in a corn silage-based total mixed ration. Fifty cows were blocked by sire breed, ranked by DIM and randomly assigned to 1 of 10 treatments. Treatments were 5 dietary inclusion levels of either alfalfa (15, 20, 25, 30 and 35% of diet DM) or orchardgrass (10, 15, 20, 25 and 30% of diet DM). Across treatments, cows averaged 86 DIM at study initiation, and cows remained on their respective treatments for 8 wk. Feed intake, feed refusals, and milk production were recorded daily, and milk composition was determined weekly. During wk 4 and 8, fecal grab samples were collected to determine in vivo diet digestibility; and eating, ruminating and resting time were recorded every 15 min for 24 h. Within alfalfa and orchardgrass treatments, 3.5% FCM yield decreased with increasing hay inclusion level (r2 = 0.59). The rate of decline was similar between hay species with cows averaging 44.6 and 37.3 kg 3.5% FCM/d at the lowest and highest hay inclusion levels, respectively, across hay species. When milk production was regressed on diet NDF concentration, within hay species, 3.5% FCM yield declined at a faster rate for the alfalfa as dietary NDF concentration increased. Range in diet NDF was 29.5 to 35.6% NDF and 29.9 to 39.8% NDF for alfalfa and orchardgrass, respectively. With each percentage unit increase in dietary NDF concentration, 3.5% FCM yield decreased 1.22 kg/d and 0.46 kg/d for alfalfa and orchardgrass, respectively. There was no difference in milk fat (3.8%) or true protein (3.0%) among treatments. Rate of in vitro NDF digestibility (IVNDFD) was similar (4.6 vs. 5.2%/h), while extent of IVNDFD was greater (79% vs. 56%) for orchardgrass compared with alfalfa hay. In this study, these alfalfa and orchardgrass hays supported similar levels of milk production when they replaced corn grain in the diet.

Key Words: dairy nutrition, alfalfa, orchardgrass

565 The effect of feed sorting on NDF, starch, and particle intake. D. D. Maulfair*, G. I. Zanton, and A. J. Heinrichs, *The Pennsylvania State University*, *University Park*.

Ration sorting occurs when cattle selectively consume certain parts of their ration, generally sorting for finer particles and against longer particles. Sorting is thought to have negative impacts on cow health and production. The objective of this experiment was to study the effects of varying TMR particle size on sorting behavior of lactating dairy cows and to evaluate effects on chewing behavior, milk yield and components, and rumen fermentation. Eight multiparous, Holstein cows (90 ± 32 d in milk; 4 rumen cannulated) were randomly assigned to replicated 4 × 4 Latin squares. Cows were fed diets that varied in chop length of dry grass hay. Diet forages and their percentage of diet DM were: corn silage (29.4), haylage (17.6), and grass hay (11.8). The geometric mean lengths (X_{gm}) of diets fed were: 4.46, 5.10, 5.32, and 5.84 mm for the short (S), medium (M), long (L), and extra long (XL) TMR respectively. Consumed X_{gm} for diets after 24 h was 4.44, 4.90, 4.82, and 5.10 mm for the S, M, L, and XL diets respectively. Differences between X_{gm} at time of feeding and after 24 h increased with increasing TMR particle size. In addition, refusal NDF concentration increased by 10.8 and 1.4%, while refusal starch concentrations decreased by 6.4% and increased by 1.5% throughout the day for the longest and shortest diets respectively. However, when NDF and starch intake were calculated after 24 h, mean NDF intakes varied by only 2.3 kg and there were no differences in starch intake. No differences were found in rumen VFA and NH_3 and mean rumen pH only varied by 0.13. Milk production and components were also similar between diets. Despite large changes in particle size distribution and NDF and starch concentrations of refusals due to sorting, there were no negative effects on rumen fermentation or milk production and components found in this study. Therefore, it is important to calculate the actual consumption of diet components to determine if sorting is a problem, because diet refusals represent only a small percentage of total diet intakes.

Key Words: chewing, particle size, sorting

566 Effects of varying inclusion rates of prairie hay and wet corn gluten feed on productivity of dairy cows. D. J. Rezac*[1], K. N. Grigsby[2], and B. J. Bradford[1], [1]*Kansas State University*, *Manhattan,*[2]*Cargill Incorporated*, *Blair, NE*.

Productivity of lactating dairy cows fed diets with wet corn gluten feed (Sweet Bran, Cargill Inc.; WGCF) as the primary energy substrate and prairie hay as the primary source of physically effective NDF (peNDF) was assessed versus a control diet. Forty-eight Holstein cows, 100–250 d in milk, were randomly assigned to 1 of 6 pens and pens were randomly assigned to treatment sequence in a replicated 3x3 Latin square. Treatments were a control ration with 18% alfalfa, 18% corn silage, 33% WCGF, and 15% forage NDF (CON); a diet with 20% prairie hay, 46% WCGF, and 13% forage NDF (PH20); and a diet with 14% prairie hay, 56% WCGF, and 9% forage NDF (PH14). However, midway through period 2, PH14 was discontinued due to numerous cases of diarrhea among cows on that treatment. Data from period 2 for PH14 pens was discarded and the pens which had been assigned to PH14 for period 3 were randomly assigned to the other treatments. Data were analyzed

with mixed models using random effects of period and pen and fixed effect of treatment. Dry matter intake was not altered by treatment. Least squares means milk yields were 36.2, 34.6, and 35.6 kg/d for CON, PH20 and PH14, respectively; milk yield was significantly greater for CON than PH20 ($P = 0.03$). Milk fat concentration was lowest for PH14 ($P < 0.01$), with means of 3.47, 3.40, and 2.82% for CON, PH20, and PH14, respectively. Fat yield was significantly greater for CON compared with PH14 ($P < 0.01$) but was not different from PH20. Milk urea nitrogen was the greatest for PH20 and least for CON ($P < 0.01$) with PH14 being intermediate, consistent with differences in dietary protein. Efficiencies, expressed as energy corrected milk divided by DMI, were 1.45, 1.40, and1.30 for CON, PH20, and PH14, respectively, and were not significantly different. These data suggest that PH14 did not provide adequate peNDF to support normal rumen function in midlactation dairy cows; however, PH20 offered a feasible diet for use on dairies where high-NDF grass hay and WCGF are available.

Key Words: non-forage fiber, physically effective fiber, wet corn gluten feed

567 Fiber digestion kinetics in muskoxen. E. M. Ungerfeld*[2], R. J. Forster[2], P. B. Barboza[1], M. B. Leigh[1], and C. Glover[1], [1]*University of Alaska Fairbanks*, *Fairbanks,* [2]*Agriculture and Agri-Food Canada*, *Lethbridge, Alberta, Canada*.

The objective of this study was to examine fiber digestion in the muskox rumen as a potential source of enzymes and microbes for biofuel production from fibrous biomass. We measured the kinetics of ruminal digestion in situ for triticale straw (low quality diet) and brome hay (medium quality diet) in a 2-period crossover design (n = 4). Each period consisted of 3 weeks adaptation to diets, after which pairs of polyester bags containing triticale straw or brome hay ground through 1mm mesh were placed in the rumen for 24 to 120 h. Negative exponential regressions were fitted to calculate fractional rate and extent of digestion of cellulose (defined as ADF – lignin), hemicellulose (NDF – ADF) and lignin for each animal-diet-substrate combination. Responses were initially modeled as functions of animal (random), period (random), diet, substrate, animal × substrate (random), period × substrate (random) and diet × substrate. Interactions were not significant for any response variable and were dropped from models. Cellulose digestion rate of both substrates was greater ($P = 0.004$) in animals fed straw than in those fed hay, indicating dietary induction of cellulotyic activity. Cellulose digestion rate was similar between substrates ($P = 0.69$) even though more cellulose was digested from hay than from straw ($P < 0.001$). Diet did not affect the rate ($P = 0.86$) or extent ($P = 0.24$) of hemicellulose digestion from either substrate. Hemicellulose digestion rate was greater ($P = 0.033$) in straw than in hay substrate, but its extent of digestion was greater ($P = 0.001$) in hay. Small values for lignin digestion at 120 h were greater for hay as substrate ($P < 0.001$) and for straw as a diet ($P = 0.012$). Results suggest that, for the substrate processing used, cellulose digestion rate, but not extent, was limited by microbial enzymatic activity, whereas hemicellulose digestion rate and extent was limited by surface available for microbial colonization and digestion. Muskoxen consuming low quality forages may induce cellulolysis and could be a potential source of useful fibrolytic microbes and enzymes.

Key Words: muskox, rumen, digestion

568 Nutrient utilization of different levels of dietary fiber in dairy heifers limit-fed high and low concentrate diets. G. J. Lascano* and A. J. Heinrichs, *The Pennsylvania State University*, *University Park*.

The objective of this experiment was to assess the optimal levels of dietary fiber (DF) incorporated in high concentrate (HC) and low concentrate (LC) diets for limit-fed dairy heifers. Eight Holstein heifers (335.6 ± 7.41 kg BW) were randomly assigned to 2 levels of concentrate: HC (20% forage) and LC (80% forage) and to a forage type sequence (0% of forage as corn stover (CT), 100% corn silage (CS); 20% CT, 80% CS; 40% CT, 60% CS; 60% CT, 40% CS) within forage level administered according to a split-plot, 4 × 4 Latin square design (21-d periods). All diets provided similar intakes of ME and allowed 800 g/d of ADG. DF (NDF and ADF) and non fiber carbohydrates composition were allowed to vary with the dietary ingredients. HC-fed heifers had higher apparent total tract (TD) digestibility of dry matter (DM; 72.6 vs.64.9 ± 0.52%; $P \leq 0.01$) than LC. Increasing DF level by increasing the amount of CT in the diet resulted in a linear decrease of DMTD (73.3, 71.5, 66.2 and 63.9 ± 0.51%, respectively; $P \leq 0.01$). Organic matter TD followed the same pattern as DMTD. LC diets had higher NDF ($P \leq 0.01$) and tended to have lower ADF TD than HC diets ($P = 0.06$). As level of DF increased, NDF and ADF TD had a cubic response with 20% CT diets having the highest values. HC diets decreased fecal output on DM and wet-bases, and DF had a decreasing linear effect on these parameters ($P \leq 0.01$). Urine volume excretion tended to be higher for HC-fed heifers (16.2 vs. 7.7 ± 2.51 kg/d; $P = 0.06$) and increasing level of DF tended to decrease urine output ($P = 0.10$). Total purine derivatives did not differ between treatments or CT level, but uric acid tended to be higher in HC-fed heifers ($P = 0.06$), and tended to decrease linearly ($P = 0.10$) when levels of DF increased. We conclude that CT decreased DM, and OM TD linearly while NDF, and ADF TD were maximized when 20% CT was added to HC and LC diets; HC diets were more digestible and generated less fecal output, but total manure was not different between HC or LC diets.

Key Words: high concentrate diet, fiber, limit-feeding, dairy heifer

569 Dietary starch level and dose response of *Saccharomyces cerevisiae* for limit fed-dairy heifers. G. J. Lascano*[1], J. M. Tricarico[2], and A. J. Heinrichs[1], [1]*The Pennsylvania State University*, *University Park*, [2]*Alltech Inc.*, *Nicholasville, KY*.

The objective of this experiment was to determine the effects of 2 levels of dietary starch and the dose at which the effects of *Saccharomyces cerevisiae* (Yea-Sacc[1026], Alltech Inc.; YC) are maximized based on nutrient total tract digestibility (AD), rumen fermentation, microbial protein synthesis, and N utilization of limit-fed dairy heifers. A split plot design with starch level as the whole plot and YC dose as sub-plot was administered in a 4 period (21 d) 4 × 4 Latin square. Eight Holstein heifers (432.49 ± 6.81 kg BW) were allocated to 2 starch treatments (30% starch: HS; 15% starch: LS) and to a sequence of YC doses (0, 10, 30, and 50 g/d). DM ($P = 0.98$) and NDF ($P = 0.28$) AD were not different between HS and LS; however, HS decreased ADF and increased hemicellulose AD (48.5 vs 44.9 ± 1.38 and 45.0 vs. 56.4 ± 3.20% respectively). YC dose increased DM AD quadratically (68.6, 68.8, 71.3, and 69.8 ± 0.47%; $P < 0.01$). NDF, ADF, and hemicellulose AD increased or tended to increase quadratically with increasing YC dose ($P = 0.03$, 0.06, 0.10 respectively). No significant effects were noted on fecal or urine output. Mean ruminal pH was higher for LS treatment (6.18 vs. 6.05 ± 0.06), and there was a trend ($P = 0.09$) for YC dose and starch interaction. The highest pH for LS and HS diet were at 0 and 50 g/d respectively. Total volatile fatty acid concentration was not different among YC doses or starch level. Concentrations of propionate, isobutyrate and iso-valerate were higher for HS than LS. Isovalerate was reduced linearly with increasing addition of YC and acetate: propionate responded quadratically to YC addition with 10 g/d having the lowest

value. Estimated microbial N outflow was not different among starch treatments or YC doses. We conclude that starch level did not affect DM AD, but influenced ADF and hemicellulose AD. YC dose had a greater effect on DM, NDF, ADF, and hemicellulose AD when added at 30 g/d. Fermentation parameters were not different among dietary treatments, but rumen pH was higher for LS diets.

Key Words: yeast culture, starch, limit-feeding, dairy heifer

570 Effects of limit-feeding on the feeding behavior of dairy heifers. B. L. Kitts*, B. W. McBride, I. J. H. Duncan, and T. J. DeVries, *Department of Animal and Poultry Science, University of Guelph, Kemptville Campus*, *Kemptville, Ontario, Canada*.

Limit-feeding replacement dairy heifers has been shown to control growth, while reducing feed costs and increasing efficiency; however, it also poses behavioral concerns. The objective of this study was to determine if these concerns are mitigated by providing straw alongside a limit-fed ration. Twenty-four Holstein dairy heifers (187 ± 11.3 d of age, 231.1 ± 12.0 kg), divided in groups of 4, were exposed to each of 3 treatments in a replicated Latin square design with 28-d periods. The treatment rations were: 1) TMR, 2) TMR with straw (2kg/d/heifer) offered as a choice (TMR-C) and 3) TMR with straw (2kg/d/heifer) mixed in (TMR-M). The TMR was fed at a restricted level (2.02% of BW) and contained (DM basis) 19.0% haylage, 21% corn silage, 45% high moisture corn, and 15% protein supplement. Feeding behavior was recorded for the last 14 d of each period. Standing time was recorded for the last 7 d of each period. Rumination behavior was recorded twice weekly in the last 14 d of each period. BW was recorded weekly and group DMI was recorded daily. Data were averaged per treatment per group, and analyzed in a GLMM with treatment, period and square as fixed effects and group within square as a random effect. DMI was lowest for the TMR treatment compared with the treatments with straw (5.7 vs 7.3kg/d; SE = 0.02, $P < 0.001$). Heifer ADG tended to be lower on the TMR-M compared with the TMR and TMR-C treatments (0.78 vs 0.94kg/d; SE = 0.04, $P = 0.1$). Feed efficiency (DMI/ADG) improved (SE = 0.01, $P < 0.001$) on the TMR (6.3) compared with TMR-C (7.8) and TMR-M (9.9). Daily feeding time differed (SE = 6.6; $P < 0.001$) between TMR (76.1 min/d), TMR-C (206.9 min/d), and TMR-M (279.2min/d). Inactive standing time differed between treatments (SE = 6.4; $P < 0.001$); with TMR being the highest compared with TMR-C and TMR-M (556.4 vs 409.9 vs 340.1 min/d). There tended to be fewer heifers ruminating on the TMR compared with TMR-M (14 vs 21.9%; SE = 2.0; $P = 0.1$). The results suggest that provision of straw as a choice, alongside a limit-fed ration, will allow heifer growth rates to be targeted, as well provide a suitable foraging source that heifers can use to satisfy their natural feeding behavior patterns.

Key Words: limit-feeding, dairy heifer, feeding behavior

571 Evaluation of potential carry over effects associated with limit feeding gravid Holstein heifers. K. A. Kruse*, N. M. Esser, P. C. Hoffman, and D. K. Combs, *University of Wisconsin, Madison*.

To evaluate potential carry over effects associated with limit feeding dairy heifers 96 Holstein heifers (400 ± 6 kg, 15.2 ± 0.1 mo) including 9 heifers with ruminal cannula were fed one of 3 dietary treatments for 180 ± 8 d in a randomized replicated pen design. Treatment diets included a control diet (C100) and 2 limit fed (LF) diets. The LF diets were formulated to provide similar nutrient intakes to C100. One LF diet (L85) was fed at 85% of C100 intake, and the other contained an ionophore (I; 325 mg/hd/d of Lasalocid) and was fed at 80% of C100 intake (L80+I). Heifers were evaluated for growth, rumen digesta volume, nutrient excretion and lactation performance. Data were analyzed using SAS proc mixed procedure with the replication of pen being the experimental unit. The LF heifers consumed less DM, NDF, and had greater ADG (0.96, 0.89 vs 0.81 kg/d), and lower feed:gain ratios (9.1, 9.3 vs. 13.0 kg/kg) as compared with heifers fed C100. No differences in rumen pH, NH_3-N, or VFA concentrations were observed between C100 or LF heifers. Limit fed heifers tended to excrete less DM (3.9, 3.2 vs 4.3 kg/d), whereas N and P excretion values were not different. Apparent N retention was improved in LF over C100 heifers (84.1, 96.8 vs. 77.1 g/d). Limit feeding did not alter rumen digesta volume, weight or density ($P > 0.05$). No differences were observed for dystocia index (≤1.0), calf BW (40.6 kg), or 7 d postpartum BW (566 kg) between LF and C100 fed heifers. After parturition, all heifers were fed a common high fiber diet. Lactation BW (551 kg), DMI (19.9 kg/d), and feed efficiency (1.6 kg/kg milk) were similar between treatments at 45 or 90 DIM. Milk yield (33.2 kg/d), milk fat (3.70%) and milk protein (2.90%) also were similar. At 45 DIM, rumen digesta volume was greater (99.1 vs. 66.1 L) for cows fed L85 as compared with cows fed L80 + I as heifers, but this effect was not observed at 90 DIM. Rumen digesta volume, lactation DMI, and milk yield of LF gravid Holstein heifers for 180 d did not result in negative carryover affects.

Key Words: limit feeding, heifers, ionophore

Small Ruminant Symposium: Going, going, gone! How Curtailment of Livestock Grazing on Federal Lands Could Alter the US Sheep Industry

572 How curtailment of livestock grazing on public lands could alter the US Sheep Industry. J. B. Taylor*, *USDA, Agricultural Research Service*, *Dubois, ID*.

This symposium will demonstrate how the potential curtailment of livestock grazing on federal lands will alter the US sheep industry, and what policies, perceptions, and biases are being used to challenge the use of federal lands for agricultural production. Five speakers will demonstrate the influence of land management policies and other related legislation, judicial decisions, and nonlitigation activities on availability of federal lands for sheep grazing, and detail the potential economic impact on the US sheep industry if livestock grazing is prohibited on federal lands in the future. The overall goal of the symposium is to challenge attendees to consider where to best place their information dissemination and research efforts in light of current policies, judicial decisions, and events that threaten the continued availability of federal lands for livestock production.

Key Words: public lands, sheep, symposium

573 The future of livestock grazing on federal lands: Opportunities for change. J. Kaiser*, *USDA, Forest Service*, *Washington, DC*.

The regulatory, environmental, social, and judicial aspects of grazing livestock on federal lands are duplicative, complicated, and litigious. Environmental laws and policies are enacted with good intentions, but often take a short-term approach to save a species without consideration of long-term effects, which may result in the demise of that same species. The threat of disease transmission from domestic to wild species has alarmed the public and various land-management agencies. A consequential reaction to this threat has been to completely separate domestic and wild species. For example, management decisions were instituted that resulted in removal of domestic sheep from federal lands that wild sheep inhabit. Although seemingly prudent for the short-term, such action fails to address long-term management needs and simultaneously threatens the vitality of sheep enterprises dependent upon federal lands. Land management policies and resulting actions must be based on sound science and a ″balance of harms″ approach, which takes the long-term view. The challenge is to override perceptions and deliver credible information that forms sound policy and drives workable solutions. To successfully develop sound policies, one should consider relevant regulatory, environmental, social, and judicial aspects of federal-land grazing; understand ″balance of harms″ approach for managing federal lands; and be aware of perceptions that drive policy related to separation of domestic and wild species using the same federal lands. Ultimately, policy should enable management that sustains healthy federal lands that provide habitat for thriving and diverse populations of wildlife and forage for productive sheep enterprises.

Key Words: policy, public lands, sheep

574 The future of livestock grazing on federal lands: Real and perceived threats. W. G. Myers*, *Holland & Hart LLP*, *Boise, ID*.

Various special interest groups want to nudge federal lands out of reach of livestock producers. In the 11 western Public Land States, federal lands that are administered by the US Department of Agriculture, Forest Service and the Department of Interior, Bureau of Land Management are an important and sustainable source of forage for many sheep enterprises. Preservation, conservation, and antiagriculture groups that are opposed to the use of federal lands for agricultural purposes have initiated species- and process-based litigation and other tactics to advocate removal of sheep grazing from public lands. For example, litigation that relates to Federal Land Policy and Management Act, Endangered Species Act, National Environmental Policy Act, and National Forest Management Act has been initiated to limit or restrict grazing access to federal lands. Furthermore, a variety of nonlegal tactics have been employed that result in unbearable fiscal, management, or labor burdens for sheep owners using federal lands. These antigrazing actions have resulted in closure of some federal lands to sheep grazing and(or) producers forfeiting grazing leases. Ultimately, closure of federal lands to sheep grazing may set precedents for removal of all livestock grazing, including beef cattle, on federal lands.

Key Words: grazing, litigation, public lands

575 Economic considerations of sheep grazing on federal and public lands. N. R. Rimbey*[1] and L. A. Torell[2], [1]*University of Idaho*, *Caldwell,* [2]*New Mexico State University*, *Las Cruces*.

Dependency of the western livestock industry on federal lands varies widely. Federal lands administered by the US Department of Agriculture, Forest Service and the Department of Interior, Bureau of Land Management contribute significant portions of the annual forage base for sheep and cattle in the western United States. These lands also provide critical habitat for wildlife and recreational opportunities to the public. Conflicts over the use and management of federal lands have greatly influenced development of grazing regulations and policies, which significantly impact the availability of federal lands for grazing. Relatively low grazing fee levels contribute to the image that federal-land grazing is heavily subsidized. These real and perceived subsidies have led to the development of asset values of federal grazing permits and of livestock enterprises that hold these permits. Therefore, administration of grazing regulations and policies that affect the availability of federal grazing permits directly influence the overall worth and viability of many western sheep enterprises. The focus of this presentation will be to discuss historic legal and regulatory basis for managing federal land grazing resources, methods for estimating grazing-use dependency, how the federal grazing fee formula is derived from federal and private grazing costs, the role that grazing permit value plays in the grazing fee debate, and policy-based alternatives related to the future of federal land grazing management.

Key Words: grazing permit, public lands, sheep

576 Impact of reduced federal and public land grazing on viability of the US sheep industry. D. P. Anderson*, *Texas A&M University*, *College Station*.

The sustained viability of the US sheep industry is linked to grazing on federal lands. As of January 1, 2010, the 11 western Public Land States contained 46 percent of the US mature ewe flock. Many of those sheep spend some portion of their lives on federal lands, which are mainly administered by the US Department of Agriculture, Forest Service and the Department of Interior, Bureau of Land Management. Loss of access to federal lands for grazing purposes would have a negative impact that is beyond the sheep enterprises that are dependent upon these lands. For example, factors that further aggravate the long-term decline in US lamb

inventory could be enough to reduce the US sheep industry to levels below a critical mass for industry infrastructure, e.g., meat packers and wool warehouses, to survive. In addition to lambs from the western Public Lands States, many meat packers also process a significant number of lambs and goats from non-public land states (e.g., Texas, the largest sheep producing state) to maintain a critical volume that is essential to keeping the plant operational. This presentation examines the economic impact of the loss of federal land grazing on the US sheep industry. Components of the US sheep industry that will be discussed are regional flock inventory in the US, lamb packing capacity, seasonal lamb production affecting packing capacity, regional wool production and quality effects, regional lamb prices, and import levels.

Key Words: economic viability, public land, sheep industry

577 So what? What is a scientist supposed to do? G. S. Lewis*, C. A. Moffet, and J. B. Taylor, *USDA, ARS, U.S. Sheep Experiment Station*, *Dubois, ID*.

Scientists can do what they do best: research and publish. But, if that is where it starts and ends, the publications are not likely to be focused on issues that matter to Federal regulatory processes. Scientists interested in conducting research pertinent to laws and regulations governing livestock grazing on public lands should 1) understand applicable laws and regulations; 2) work with stakeholders, including livestock producers, public land-management agencies, groups who oppose livestock grazing, and experts in the process of complying with the various laws and regulations, to identify critical research needs; 3) convert critical needs into focused research; 4) conduct statistically valid research to provide unbiased tests of null hypotheses and robust data; and 5) publish timely articles in well-known peer-reviewed journals that are organs of highly respected scientific organizations. In their publications, scientists should discuss and cite the "best available" published data that bear on the topic of their research. They should also describe the shortcomings of poorly designed research that appears in recognized scientific journals, and of bad science, phony science, and pseudoscience that appears in gray literature aimed at supporting a cause. Unfortunately, some Federal judges and key decision makers in land-management agencies may not be able to distinguish between outstanding "real" science and bad science, phony science, or pseudoscience. In some cases, there is a dearth of "real" science, and land-management decisions are not science based. Thus, scientists should develop close working relationships with public land managers and become trusted scientific advisors. However, scientists must understand that aesthetic, historical, and recreational considerations, rather than sound science, may dominate public land management decisions and policies. Nevertheless, scientists must remain committed to the process and to the idea that sound science will eventually lead to policies that permit the continuation of appropriate livestock grazing on public lands.

Key Words: livestock grazing, public lands, research

Teaching/Undergraduate and Graduate Education Symposium: Surviving Promotion and Tenure with a Teaching Appointment

578 Going beyond the minimum for promotion: Building a toolbox for documenting teaching effectiveness and a pathway to improving teaching. D. R. Mulvaney*1,2 and J. E. Groccia[3], [1]*Coll. of Ag., Auburn University*, *Auburn, AL*, [2]*Dept. Anim. Sciences*, *Auburn, AL,* [3]*Biggio Teaching Center, Auburn University*, *Auburn, AL*.

For the professional scientist in academia, failure to document effective teaching practices beyond that which is minimally required by the institution can lead to underrepresentation of a faculty member's effort and expertise. Consistent with national trends and demands of accrediting bodies for accountability to the profession and public sectors served by our programs, the need for documentation of teaching practices and learning outcomes has never been higher. Departments and institutions vary in the minimum amount and type of information required to document teaching. Our objectives are to illustrate approaches for documenting teaching expertise, analyze the key components of teaching portfolios, and summarize factors in standard evaluations most closely related to student learning outcomes. Teaching portfolios are a collection of materials reflecting one's professional strengths as a teacher and can be useful in formative and summative evaluation processes. From student course evaluations, surveys, mid-semester evaluations, restructured course evaluations, student focus groups and many more examples of classroom assessment techniques, we include innovative and proven examples of generating objective information toward one′s teaching for use by departments, programs, and institutional assessment groups. Participants of the session will be challenged and stimulated to consider simple yet novel approaches to documenting their effective practice of teaching.

Key Words: teaching effectiveness, learning outcomes assessment, teaching animal sciences

579 Getting scholarly teaching projects published. M. A. Wattiaux*, *University of Wisconsin-Madison*, *Madison*.

In spite of a diversity of intentions and forms of expression, abstracts, portfolio, online educational resources, book chapters, textbooks and peer-reviewed journal articles are examples of teaching publications because they represent various forms of documentation and dissemination of a teaching-related scholarly activity. According to a recent survey, animal science faculty believe that authorship of peer-reviewed publications is currently over-emphasized as an indicator of excellence in teaching. However, the scholarship of teaching and learning (SoTL) is based upon the premise that one can assemble sufficient evidence to provide generalizable knowledge to improve teaching and learning within a discipline. There is a great variety of expectations among journals, but the project design, the mode and rigor in data collection, and the methods of analysis provide the basis for the scope of inference and frequently set the suitability for publication as determined by editorial boards and individual reviewers. Although reliance on original (quantitative or qualitative) data collected to address a hypothesis is a common standard of publication, sharing cumulative years of teaching experience as a memoirs has been recognized also as a form of scholarship. Unfortunately, in spite of a call by national leaders to encourage teaching publications within the discipline, teaching-related articles in the animal sciences are rarely published in the main disciplinary journals. A search of the Agricola database revealed that in the last 25 years, 39 of the 39,502 articles in JDS, JAS, or Poultry Science included the words undergraduate or higher education in the text. In contrast, the same words were in 27% or 304 of the 1135 articles published in The North American Colleges and Teachers of Agriculture (NACTA) Journal and the Journal of Natural Resources and Life Science Education (JNRLSE), the 2 most common venues for publications in the Food and Agricultural Sciences. Another option is to publish in journals outside of the discipline but dedicated to SoTL. A list of 26 non-discipline-based SoTL journals can be found at: http://www4.uwm.edu/sotl/help_support/pub_outlets/index.cfm?a1 = search .

Key Words: scholarship of teaching

580 In the same boat—Facing the challenges of tenure and promotion. O. U. Bolden-Tiller*, *Tuskegee University*, *Tuskegee, AL*.

Getting the big job is all one may think about upon completing graduate and postdoctoral training and moving into the professional arena of academia. Only to find that once there, another hill, promotion and tenure, must soon be scaled. Many arguments surrounding tenure and promotion have abounded since the practice was first instituted decades ago. Whether one is for or against promotion and tenure, it remains a reality if one is committed to academia, as tenure is alive and well at most institutions and of the utmost importance to faculty, particularly junior faculty. Overall, the expectations seem clear, but once in the boat, many unexpected challenges arise. How does one identify the best course to address the challenges, including balancing service, teaching and research, all of which are critical to a successful promotion and tenure based on one's appointment? This seminar will highlight some of the challenges junior faculty currently face in various academic settings, including a small liberal arts college, a minority serving institution, and a research intensive university, on their road to tenure. How does one prepare for tenure? From institution to institution, what is the same and what is different? How can the tenure process be used to one′s benefit? Lastly, with changes in teaching delivery systems, such as distance education, which often utilizes faculty in a part-time or adjunct position, the question ''Does tenure really matter, especially to a junior faculty person"? will also be addressed.

Key Words: promotion, tenure, junior faculty

Animal Behavior and Well-Being: Poultry 2: Broilers

581 The effect of lighting regimen on broiler behavior and health. R. A. Blatchford*, G. S. Archer, and J. A. Mench, *University of California*, *Davis*.

Although long dim photoperiods are commonly used in commercial broiler production, evidence suggests that moderate-length photoperiods with brighter light intensities could be beneficial for broiler welfare. We evaluated the effects of long (20L:4D) and moderate (16L:8D) photoperiods at dim (1 lx day, 0.5 lx night) and bright (200 lx day, 0.5 lx night) light intensities on the behavior and health of broilers (n = 1004; 6 replicate pens/treatment). General activity was measured using passive infrared detection, and feeding activity measured by the amount of feed consumed per hour during one 24-h period per pen each week. Broilers were gait scored using a 0–5 scoring system, weighed, and killed at 6 weeks of age. Eyes were dissected from 30 birds/treatment and measured for size and weight. Behaviors and performance were analyzed using a general linear model, gait score using a Kruskal-Wallis test, and eye measures using a MANOVA. There were no differences in feed conversion ratio (mean = 1.63 ± 0.01 kg feed/kg body weight), however 1 lx broilers (2.79 ± 0.01kg) were slightly heavier ($P = 0.02$) than 200 lx broilers (2.72 ± 0.01 kg). The 200 lx broilers were more active during the day ($P = 0.03$), but less active at night ($P = 0.02$), than those reared with 1 lx. They also fed more ($P = 0.001$) during the day but less at night ($P = 0.0001$) than those reared with 1 lx. Similarly, broilers reared with 16L:8D fed more ($P = 0.007$) at night than those reared with 20L:4D. The 200 lx broilers had the best ($P = 0.0002$) gait scores, although treatment differences were small. The 1 lx broilers had greater side-to-side (18.86 ± 0.11 mm vs. 17.63 ± 0.11 mm, $P < 0.0001$) and back-to-front (13.39 ± 0.09 mm vs. 12.89 ± 0.09 mm, $P = 0.0002$) eye diameters, as well as heavier eyes (2.42 ± 0.03 g vs. 1.99 ± 0.03 g, $P < 0.0001$) than those reared with 200 lx. These results show that light intensity, rather than photoperiod, is the major factor affecting broiler behavior and eye health. Light intensity of 1 lx dampens behavioral rhythms, with possible physiological effects such as the observed differences in eye health.

Key Words: broiler, lighting, behavior

582 Effect of daylength on physiological and behavioral rhythms in broilers. K. Schwean-Lardner*[1], B. I. Fancher[2], and H. L. Classen[1], [1]*University of Saskatchewan*, *Saskatoon, SK, Canada*, [2]*Aviagen*, *Huntsville, AL*.

The impact of day length (14, 17, 20 and 23 h) on melatonin and behavioral rhythms was studied in Ross × Ross 308 male broilers. Blood samples were collected 6 times (n = 6) over 24 h at 21 d of age to provide serum for RIA melatonin analysis. Behavior was recorded with infrared cameras for 24 h per replicate (2 per trial) in trial 1 (27–28 d of age (d 27)) and 2 (42–43 d (d 42)) in one pen of 53 male broilers (30 kg/m^2). The recordings were observed using scan sampling (10 min intervals) for the full 24 h. Data were analyzed with Proc Reg and RSReg of SAS to determine if relationships existed between the variable and time of day. Serum melatonin in birds raised on 14, 17 and 20 h day length showed quadratic (Q) relationships with time of d, with high and low values during the scotophase and photophase respectively, suggesting flock synchrony. No relationship was found for birds raised under 23 h, suggesting unsynchronized free-running rhythms. No scotoperiod activity occurred except in birds raised under 14 h day length, where stretching and feeding occurred before the photophase. Regression analyses revealed quadratic (or linear (ln) where noted) relationships ($P < 0.05$) between behavior and time within the photoperiod for percent inactive resting (27 d - 14, 17L; 42 d - 14, 20L),where the lowest values occurred at the start and just before the end of photophase; walking (27 d - 14, 17L), standing (27 and 42 d - 14, 17L, ln 20L), feeding (27 d - 14, 17L), and drinking (27 d - 14, 17, 20 L), with peaks at start and end of photophase; and finally preening (27 d - 14, 17L), and dustbathing (27 d - 14, 17, 20L), with the peak toward the center of the photophase. No relationships between behavior and time were noted for birds under 23 h day length. The melatonin and behavioral data in this work strongly suggest that flocks raised under 23 h do not develop synchronized circadian rhythms. Sleep fragmentation, a form of sleep deprivation, may result from the unsynchronized behavioral activity.

Key Words: circadian rhythm, melatonin, behavior

583 The effect of providing lighting during incubation on stress responses of broiler chickens post-hatch. G. S. Archer* and J. A. Mench, *University of California, Davis*.

Lighting conditions during incubation affect brain development and hormone regulation in chickens, thus potentially affecting the stress response. We examined the effects of 4 lighting conditions during incubation on stress responses of broilers post hatch. Throughout incubation, Cobb broiler eggs were provided with either 0, 1, 6, or 12 h of 550 lx full-spectrum fluorescent light daily. Each treatment was divided over 3 incubators and was replicated once in time. Broilers were housed in pens with others from their own incubator. Post-hatch, broilers were subjected to an adrenocorticotropic hormone (ACTH) challenge (n = 12 per treatment) and a stress test (1 h of crating, n = 24 per treatment, treatments were equally distributed across crates) at 4 weeks of age. Half of the crated broilers had blood collected via brachial vein (1.5 to 2 mL) pre- and post-crating to determine the effect of crating on corticosterone levels, while the other half were challenged with keyhole limpet hemocyanin (KLH). Bilateral traits (middle toe length, metatarsal width and length) were also measured in 60 broilers per treatment to assess developmental asymmetry at 6 weeks of age. There was no difference ($P > 0.05$) between treatments in the corticosterone response to ACTH challenge (18.1 ng/mL). However, 12L broilers had lower ($P < 0.05$) corticosterone concentrations after crating (0.31 ng/mL) than 0L (0.64 ng/mL) broilers. The 12L broilers also had higher ($P < 0.05$) anti-KLH IgG titers (93295 U/mL) and lower ($P < 0.05$) composite asymmetry scores (0.92) than the 0L broilers (62239 U/mL, 1.21). Broilers provided with 12 h of light during incubation were thus less affected by stressors post-hatch, as indicated by corticosterone and IgG concentrations and composite asymmetry score.

Key Words: incubation, light, stress

584 The effect of providing light during incubation on fear responses of broiler chickens post-hatch. G. S. Archer* and J. A. Mench, *University of California, Davis*.

Lighting conditions during incubation affect brain development and hormone regulation in chickens, thus potentially affecting post-hatch behavior, including fear-related behavior. We examined the effects of 4 incubation lighting conditions on the fear responses of broilers post-hatch. Throughout incubation, Cobb broiler eggs were provided with either 0, 1, 6, or 12 h of 550 lx full-spectrum fluorescent light daily. Post-hatch, the broilers (n = 60 per treatment) were subjected to the following fear tests: chute/emergence test (3 weeks of age), approach/

isolation test (3 weeks of age), tonic immobility test (5 weeks of age), and inversion after catching test (6 weeks of age). All data were analyzed using GLMs differences were considered when $P > 0.05$. During all tests, the responses of the 12L broilers indicated that they were less fearful than broilers in other treatment groups. During the chute test, 12L broilers emerged faster from the darkened start box (28.9 ± 3.3 s, $P < 0.05$) than broilers from all other treatments. During the approach test, 12L broilers vocalized less (179 ± 9 times), were less active (28 ± 2% of the time), and spent more time in the area closest to the observer (63 ± 3% of the time) than the 0L broilers (211 ± 10 times, 35 ± 3% of the time, 51 ± 4% of the time, $P < 0.05$). During the tonic immobility test, 12L broilers had shorter ($P < 0.05$) latencies to first head movement (26 ± 3 s) and to right (120 ± 17 s) than 0L (57 ± 14 s, 201 ± 25 s) and 1L (51 ± 9 s, 213 ± 22 s) broilers. During the inversion test, 0L broilers wing-flapped more intensely (5.5 ± 0.1 flaps/sec, $P < 0.05$) than broilers in all other treatment (5.9 ± 0.1 flaps/sec). These results indicate that providing 12 h of light during incubation reduced the fear response of the broilers when compared with the broilers incubated in complete darkness.

Key Words: fear, incubation, lighting

585 Impact of light intensity on broiler biological rhythms and welfare. A. Deep*[1], K. Schwean-Lardner[1], T. G. Crowe[1], B. I. Fancher[2], and H. L. Classen[1], [1]*University of Saskatchewan*, *Saskatoon, Canada*, [2]*Aviagen*, *Huntsville, AL*.

Light intensity (LI) manipulation is an important management tool affecting broiler behavior and physiology but still there is debate regarding the optimum level to be used. Two trials were completed to study the impact of light intensity (LI) within the practical levels in confinement barns (1, 10, 20 and 40 lx) on biological rhythms and welfare of broilers raised to 35 d of age. In each trial, 950 Ross × Ross 308 chicks were housed per room with replication of individual LI treatments in 2 environmentally controlled rooms. Within each large room, a small pen with 25 male and 25 female chicks was used for recording behavior. Data were analyzed as a randomized complete block design with trial serving as a block. All chicks were provided with 40 lx intensity and 23 h light until shifting to treatment LI and 17 h day length at 7 d of age. For each replicate, behavior was recorded for a 24 h period, starting at 16 or 17 d of age. At 23 d of age, 3 birds per room were bled at the start, middle and end of light and dark periods for melatonin estimation using RIA. Skeletal and foot pad, and ocular health were monitored at 31 and 32 d of age, respectively. When summarized over the 24 h observation period, birds exposed to 1 lx rested more and had reduced expression of foraging, preening, dust-bathing ($P = 0.09$), stretching and wing-flapping ($P = 0.07$) behaviors in comparison to other light intensities. Diurnal rhythms of serum melatonin were unaffected by LI. Broilers exposed to 1 lx had heavier and bigger eyes as compared with other treatments. LI had no effect on skeletal health but deep ulcerative foot pad lesions decreased linearly with increasing LI. In conclusion, despite having prominent melatonin rhythms, broilers exposed to 1 lx demonstrated reduced welfare as indicated by altered behavioral expression, and increased foot pad lesions and eye size.

Key Words: broiler, light intensity, welfare

586 Broiler behavior under lighting programs with a sectioned dark period and its welfare considerations. C. Raginski*[1], K. V. Schwean-Lardner[1], H. W. Gonyou[1,2], and H. L. Classen[1], [1]*University of Saskatchewan*, *Saskatoon, SK, Canada*, [2]*Prairie Swine Centre*, *Saskatoon, SK, Canada*.

Light provision can influence broiler performance and also impact bird welfare. Therefore, understanding how much light, and in what pattern it is given, is required to provide guidance to organizations responsible for codes of practice. The objective of this research is to establish the impact of 9 h of darkness provided in one (9 h), trt 1, 2 (2 × 4.5 h), trt 2, and 3 (3 × 3 h), trt 3, periods on the welfare of broiler chickens as assessed by bird behavior. Each lighting treatment was replicated 3 times and behavior was recorded over a 24 h period in one room per treatment (12 pens per room each with 50 birds at housing) with a different room at each of 32, 33 and 34 d of age using infrared cameras. Behavior was quantified by instantaneous scan sampling at 10 min intervals over a 24 h period and compared between treatments over 24 h, overall photo- and scotoperiods, and within treatments between individual photo- and scotoperiods. Comparisons between the 3 treatment means by ANOVA indicate lighting treatment had little to no effect on feeding, drinking, resting, standing, walking, running, foraging, stretching, dust bathing, wing flapping and feather ruffling behaviors ($P > 0.10$). Preening (mean trt 1 = 4.74, trt 2 = 3.48, trt 3 = 3.33; $P = 0.03$) and comfort behaviors (meant trt 1 = 5.25, trt 2 = 3.86, trt 3 = 3.71; $P < 0.01$) show a reduction when the scotoperiod is increased from one to more. Behavioral expression over time was examined within major photoperiods using regression analyses to determine rhythms and patterns of activity. Quadratic patterns were seen for feeding ($P < 0.05$) and drinking ($P < 0.05$) with peaks at the initiation and end of the day. Dust bathing occurred consistently at mid-day for all treatments, indicating the presence of a biological rhythm. The reduced proportion of broilers partaking in comfort behaviors alone does not clearly indicate a reduction in welfare for broilers exposed to multiple scotoperiods in comparison to those given one longer period.

Key Words: broilers, lighting, behavior

587 Heat and moisture production in broilers during simulated winter transport. J. M. Watts*, L. J. Graff, M. L. Strawford, T. G. Crowe, N. A. Burlinguette, H. L. Classen, and P. J. Shand, *University of Saskatchewan*, *Saskatoon, Saskatchewan, Canada*.

To ensure broiler welfare during winter transport it is necessary to manage heat and moisture accumulation within transport vehicles. Heat production (HP) and moisture production (MP) in broilers are affected by many factors, both intrinsic and environmental. Hence, it is necessary to determine HP and MP rates under representative conditions. A transport simulation chamber containing 1 or 2 standard transport drawers was used in 2 configurations. (Divided: 2 drawers were each partitioned into 15 small compartments, each containing 1 bird and stacked together in the chamber; Grouped: a single drawer contained 15 birds able to move and huddle together). Cold air was drawn into the system, at 0.35 m^3/s, from outside the building. A control system operated a heater to warm the air to the desired temperature before it passed through the drawer(s) and was exhausted from the building. Broilers were fasted for 7 h, placed into the chamber, and exposed to test conditions for 3 h. Air temperature and relative humidity (RH) were measured upstream and downstream of the insulated bird compartment at -min intervals. Differences in the paired temperature and RH values were a result of metabolic activity and were used to calculate a mean HP and MP value for the 3 h, per unit of bird weight, for n = 36 trials (12 Divided, 24 Grouped). The effects of temperature (−4, −5, −8, −10, −12, −15, −17, −18 or +20°C) and bird age (5 or 6 weeks) were studied. Drawers were balanced for numbers of male and female birds. At 20°C, HP was 6.1–8.1W/kg and MP was 3.6–5.7g/h-kg (n = 3). In both configurations HP and MP tended to increase with each colder temperature increment. Pooled observations between −4 and −18°C

were categorized by bird age and confinement type. Younger Grouped birds (n = 9 trials) had mean HP of 73.1W/kg (range 59.1–87.5) and MP of 20.5g/h-kg (range18.4–21.1), older Grouped birds (n = 11 trials) 41.4W/kg (range 35.5–46.8) and 12.8g/h-kg (range 5.5–14.1), younger Divided birds (n = 5 trials) 24.0W/kg (range 16.5–27.3) and 4.26g/h-kg (range 3.1–7.1) and older Divided birds (n = 5 trials) 19.5W/kg (range 15.8–22.2) and 3.54g/h-kg (range 2.9–4.5).

Key Words: broiler, heat production, cold weather transport

588 Humane slaughter methods for small- and mid-scale poultry operations. V. B. Brewer*[1], A. C. Fanatico[2], W. J. Kuenzel[1], C. M. Owens[1], V. A. Kuttappan[1], and A. M. Donoghue[2], [1]*University of Arkansas Department of Poultry Science*, *Fayetteville,* [2]*USDA Agricultural Research Service, Poultry Production and Product Safety Research*, *Fayetteville, AR*.

Interest is growing in humane handling of poultry and other livestock. Due to the cost of humane slaughter devices, small-scale poultry producers may cut birds necks without prior stunning. With the objective of determining low-cost humane slaughter methods, a trial was conducted to evaluate impact on blood loss, bird reactions, and carcass quality. Groups of slow-growing hybrid broilers (n = 20) were assigned to stun/kill treatments: no stun (NS; control); cervical dislocation (DIS); electrical knife at 40V/7s (LOW); electrical knife at 50V/7s (HIGH); and electrical head-only prong at 40V/7s (HEAD). There were 2 replications of treatments. Necks were cut immediately after all methods. Body movements were scored by 2 workers during bleeding with a 4-point scale (1 = mild; 4 = most severe), and measured in 3 phases (0–10, 10–60, and 60–120 s) post stun/kill. Carcasses were evaluated for hemorrhage and broken bones. When comparing the treatments to the control NS, blood loss was lower in DIS birds, probably due to internal tearing of vessels, and higher in LOW and HEAD birds, because low-voltage stuns help provide uniform heartbeat and facilitate bleeding ($P < 0.05$). Under Chi Square analysis, distributions of body movement scores differed significantly ($P < 0.05$). NS and DIS treatments displayed intense motor contractions early in the post stun/kill period: 44% and 95% of NS birds had Level 4 uncontrolled muscle contractions in phases 1 and 2, and 100% and 85% of DIS birds. Contractions in HIGH birds were Level 1 in phases 1 and 2, presumably due to immediate death. Muscle contractions of LOW birds were also minor at first and increased in phase 3 where 16% experienced Level 3 movements. Wing hemorrhage was higher in DIS birds and broken wings were higher in NS compared with other treatments ($P < 0.05$), probably due to increased wing flapping. Cervical dislocation, while a low-cost kill method for small numbers of birds, resulted in poor bleedout and wing hemorrhage. In conclusion, hand-held electrical stun devices can be effective methods used at low and high settings and warrant additional research for best welfare practices for small broiler operations.

Key Words: poultry, stun, welfare

589 Genetic and non-genetic factors affecting the prevalence of mastitis in dromedary camels. S. Ahmad*[1,2], M. Yaqoob[1,2], M. Q. Bilal[1,2], G. Muhammad[1,3], A. Iqbal[1,2], and M. K. Khan[1,3], [1]*university of Agriculture, Faisalabad-Pakistan*, [2]*University of Agriculture, Faisalabad-Pakistan*, *Department of Livestock Management*, [3]*University of Agriculture, Faisalabad-Pakistan*, *Department of Clinical Medicine and Surgery*.

The present study was designed to determine the prevalence and associated determinants (age, parity, stage of lactation, season and breed) of mastitis in the camel of Thal areas of Pakistan. Based on multistage cluster random sampling, 200 she-camels were screened for subclinical mastitis. Milk samples from each quarter of selected animals were collected and analyzed using Surf Field Mastitis Test (SFMT). Overall prevalence of subclinical and clinical mastitis was 38% (304/800) and 28% (224/800), respectively. Age, parity, stage of lactation, season and breed were found significantly associated ($P < 0.05$) with the prevalence of mastitis in she-camels. The prevalence of mastitis was significantly higher ($P < 0.05$; 60%) in camels of 5–7 years of age (1st and 2nd parities) compared with that of 14 to 16 years of age (5th and 6th parities) (26.67%). Samples collected in winter showed significantly ($P < 0.05$) higher (48%) prevalence of mastitis as compared with summer samples (28%). Stage of lactation significantly affected ($P < 0.05$) the prevalence of mastitis being highest during the last 2 mo (10–12 mo) (50%) followed in order by initial stage of lactation (0–1 mo) (45.45%) and mid stages (1–3 and 3–10 mo) of lactation (0% and 25%, respectively). According to breed of camels, the prevalence of mastitis was significantly higher ($P < 0.05$) in crossbred (45.83%) followed in order by mareecha (35.29%) and desi (22.22%). The present study may provide baseline data for the researchers and veterinarians to plan mastitis control program in camels of Pakistan.

Key Words: prevalence, mastitis, associated determinants, camels, thal, Pakistan

590 Use of a lipopolysaccharide (LPS) challenge to evaluate the innate immune response of Angus heifers with genotypic differences in GeneSTAR Markers for intramuscular fat deposition. J. O. Buntyn*[1], J. A. Carroll[2], T. Smith[1], S. M. Falkenberg[1], J. D. Rivera[3], C. Collier[2], and T. B. Schmidt[1], [1]*Department of Animal, Mississippi State University and Dairy Sciences*, *Mississippi State,* [2]*Livestock Issues Research Unit, USDA-ARS*, *Lubbock, TX*, [3]*South Mississippi Branch Experiment Station*, *Mississippi State*.

Due to increased nutritional requirements during an immune challenge, intramuscular fat (IMF) can serve as an energy reserve for cattle. Cattle with a genotypic variation in DNA markers (DNAm) for IMF may have an altered response to an immune challenge. The objective of this study was to evaluate the innate immune response of Angus heifers selected for genotypic variation in intramuscular fat deposition (IMFD). Genotypic variation (QG1 and QG2) in heifers was determined by presence or absence of DNA markers for IMFD. Twenty-three heifers (223 ± 44 kg) were sorted into 2 treatment groups based upon DNAm; heifers with no DNAm for IMFD (n = 11; NoDNAm), and heifers with one or more DNAm for IMFD (n = 12; DNAm). Prior to challenge (24 h), indwelling jugular catheters and indwelling rectal thermometers were inserted. Blood samples were collected at 30-min intervals and rectal temperatures (RT) at 1-min intervals from −2 to 8 h relative to the immune challenge (LPS: 0.25 μg/kg BW) at time 0. Heifers with DNAm displayed greater ($P < 0.05$) RT temperature 2 h post LPS challenge compared with heifers with NoDNAm heifers (40.92 and 39.93 ± 0.07°C, respectively) and greater concentrations of cortisol at 2.5 (281.5 vs. 267.7 pg/mL, respectively) and 3 h (252.2 vs. 215.2 pg/mL, respectively) post LPS compared with NoDNAm heifers. NoDNAm heifers had greater ($P < 0.05$) concentrations of IFNγ 2 h post-LPS compared with DNAm heifers for IMFD (17.2 ng/mL and 11.4 ng/mL, respectively). No differences ($P > 0.05$) were observed between groups of heifers for IL-6 concentrations; however, NoDNAm heifers had greater ($P < 0.05$) sustained IL-6 responses over time. These results suggest that there is a difference to an LPS challenge in heifers with genotypic variation in intramuscular fat deposition.

Key Words: pro-inflammatory, GeneSTAR, Angus

591 Impact of vaccination on the incidence of liver abscesses in natural-fed finishing cattle. J. T. Fox*[1], D. U. Thomson[1], N. N. Lindberg[2], and K. Barling[3], [1]*Kansas State University*, *Manhattan,* [2]*Progressive Beef Consulting Service*, *Great Bend, KS,* [3]*Novartis Animal Health*, *College Station, TX*.

A blinded clinical trial was conducted with the objective of determining the ability of vaccines to reduce liver abscess incidence in natural-fed cattle as well as evaluating the impact of liver abscesses on performance and carcass characteristics. Feedlot cattle (n = 1,307; initial body weight (BW) = 279 ± 32 kg) were randomly assigned to 1 of 3 treatments. Treatments were control (no vaccine), vaccination with a *Fusobacterium necrophorum* bacterin or vaccination with an *Arcanobacterium pyogenes-Fusobacterium necrophorum* toxoid. Vaccines were administered to animals in accordance with label directions. Cattle were fed a series of 4 step-up diets and a finishing diet consisting of 73% steam-flaked corn and 13% roughage (as-fed basis). Cattle were selected for harvest on a weekly basis based upon phenotypic evaluation of finish. At harvest, livers were scored following the Elanco system: 0, no abscesses evident; A-, 1 or 2 small abscesses or scars; A, 2 to 4 well-organized abscesses less than 2.5 cm in diameter; or A+, 1 or more large active abscesses greater than 2.5 cm in diameter. Incidence of liver abscesses (56%) and severe (A and A+ scores) liver abscesses (39%) was relatively high in this study. Data were analyzed with either general linear or general linear mixed models. No differences were observed ($P > 0.60$) between treatments with regard to the incidence of liver abscesses, incidence of severe liver abscesses, or liver abscess score. Initial BW, 60-d BW, 60-d average daily gain, total days on feed (DOF), hot carcass weight (HCW), yield grade and quality grade were not different ($P > 0.10$) among treatments. Liver abscess present at harvest increased ($P = 0.02$) total DOF, but this difference (2 d) was somewhat minor. Severe liver abscesses reduced ($P < 0.01$) HCW and increased the number grading USDA Select instead of USDA Choice ($P = 0.01$). In conclusion, we did not observe any treatment differences in liver abscess incidence or severity. We did identify some important differences in performance and carcass parameters between cattle with and without liver abscesses at harvest.

Key Words: natural-fed cattle, liver abscesses, vaccines

592 Physiological responses of heat tolerant and sensitive *Bos taurus* breeds of cattle to different levels of heat stress. D. E. Spiers*, H. L. Vellios, P. A. Eichen, B. Scharf, J. S. Johnson, D. K. Kishore, and E. A. Coate, *University of Missouri*, *Columbia*.

Bos taurus cattle from different regions of the US may differ in their response to heat stress. In the present study, Angus steers from Oklahoma (OK; n = 6) and Missouri (MO; n = 6) were compared against Romosinuano (heat tolerant) cattle (RO; n = 5) from Florida in the University of Missouri Brody Environmental Center to identify specific differences in thermoregulatory responses to thermal conditions above thermoneutrality. Animals were fed ad libitum, and intake was recorded daily. Rectal temperature (Tre) and respiration rate (RR) were measured 6 times daily. Initially, animals were exposed to a constant 20°C (TN) for 8 d, followed by 2 cyclic heat stress periods that consisted of 28°C (night) to 38°C (day) daily cycle for 8 d (HS1), followed by a greater heat stress of 30°C (night) to 40°C (day) for an additional 8 d (HS2). Feed intake rapidly decreased by ~2 kg/d for all breeds during HS1, with partially recovered after several days. No differences were found across breeds in feed intake/kg BW ($P = 0.16$). Tre for all breeds at TN increased from 1100 (38.8°C) to 2100 (39.0°C), with RO being 0.3°C below OK. In contrast, RR of RO was less than Angus (19 bpm; $P \leq 0.05$) at TN. RR for all breeds increased (33 bpm; $P \leq 0.05$) during HS1 and again during HS2 (11 bpm; $P \leq 0.05$), with RO maintaining a lower level (19 bpm; $P \leq 0.05$) than Angus. Tre for RO was below Angus throughout (1.0°C; $P \leq 0.05$), with no increase during either HS1 or HS2. Both Angus groups increased Tre from TN to HS1 (0.9°C; $P \leq 0.05$), with partial recovery, followed by a second increase to HS2 (0.6°C; $P \leq 0.05$) for MO steers. This study identified the time-related differences in thermoregulatory ability of Angus and Romosinuano breeds of cattle that were unrelated to feed intake.

Key Words: cattle, heat, breed

593 Early stage diagnosis of mastitis of dairy cows using ^{1}H NMR–based metabolomics. Y. Lv and Q. Z. Li*, *Key Laboratory of Dairy Science of Education Ministry, Northeast Agricultural University*, *Harbin, China*.

Mastitis is one of the main diseases in dairy cows worldwide with considerable economic consequences, mainly due to reduced milk production, discarded milk, an increased culling rate and higher treatment costs. Most mastitis cases are subclinical or chronic mastitis with little inflammation, but many of these infections eventually develop into clinical mastitis. Clinical mastitis is easy to detect for veterinarians whereas the detection of subclinical mastitis cases can be a challenge. Nuclear magnetic resonance (NMR) based metabolomics, combined with multivariate statistics, assessment of a biological system by means of global and non–targeted metabolite profiling, is a powerful tool to analyze the small molecule composition. Many metabolomics applications exist for finding biomarkers and could assist diagnosis and prognosis of disease. In this study, several constituents in cow milk were identified through 1D and 2D NMR experiments. A pilot study analyzed whey samples from several cows with mastitis and normal control individuals to identify characteristic changes of metabolites profiles in cows with mastitis. Multivariate data analysis using SIMCA software differentiated these whey ^{1} H NMR spectra identifying any discriminating metabolite patterns. We found distinct metabolic change in milk between subclinical mastitis cows and healthy cows. Our results indicated the metabolic change in milk of cows with subclinical mastitis and healthy cows. Compared with healthy cow milk, especially lower levels of lipid (mainly very low density lipoproteins), phosphatidylcholine/choline and lactate in milk of cows with subclinical mastitis, might be one pathogenesis of early stage mastitis of cows. The present study demonstrated that PCA results of milk CPMG spectra are clearly different in subclinical mastitis cows and healthy cows. Milk NMR spectra combined with principal component analysis techniques may be able to assist early diagnosis and postoperative of cow mastitis using a little milk sample.
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Key Words: dairy cow, mastitis, metabolomics

594 Clinical trial to evaluate the effect of ceftiofur intramammary treatment on non-severe clinical coliform mastitis. Y. H. Schukken[1], G. J. Bennett[1], B. J. Rauch[1], H. L. Sharkey[1], and R. L. Saltman*[2], [1]*Cornell University*, *Ithaca, NY*, [2]*Pfizer, Inc.*, *New York, NY*.

The objective of this study was to evaluate the effectiveness of treatment of non-severe, clinical coliform mastitis with intramammary ceftiofur (Spectramast LC). Particularly, the cure rates and clinical symptoms of cows treated with Spectramast LC were compared with those of control cows that were not treated with antimicrobials (negative controls). In a controlled clinical trial we enrolled 104 cows from 5 New York dairy herds with non-severe gram-negative clinical mastitis. Cows were either treated for 5 d with once a day intramammary Ceftiofur or received no treatment in the control group. Post treatment milk production, somatic cell counts, clinical cure and bacteriological cure were evaluated. The continuous data (somatic cell count (after transformation to linear score) and milk production) was analyzed using a linear mixed model, while the discrete data (clinical and bacteriological cure rates) was analyzed using a generalized linear mixed model. For both models, treatment was considered a fixed effect and herd was also treated as a fixed effect. For all of the outcome variables, treatment was compared with the control group using one-sided tests with 5% significance level. Treatment of non-severe clinical gram-negative mastitis with 5 days of Spectramast LC resulted in a significant increased bacteriological cure compared to non-treated control animals (73% versus 38%), particularly in animals infected with *E. coli* or *Klebsiella* species. Cured animals also showed a lower loss in milk production (6 kg per day), improved SCC (1 LS unit) and higher clinical cure compared to non-cured cows. Clinical cure was notably improved in Ceftiofur treated cows with a Klebsiella infection. In treated *Klebsiella* cows 62% clinically cured while 42% of control cows showed clinical cure. However, the differences between the treatment groups in production, SCC and clinical improvement were not statistically significant. In conclusion, intramammary Ceftiofur treatment of non-severe coliform mastitis resulted in a significant improved bacteriological cure and numerically improved clinical parameters.

Key Words: mastitis, coli, clinical trial

595 Cytological and clinical endometritis in dairy cows. J. Dubuc*[1], T. F. Duffield[1], K. E. Leslie[1], J. S. Walton[2], and S. J. LeBlanc[1], [1]*Department of Population Medicine, University of Guelph*, *Guelph, Ontario, Canada*, [2]*Department of Animal and Poultry Science, University of Guelph*, *Guelph, Ontario, Canada*.

The objective of this study was to compare cytological and clinical endometritis. Data from 2178 Holstein cows (6 herds) enrolled in a randomized clinical trial were used. Cows were followed from parturition until 300 d after parturition (dap). Data on periparturient disease incidence, calving history, and body condition score (BCS) at parturition were collected. Serum BHB, NEFA and haptoglobin were measured at 4, 11, and 18 (±3.5) dap. Examination for endometritis was performed 35 (±3.5) dap and the voluntary waiting period for breeding was 60 d. Endometritis was diagnosed cytologically (cytobrush technique) and clinically (Metricheck technique and score, and cervical diameter by transrectal palpation). Diagnostic criteria for endometritis were determined based on impaired subsequent reproductive performance.

Statistical analyses were performed using Cox proportional hazard models and logistic regression models in SAS, accounting for the effects of treatments and herd clustering. Cytological endometritis (CYTO) was defined as ≤ 6% polymorphonuclear cells in endometrial cytology. Clinical endometritis (CLIN) was defined as the presence of mucopurulent or purulent vaginal discharge. Prevalence of CYTO and CLIN were 20% and 16%, respectively. Among cows with CLIN, only 38% had CYTO. Risk factors for CYTO were hyperketonemia during the first 7 dap (≥1100 μmol/L; OR = 1.4; $P = 0.03$), hyperhaptoglobinemia during the first 7 dap (≥0.8 g/L; OR = 1.5; $P < 0.01$), and thin BCS at parturition (≤2.75; OR = 1.9; $P = 0.03$). Risk factors for CLIN were twins (OR = 2.2; $P < 0.01$), dystocia (OR = 2.1; $P < 0.01$), metritis (OR = 2.3; $P < 0.01$), and hyperhaptoglobinemia during the first 7 dap (OR = 2.0; $P < 0.01$). Cytological endometritis and CLIN increased median time to pregnancy (Unaffected: 132 d; CYTO: 156 d; CLIN: 168 d; $P < 0.01$). Their impacts were additive in cows affected by both conditions (BOTH: 193 d; $P < 0.01$). These findings suggested that CYTO and CLIN represent 2 different conditions. The source of vaginal discharge is unclear. It is proposed that uterine health status should be described as unaffected, CYTO only, purulent vaginal discharge (PVD) only, and BOTH.

Key Words: dairy cow, uterine disease, endometritis

596 Impact of postpartum uterine diseases on milk production and culling in dairy cows. J. Dubuc*[1], T. F. Duffield[1], K. E. Leslie[1], J. S. Walton[2], and S. J. LeBlanc[1], [1]*Department of Population Medicine, University of Guelph*, *Guelph, Ontario, Canada*, [2]*Department of Animal and Poultry Science, University of Guelph*, *Guelph, Ontario, Canada*.

The objective of this study was to quantify the impact of postpartum uterine diseases on milk production and culling. Data from 2178 Holstein cows (6 herds) enrolled in a randomized clinical trial were used. Data were collected from parturition until 300 d after parturition (DAP). Metritis (MET), retained placenta (RP), displaced abomasum, and culling data were recorded by farm managers. Milk production data were retrieved from DHI test-day records. Metritis was defined as rectal temperature ≥ 39.5°C and a foul-smelling discharge occurring ≤ 15 DAP; clinical endometritis (CLIN) as mucopurulent or purulent vaginal discharge (Metricheck device); and cytological endometritis (CYTO) as ≥ 6% polymorphonuclear cells in endometrial cytology (cytobrush technique). All cows were examined for endometritis 35 (±3.5) DAP. Milk production and culling were considered as outcomes. Statistical analyses, accounting for the effects of treatments, were performed using linear mixed models and logistic mixed models for milk production and culling, respectively. Primiparous and multiparous cows were modeled separately for milk production. Milk production of primiparous cows was unaffected by uterine diseases. The impact of MET and RP on milk production was additive in multiparous cows. The impact of MET on milk production was variable over time in multiparous cows, as it reduced the milk production per cow by 3.7 kg at first DHI test on average ($P < 0.05$), but was not significantly different at later tests. Retained placenta reduced milk production by 2.6 kg/day in multiparous cow, which was consistent through the first 4 DHI tests. The projected impact of MET and RP in multiparous cows was a reduction of 259 kg and 753 kg over 305 d, respectively. Endometritis (CYTO and CLIN) had no effect on milk production. Culling risks at 63 and 300 DAP were not affected by uterine diseases, after accounting or not for pregnancy status, parity, and milk production level. Overall, these findings suggested that although uterine diseases have negative impact on milk production and reproduction, they did not influence the culling risk of affected cows up to 300 DAP.

Key Words: dairy cow, uterine disease, impact

597 Evaluation of the hand-held Precision Xtra system for diagnosing ketosis in early lactation dairy cows. G. R. Oetzel*, *University of Wisconsin*, *Madison*.

The objective of this study was to evaluate the sensitivity, specificity, and repeatability of a hand-held meter (Precision Xtra System, Abbott Laboratories) for cowside diagnosis of ketosis in early lactation dairy cows. Experimental cows were 753 early lactation cows in 5 different commercial dairy herds. Each herd was visited twice and all cows in the herd between 5 and 25 d in milk were tested at each visit. Blood samples were collected from the tail vein of each cow. A drop of whole blood was applied to the Precision Xtra meter and analyzed for BHBA concentration. The remainder of the blood was allowed to clot. Serum was later separated and analyzed for BHBA concentration at a commercial laboratory (Marshfield Clinic Veterinary Diagnostic Services) using an automated chemistry analyzer. For a subset of 71 cows, 2 additional blood samples were collected to evaluate the repeatability of both the serum and whole blood BHB tests. Serum chemistry was the gold standard test, with BHBA ≥1.4 mmol/L classified as ketosis. Serum BHBA concentrations ranged from 0.2 to 5.4 mmol/L, and 76 cows (10%) were classified as ketotic. Herd prevalence of ketosis ranged from 7 to 31%. BHBA concentrations determined by the meter were highly correlated to serum chemistry results ($R^2 = 0.86$, $P < 0.01$). A threshold of ≥1.3 mmol/L using the meter resulted in the best combination of sensitivity (98.7%) and specificity (98.4%) compared with the gold standard of ≥1.4 mmol/L serum BHBA. Coefficient of variation was 4.3% for repeated serum laboratory BHBA results and 10.9% for repeated whole blood BHBA results using the meter. Repeated testing of cows using the meter resulted in no changes in ketosis classification. Results indicate excellent usefulness of the Precision Xtra hand-held meter for cowside diagnosis of ketosis in early lactation dairy cows using whole blood samples collected from the tail vein.

Key Words: BHBA, ketosis, hand-held meter

598 Effect of 1 or 2 dose circovirus and mycoplasma vaccines and day of vaccination on growth performance of nursery pigs. K. L. Saddoris-Clemons*, S. B. Wiliams, N. D. Paton, and D. R. Cook, *Akey*, *Lewisburg, OH*.

880 nursery pigs (PIC genetics) with an initial BW of 6.1 kg were utilized to determine the effects of circovirus and mycoplasma vaccines timing and number of doses on feed intake, weight gain, and BW. Pens (22 pigs/pen) were randomly assigned to one of 5 treatment groups: Unvaccinated (NC), 1-dose early (d 0), 1-dose late (d 14), 2-dose early (d 0 and 14), 2-dose late (d 14 and 28). The vaccine products tested were 2 doses (2 mL/dose) of Circumvent PCV (Intervet) and Respisure (Pfizer) or 1 dose (1 mL/dose) of Circoflex (BI) and Mycoflex (BI). Pigs were allowed ad libitum access to a commercial nursery diet and water. Feed intake was determined daily from d 1–7, 15–21, and 29–35 and weekly from d 8–14 and 22–28. Pigs were weighed weekly. Cumulative ADFI from d 1–7 tended to be higher ($P < 0.10$) for vaccinated pigs compared with unvaccinated pigs, however, ADG, and G/F were not different ($P > 0.10$). Following d 14 vaccination, vaccinated pigs had a lower ($P < 0.05$) d 15–21 ADFI compared with NC pigs. Pigs vaccinated with 2 dose products tended to have a lower ($P < 0.10$) ADG for d 15–21 than pigs vaccinated with 1 dose products. Vaccinating pigs for the second time on d 14 with 2 dose products decreased ADFI compared with vaccinating pigs for the first time on d 14 with either 1 or 2 dose products (time × dose, $P < 0.05$). From d 29–35, vaccinated pigs had a lower ADFI ($P < 0.01$) and tended to have a lower final BW ($P < 0.10$) compared with NC pigs. Vaccinating on d 28 with 2 dose products resulted in lower ADG, ADFI, and poorer feed efficiency compared with pigs vaccinated

on d 0 and 14 with 2 dose products or vs. pigs vaccinated with 1 dose products on either d 0 or 14 (time × dose, $P < 0.05$). Overall, vaccinated pigs tended to have a lower ($P < 0.10$) ADG, ADFI, and 0.53 kg lower final BW compared with NC pigs. Additionally, pigs given the 2 dose vaccination products tended to have a lower ($P < 0.10$) overall ADFI compared with pigs given the 1 dose vaccination products, regardless of the timing. Vaccination tended to reduce growth performance of nursery pigs and effects were greater with 2-dose vaccines given late in the nursery period.

Key Words: vaccination, nursery, pigs

599 The effect of breeder source flock age on 7- and 14-day turkey poult mortality. B. J. Wood*, D. R. McIntyre, and G. Norwell, *Hybrid Turkeys*, *Kitchener, ON, Canada*.

There are many factors that affect early mortality in turkeys such as breeder flock age, genetics, hatchery and management. With multifactorial problems quantifying individual effects in an observational study is difficult; consequently, little has been published on poult mortality under commercial conditions. This study quantifies the effect of breeder flock age on poult mortality at 7 and 14 d of age. Mortality data over a 10-yr period was used in which flocks were placed at biweekly intervals with each flock composed of poults from breeders varying in age from 29 to 56 weeks. All flocks were ring and conventional brooder stove brooded. Each flock had a minimum of 3 and up to 5 contributing breeder flocks with each of the 245,000 poults having a wing band to identify dam origin. Contributing breeder flocks had a distinct age class compared with other contributing flocks. Average mortality was 2.2%, 3.1% for hens and 4.4% and 5.3% for toms, at 7 and 14 d respectively. The table shows within flock tom poult mortality and standard errors (SE) against breeder age. Relative mortality against flock age decreased sharply from 30 to 38 weeks of age, leveled and rose again late in lay. Female poult mortality showed a similar proportional mortality pattern. Poults from breeder flocks 32 weeks of age and under were approximately 2 times more likely to record a mortality compared to breeders between 38 and 52 weeks of age. This shows the approximate change in mortality that can be expected based on the relative differences in breeder source flock age accounting for other early mortality factors.

Table 1. Tom poult mortality at 7 and 14 days against breeder source flock age

Flock age (weeks)	7d mortality (SE)	14d mortality (SE)
≤ 30	10.9 (0.89)	12.2 (0.94)
32	6.6 (0.38)	7.7 (0.41)
34	4.7 (0.29)	5.7 (0.35)
36	4.1 (0.31)	5.1 (0.33)
38	3.4 (0.31)	4.4 (0.33)
40	3.4 (0.32)	4.2 (0.35)
42	3.4 (0.40)	4.2 (0.42)
44	4.2 (0.60)	5.0 (0.61)
46	3.7 (0.66)	4.6 (0.67)
48	3.8 (0.61)	4.4 (0.65)
50	3.2 (0.48)	3.6 (0.49)
52	2.6 (0.60)	3.1 (0.64)
≥ 54	5.2 (1.88)	5.5 (1.88)

SE = standard error.

Key Words: early mortality, liveability, turkeys

600 Development of an inflammation model for use in the commercial duck. P. Cotter*[1], T. Applegate[2], R. Murdoch[3], K. Daugherty[3], and M. Turk[3], [1]*Cotter Laboratory*, *Arlington, MA,* [2]*Purdue University*, *West Lafayette, IN,* [3]*Maple Leaf Farms*, *Milford, IN*.

The response to injection with *E. coli* LPS was tested as a means to assess the effects of inflammation on performance of young commercial ducks. Inflammation was measured by temperature changes, feed consumption, and body weight. Natural antibody titer and complement activity were used as immunity measures. It was determined by a preliminary trial that of 3 doses (n = 4 per dose) of LPS, 0.1, 1, and 5 mg/kg BW only the high dose (5 mg/Kg) resulted in fever (+ 1 C increase in cloacal temperature). A second trial using 6 ducks at each of 4 injection treatments: none, non-pyrogenic saline, 5 mg LPS, and *Riemerella anatipestifer* bacterin (RAB) given on day of age 21 and 23 was conducted. Pre-injection measurements obtained at d 18 compared with post injection measurements through d 25 indicated that both LPS and RAB were associated with reduced feed intake ($P = 0.008$), reduced BW gain: 0.73Kg (LPS) 0.86Kg (RAB) 0.95Kg (no inj.) 1Kg (saline)($P = 0.06$); but only LPS caused fever ($P = 0.001$). Immunity was measured by comparing natural (anti-rabbit erythrocyte) agglutinins and lysins. Four parameters: HA1, HA2 (agglutination), L100, L50 (lysis) assessed agglutination and complement activity in serum at d 25. As C′ activity was anticipated to be an important component of the inflammatory response serum diluents were (PBS) supplemented with Ca, Mg, or both. HA1 (IgM type) agglutination (log 2 titer) was not affected by injection treatments but HA2 (IgG type) agglutination was lower in LPS (7.0) and saline (7.7) (vs. 8.4 no injection, and 9.7 RAB injection treatments) when assessed with Ca or Mg supplemented PBS ($P < 0.02$) but not when assessed with un-supplemented PBS. More C′ activity was detected using diluents supplemented with both Ca and Mg than with either alone. Ca supplemented lysis of rabbit cells (L50) was lowered by RAB injection more than by LPS ($P < 0.002$). This duck inflammation model appears useful and might have application in testing the effectiveness of dietary products designed to modulate immunity in this species.

Key Words: ducks, inflammation, LPS

601 Comparison of water-based foam and inert gas mass emergency depopulation methods of turkeys. M. K. Rankin*, E. R. Benson, R. L. Alphin, D. P. Hougentogler, and P. Mohankumar, *University of Delaware*, *Newark*.

Current control strategies for avian influenza (AI) and other highly contagious poultry diseases include surveillance, quarantine, depopulation, disposal, and decontamination. Selection of the best method of emergency mass depopulation needs to maximize human health and safety while minimizing disease spread and animal welfare concerns. The method used must be compatible with species, age, housing type, and disposal options. Research has shown differences in gassing and foam depopulation procedures when comparing time to and consistency of time to brain death. Unconsciousness precedes terminal convulsions. The objective of this study was to compare the time to death and other physiological markers for water based foam and CO_2 gas depopulation methods. An experiment was conducted individually comparing the use of water based foam and CO_2 gas for depopulation of turkeys. The time to death of the birds was evaluated using electroencephalogram (EEG), electrocardiogram (ECG) and motion cessation. Each bird was instrumented with a surgically implanted EEG transmitter and an external accelerometer and ECG pads. Eighteen turkeys, aged 14–26 weeks, were individually depopulated per treatment. The EEG results showed that foam caused more rapid brain death (mean of 190 s (foam) versus

a mean of 242 s (CO_2 gas)) and the differences were statistically significant. Although ECG results showed that foam caused more rapid cardiac suppression (200 s (foam) versus 220 s (CO_2 gas)), the differences were not statistically significant. Onset of terminal convulsions occurred at similar times (166 s (foam) and (174 s (CO_2 gas)) for both treatments. Additional analysis of brain activity before and during treatment was also conducted. The use of water based foam depopulation results in more rapid brain death than available gassing procedures, reducing the time that the bird is conscious and aware during depopulation.

Key Words: foam, depopulation, EEG

ASAS-ADSA Cell Biology Symposium: Receptors and Signaling

602 The GnRHR: GPCR trafficking in health and disease. P. M. Conn*[1,2] and J. A. Janovick[1,2], [1]*Oregon Health and Science University*, *Portland,* [2]*Oregon National Primate Research Center*, *Beaverton*.

The GnRH receptor (GnRHR) is a heptahelical G protein coupled receptor (GPCR) found in gonadotrope cell plasma membrane. GnRHR mutants from patients with hypogonadotropic hypogonadism are frequently misfolded and mislocalized proteins, retained in the ER by the cell's quality control system (QCS). The vast majority of these mutants (16 of the 19 point mutations reported from patients) can be restored to function by peptidomimetic antagonists, acting as pharmacological chaperones or "pharmacoperones." Pharmacoperones are a newly appreciated class of drugs, made up of small, target-specific molecules that diffuse into cells and serve as folding templates to cause otherwise misfolded proteins to fold in a manner that is acceptable to the QCS. Accordingly, these drugs rescue misfolded proteins, restore them to the correct location in the cell and allow normal function.It has become obvious that many protein mutants retain or regain their fundamental properties as ion channels, enzymes or receptors when re-routed correctly and so, the use of pharmacoperones has general application. Among the diseases caused by misfolding (which may benefit from this approach) include cystic fibrosis, hypogonadotropic hypogonadism, nephrogenic diabetes insipidus, retinitis pigmentosa, hypercholesterolemia, cataracts, neurodegenerative diseases (Huntington's, Alzheimer's and Parkinson's), cancers and digestive disorders. It is fair to say that virtually every person will be affected by protein folding diseases during his or her lifetime, either directly or due to the illness of a loved one. This presentation will provide an overview of the GnRHR, emphasizing its role as a model for protein folding and mutant rescue. Among the topics that appear to have general application are the interaction and molecular mechanism of action of pharmacoperones, the "dominant negative" effect, whereby oligomerizing GnRHR (WT and mutants) cause the retention of WT-mutant hetero-aggregates because the oligomer is recognized as misfolded and the mechanism by which the cells protects itself against constitutively active mutants.

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Key Words: g-protein coupled receptors, protein trafficking, pharmacoperone

603 Function and regulation of the toll-like receptor family. G. M. Barton*, *University of California, Berkeley*.

The toll-like receptors (TLRs) are a family of innate immune receptors that have evolved to recognize conserved features of microbes. These receptors link the recognition of invading microbes to induction of innate and adaptive immune. Accordingly, TLRs have been implicated in immunity to many pathogens. Inappropriate activation of these receptors can also lead to autoinflammatory or autoimmune disorders. Our group has been studying the regulatory pathways responsible for maintaining the balance between immunity and tolerance. In this presentation I will provide an overview of TLRs and will highlight our recent work on the regulation of these receptors in immunity and autoimmunity.

Key Words: toll-like receptors, innate immunity, autoimmunity

604 Insulin signaling is a modulator of muscle growth. T. A. Davis*, A. Suryawan, R. A. Orellana, and M. L. Fiorotto, *USDA/ARS Children's Nutrition Research Center, Department of Pediatrics, Baylor College of Medicine, Houston, TX.*

The growth rate of skeletal muscle during the neonatal period is higher than at any other stage of postnatal development and is driven by an elevated rate of protein synthesis. The high rate of muscle protein synthesis in neonatal mammals is in part due to a marked stimulation of protein synthesis after feeding. This response to feeding is, in part, due to an enhanced sensitivity to the postprandial rise in insulin. The effect of insulin on protein synthesis is most pronounced in skeletal muscle. The decline with age in the response of muscle protein synthesis to insulin parallels the developmental decline in the rate of muscle protein synthesis. The high rate of protein synthesis in neonatal muscle is in part due to an enhanced activation of the insulin signaling pathway. Thus, the postprandial rise in insulin activates in muscle the insulin receptor, insulin receptor substrate 1/2, phosphatidylinositol 3-kinase, phosphoinositide-dependent kinase 1, protein kinase B, mammalian target of rapamycin, ribosomal protein S6 kinase-1, eukaryotic initiation factor (eIF) 4E-binding protein 1, and eIF4E associated with eIF4G and these responses decrease with development. The reduced activation of negative regulators of insulin signaling also contributes to the high rate of neonatal muscle protein synthesis. These include protein tyrosine phosphatase 1B, phosphatase and tensin homolog deleted on chromosome 10, protein phosphatase 2A, tuberous sclerosis 2, and proline-rich Akt/PKB substrate 40 kDa. These studies demonstrate that the high rate of protein synthesis and rapid gain in skeletal muscle mass in neonatal pigs are in part modulated by changes in the activation of components in the insulin signaling pathway.

Key Words: muscle, protein synthesis, insulin

605 Imaging the organization and trafficking of lipolytic proteins in adipocytes. J. G. Granneman*, *Wayne State University School of Medicine*, *Detroit, MI*.

Growing evidence indicates that hormone-stimulated lipolysis involves protein kinase A (PKA)-regulated protein trafficking at the surface of lipid droplets and that perilipin A (Plin), a lipid droplet scaffold protein, plays an essential role. We investigated mechanisms whereby Plin regulates hormone stimulated lipolysis with a panel of fluorescently-tagged proteins and novel protein-protein interaction assays that allow monitoring of dynamic interactions in live cells. Our data show that Plin regulates lipolysis by direct and indirect means. First, Plin directly regulates HSL activity by providing a docking site for phosphorylated HSL to bind and gain access to triglyceride substrate. Second, Plin indirectly regulates the activity of adipose triglyceride lipase (Atgl) by controlling the availability of its coactivator, Abhd5, in a manner that requires Plin phosphorylation. Our results demonstrate that Plin binds Abhd5 in the basal state which greatly inhibits Abhd5/Atgl interactions and reduces basal lipolysis. PKA activation leads to rapid release of Abhd5 from Plin. We identify the PKA phosphorylation sites on Plin that are necessary both for releasing Abhd5 from Plin and promoting its interaction with Atgl. Finally, we show that the PKA-dependent interaction of Abhd5 and Atgl occurs mainly on lipid droplets containing Plin.

Key Words: lipolysis, perilipin, adipocytes

Bioethics Symposium: Should Animal Welfare be Law or Market Driven?

606 Bioethics symposium introduction: Should animal welfare be law or market driven? C. C. Croney*, *The Ohio State University*, *Columbus*.

In recent years, concern about the welfare of food producing animals has provided the impetus for greater regulation of US animal production practices and policies. Annual polls conducted within the United States indicate strong and consistent public support for such regulation. Intensive confinement of animals, relief of animal pain, humane handling of animals and timely and appropriate euthanasia remain high on the list of concerns articulated by consumers, animal activists, scientists and other key stakeholders. Consequently, the rate of passage of state legislation of farm animal production has escalated. Concurrently, most food retailers have adopted some form of animal welfare assurance scheme and audit program to meet consumer expectations relative to animal welfare. Despite these efforts, frequent undercover exposés depicting treatment of farm animals that is socially unacceptable or questionable, and occasionally, clearly abusive suggest some need for greater regulation. However, hastily regulating farm animal welfare may have unforeseen consequences, including negative implications for animal producers, food prices, concerned citizens and the animals themselves, and these should also be considered. All of this suggests the need for thoughtful debate about whether protection of farm animal welfare in the US should be legislated, voluntarily regulated by the animal industries, or driven simply by market demands.

Key Words: ethics, regulation, animal production

607 Should we legislate farm animal welfare? J. C. Swanson*, *Michigan State University*, *East Lansing*.

In the last 5 years successful state citizen initiatives and legislation has created a patchwork of farm animal welfare regulation across the United States. Consequently, some states have responded with defensive measures such as creating state livestock care boards or advisory councils charged with promulgating standards for the care of livestock and poultry within the state. Although recent citizen initiatives and state bills begin with similar themes, during the legislative process deals are struck and the enacted laws often differ. Implementation periods, minimum space requirements, and noncompliance penalties are negotiated areas that create subtle yet important differences. Similar issues could erupt between state livestock care boards. As more states opt to regulate, it will eventually force a discussion about the federal regulation of farm animal care. This presentation will explore whether farm animal welfare ought to be legislated.

Key Words: animal welfare, legislation, regulation

608 Impact of slaughter bans on horse welfare. D. L. Gies*, *Animal Assistance Foundation*, *Denver, CO*.

This session will provide attendees with an historical perspective of horse slaughter in the United States and the effects of slaughterhouse closures on horse welfare from both a scientific and non-scientific perspective. It will provide up-to-date information on the status and detail of the competing horse slaughter legislation and will discuss the ongoing efforts of the horse community to measure horse welfare. Many animal and horse welfare organizations have raised concerns for years about the slaughter of horses for human consumption. Specifically, groups stated that the horse slaughter process was inhumane, that horses should not be processed for human consumption and that horses should not be slaughtered in the U.S. for export. In 2007, the three equine slaughter plants operating in the U.S., located in Illinois and Texas, closed following state legislation that banned the slaughter of horses for human consumption. In their final year of operation, these plants processed 102,260 horses. Since 2007, questions have been raised about whether the closure of the slaughter plants has in fact improved horse welfare. In 2009, there were an estimated 170,000 unwanted horses. Approximately 100,000 of these horses were exported to Mexico or Canada for slaughter in plants not regulated by USDA inspectors.
Currently there is no federal legislation banning domestic horse slaughter for human consumption. However, USDA inspectors are prohibited from inspecting horse meat slaughtered in U.S. plants for human consumption, effectively barring horse slaughter plants from operating. As a result, a national debate regarding horse slaughter continues. The proposed Prevention of Equine Cruelty Act seeks to ban horse slaughter in the U.S. and the export of horses for slaughter. A competing bill, the proposed Humane and Optimal Restoration and Sustainability of Equines Act (HORSE), seeks to reopen slaughter plants within the U.S. by removing the regulatory roadblocks to USDA inspection of horse meat.

Key Words: horse, slaughter, welfare

609 Should animal welfare be law or market based? B. Rollin*, *Colorado State University*, *Fort Collins*.

Between 1976 and 1985, a group of people at Colorado State University engaged the task of writing federal animal welfare legislation for research animals. Between us we had over 50 years of experience in animal research. We were particularly concerned about the lack of knowledge of analgesia and pain control in research. Not only was there virtually no use of pain management in invasive research protocols, there was not even literature on the subject. Yet the knowledge existed in the research community that the failure to control pain and distress skewed key variables being studied. In other words, pain control should have been a matter of rational self-interest, assuring that one's results in experimentation were as accurate as they could be. Even self-interest could not override widespread ideological agnosticism about animal pain and consciousness rife in the scientific community, nor could it override ignoring ethical questions occasion by animal research. When we did successfully legislate pain control for research animals in 1985, both knowledge and use of analgesia in research proliferated. From a total absence of papers on pain control in animals in 1982, there now exists an estimated 10,000 such papers. In other words, legislation was essential to incorporating into animal research what should have been ethically presuppositional to its activities. If self-interest did not lead researchers to control pain, it is clear that market options would have done so. Fulfilling one's ethical obligation attendant upon using animals for human benefit should not be a matter of choice of the sort that market options provide. The animal agricultural industry knows full well that the public often chooses the cheaper product even when expressing a commitment to animal welfare or environment friendly products. This does not prove the weakness of these commitments, it rather shows what ancient Stoic philosophers call akrasia, or weakness of the will. That is why repeated polls have demonstrated that fully 75% wish to see farm animal welfare encoded in legislation. Honoring basic moral obligations should not be left to market choices, but should be presuppositional to such choices.

Key Words: pain, research animal law, market

610 Should euthanasia and pain management be mandatory? Veterinary viewpoint. G. C. Golab*, *American Veterinary Medical Association*, *Schaumburg, IL*.

The AVMA believes animal pain and suffering are clinically important conditions adversely affecting quality of life, and encourages veterinarians to make every attempt to prevent and alleviate pain in animals. Because animals vary considerably in their response to stimuli, preventive and therapeutic strategies for managing pain must be tailored to individuals. Pain management protocols must be flexible and allow professional judgment in their application.
Considerations in managing pain include species, type/breed, age, procedure performed, extent of tissue trauma, behaviors, degree of pain, health status, and availability of techniques and pharmaceuticals. Pharmacologic and nonpharmacologic approaches should be considered. Pharmacologic approaches include appropriate selection and use of sedatives/tranquilizers, anesthetics, and analgesics. Consideration should be given to multimodal approaches, as these may improve analgesia, allow reductions in dose of drugs, and minimize adverse effects. Nonpharmacologic approaches include nutritional support, good husbandry practices, and positive owner interactions. It may not be possible (or desirable) to completely avoid or eliminate pain in animals. In such cases, veterinarians should pursue strategies that improve an animal's ability to cope with pain, allow the animal to engage in as many normal activities as possible (e.g., eating, sleeping, ambulating, socializing with conspecifics and/or people), and avoid suffering. When suffering cannot be avoided, and resolution of the condition leading to suffering is unlikely, euthanasia should be considered. Delaying euthanasia, when euthanasia is the appropriate choice, is unacceptable in terms of risks to animal well being and human ethical responsibilities. Euthanasia is the act of inducing humane death. Veterinarians have a responsibility to ensure that if an animal′s life is taken, it is done with the greatest degree of respect and with an emphasis on making its death as pain- and distress-free as possible. Euthanasia techniques should result in rapid loss of consciousness, followed by cardiac or respiratory arrest and the ultimate loss of brain function.

Key Words: pain management, euthanasia

611 Consumer preferences for market and regulatory responses to farm animal welfare concerns. F. B. Norwood* and J. L. Lusk, *Oklahoma State University*, *Stillwater*.

Consumers can pursue changes in how farm animals are raised by purchasing products differentiated by the level of animal welfare provided, or by seeking regulations forcing farmers to adopt certain production practices. The desirability of market or regulatory responses depends on the extent to which animal welfare is considered a private or public good. The greater extent to which people care about the animals producing other peoples' food, the more animal welfare resembles a public instead of a private good. Consumer experiments were conducted to measure the private and public good component of livestock welfare. Over 300 individuals from 3 cities were educated about the farm animal welfare issue, and were presented with 4 different systems for producing pork and eggs. These individuals then submitted bids in a real auction to measure the extent to which they will pay premiums for animal-friendly pork and eggs. The auctions were specifically designed to measure welfare concerns for the animals producing their personal food and the animals producing other peoples' food. The results suggest that approximately one-third of Americans do not value welfare improvements, many consumers posses a relatively high value on the private good component of animal welfare, but that the public good component for the average American is small. The results suggest markets may address animal welfare concerns better than regulations.

Key Words: consumer experiments, consumer preferences, farm animal welfare

612 Utility of genomic relationship matrix to identify genotyping errors. R. Simeone*[1], I. Misztal[1], and I. Aguilar[1,2], [1]*University of Georgia*, *Athens*, [2]*INIA*, *Las Brujas, Uruguay*.

The purpose of this study was to use the genomic relationship matrix (G) as an indicator of genotyping or other analysis problems in a single-step genomic evaluation procedure. Data was obtained from Cobb-Vantress and consisted of body weights for 183,784 broiler chickens over 3 generations with pedigrees on 186,222 animals. Of these animals 3,284 were genotyped for 57,636 SNP. Loci with no variation or minor allele frequency <0.02 were removed from the data, leaving 48,006 loci for analysis. Construction of G used current allele frequencies. Theoretically, the mean of the diagonal elements in both relationship matrices should be the same. The mean of the diagonal elements of G was 1.03 ± 0.16, however, the distribution of these elements showed 3 peaks: 3,195 in the range from 0.54 to 1.19, 88 in the range from 1.73 to 2.09, and one with a value of 3.12. Animals with a diagonal element >1.2 were assumed to have abnormal genotypes. Genetic predictions were computed by a single-step procedure (SSP) that combined phenotypic, pedigree and genomic information. This procedure was applied with all genotypes or with abnormal genotypes removed and with all phenotypes or only with phenotypes of genotyped animals. Accuracies were computed by dividing the predictive ability by the square root of heritability. Removing genotypes causing abnormal diagonals increased the accuracy from 0.648 to 0.657 when all phenotypes were used and from 0.584 to 0.586 when only phenotypes of genotyped animals were used. The difference between predictions obtained with and without the abnormal genotypes was distributed close to normal but with longer tails. Analysis of diagonals in G may serve as a diagnostic tool to identify erroneous genotypes. Very large diagonals suggest an analysis problem; explanations may be presence of animals of another breed, allele frequency shifts or a genotyping error. Removing suspected genotypes is likely to improve accuracy of genetic evaluation, especially for animals with suspected genotypes or their progenies.

Key Words: genomic relationship, genotyping error, single-step procedure

613 Genetic evaluation including phenotypic, full pedigree, and genomic information: An application in broiler chickens. C. Y. Chen*[1], I. Misztal[1], I. Aguilar[1,2], S. Tsuruta[1], T. H. E. Meuwissen[3], S. E. Aggrey[4], and W. M. Muir[5], [1]*Department of Animal and Dairy Science, University of Georgia*, *Athens,* [2]*Instituto Nacional de Investigación Agropecuaria*, *Las Brujas 90200, Uruguay*, [3]*Department of Animal and Aquacultural Sciences, Norwegian University of Life Sciences*, *NO-1432 As, Norway*, [4]*Department of Poultry Science, University of Georgia*, *Athens,* [5]*Department of Animal Science, Purdue University*, *West Lafayette, IN*.

A complete phenotypic data set (FULL) consisted of 183,784 and 164,246 broilers for 2 lines across 3 generations. Genotyped subset (SUB) consisted of 3,284 and 3,098 broilers in lines 1 and 2 with 57,636 SNP available. Traits were body weight at 6 weeks (BW), ultrasound (US), and binary leg defect score (LEG). Some records were missing for US. Heritability with FULL were 0.17–0.20 for BW, 0.30–0.35 for US, and 0.09–0.11 for LEG. Genetic evaluation was performed by regular BLUP, by a single-step procedure (SSP) that combined relationships based on pedigree and the SNP data, and by Bayes A procedure. While BLUP and SSP could use the complete data set, Bayes A could use only the genotyped subset. Genotyped animals in generation 3 were treated as validation population. The average accuracies of the validation population with BLUP for BW, US, and LEG were 0.46, 0.30, and < 0 with SUB and 0.51, 0.34, and 0.28 with FULL. With SSP, those accuracies were 0.60, 0.34, and 0.06 with SUB and 0.61, 0.40, and 0.37 with FULL, respectively. Accuracies with BayesA were similar to SSP with SUB. Accuracies in lines 1 and 2 were similar for US but different for BW and LEG. For traits with high heritability, the accuracy of the evaluation using the genomic information and only records of genotyped animals may be higher than that using the complete data and BLUP. The opposite is likely for traits with lower heritability, many missing records, or undergoing pre-selection. An optimal genomic evaluation would be multi-trait and would involve all traits and records on which the selection is based.

Key Words: chicken, genetic evaluation, genomic prediction

614 Scaling the genomic relationship matrix for single-step evaluation using phenotypic, pedigree and genomic information. S. Forni*[1,2], I. Aguilar[3,2], I. Misztal[2], and N. Deeb[1], [1]*PIC/Genus Plc*, *Hendersonville, TN,* [2]*University of Georgia*, *Athens,* [3]*INIA*, *Las Brujas, Uruguay*.

Data included litter sizes for 338,346 PIC sows, of which 1,919 had genotypes using the porcine 60k SNP chip. Genotypes were also available for 70 sires. Analyses involved a complete data set or a subset of genotyped animals and their parents (n = 5,090). A genomic relationship matrix was constructed using equal (G05) or observed gene frequencies (GOB). Additional relationship matrices were the pedigree-based relationship matrix (A) and a combined pedigree-genomic matrix (H). For genotyped animals, the mean of diagonal elements in A (G05, GOB) was 1.00 (1.25, 0.94). The mean of off-diagonal elements was 0.03 (0.59, 0.00). A normalized matrix (GN) was obtained by multiplying GOB by a constant to achieve an average diagonal of 1. Using A and the complete data set, the estimate of the additive variance was 1.26(±0.03). With H that included G05, GOB or GN the additive variance estimates were 1.28(±0.03), 1.28(±0.03) and 1.27(±0.03), respectively. Using A and the subset of the data, the estimate of the additive variance was 2.28(±0.52). With H that included G05, GOB or GN the additive variance estimates were 3.43(±0.56), 2.42(±0.39) and 2.25(±0.36), respectively. Accuracies for the complete data set were estimated by inversion. The average accuracy for genotyped animals using A, G05, GOB and GN were 0.23, 0.38, 0.31, and 0.30, respectively. When the genomic relationship matrix has a different scale than the pedigree-based matrix, the estimates of the additive variance may be biased especially for small data sets. Also, estimates of the accuracies of evaluation obtained by inversion may be inflated. One solution to normalize the genomic relationship matrix is by using realized gene frequencies and scaling this matrix to obtain an average diagonal close to 1.

Key Words: genomic selection, swine, single-step evaluation

615 Accuracies of direct genomic breeding values estimated in dairy cattle with a principal component approach. N. P. P. Macciotta*[1], M. A. Pintus[1], R. Steri[1], C. Pieramati[2], E. L. Nicolazzi[3], E. Santus[4], D. Vicario[5], J. T. van Kaam[6], A. Nardone[7], A. Valentini[7], and P. Ajmone-Marsan[3], [1]*Università di Sassari*, *Sassari, Italia*, [2]*Università di Perugia*, *Perugia, Italia*, [3]*Università di Piacenza*, *Piacenza, Italia*, [4]*ANARB*, *Bussolengo, Italia*, [5]*ANAPRI*, *Udine, Italia*, [6]*ANAFI*, *Cremona, Italia*, [7]*Università della Tuscia*, *Viterbo, Italia*.

A severe risk of overfitting due to the huge asymmetry between number of markers and phenotypes usually represents the main constraint for the implementation of genomic selection in livestock species. In the present work, the number of predictors for calculating direct genomic breeding values (DGV) is reduced by using principal component (PC) analysis. Sires of 3 dairy cattle breeds farmed in Italy were genotyped with the 54K Illumina beadchip: 863 Holstein (H), 749 Brown (B), and 479 Simmental (S). SNPs retained after edits were 40,658, 37,254, and 40,179 and the number of PC extracted 2,564, 2,257, and 2,476 for H, B, and S respectively. Effect of PC on polygenic EBV was estimated in the reference population with a BLUP model. Traits considered were milk yield, protein percentage, udder score and economic index. To create reference and validation population, bulls were tagged either by birth year or randomly. Accuracies were calculated as correlation between DGV and polygenic EBV in validation bulls. High DGV accuracies are obtained with reference animals selected at random (Table 1). When older animals are used to predict younger bulls, DGV accuracy drops dramatically for milk yield, especially for B and H, while it remains almost unchanged for udder score, protein percentage in B and milk yield in S.

Table 1.

	Random			By Year		
Trait	Holstein	Brown	Simmental	Holstein	Brown	Simmental
Milk yield	0.62	0.82	0.72	0.21	0.18	0.46
Protein percentage	0.52	0.58	0.32	0.37	0.54	0.36
Udder score	0.63	0.64	0.58	0.61	0.52	0.46
Economic index	0.67	0.84	0.64	0.44	0.33	0.28

Key Words: genomic selection, principal components, dairy cattle

616 Choice of parameters for single-step genomic evaluation for type. I. Misztal*[1], I. Aguilar[1,2], A. Legarra[3], and T. J. Lawlor[4], [1]*University of Georgia, Athens,* [2]*INIA, Las Brujas, Uruguay*, [3]*INRA, Toulouse, France*, [4]*Holstein Association, Brattleboro, VT.*

In a single step procedure, the pedigree-based matrix A is replaced by a matrix H that blends pedigree and genomic relationships. The inverse of matrix H involves an expression $G^{-1} - A_{22}^{-1}$, where G is a genomic relationship matrix and A_{22} is a pedigree relationship matrix for genotyped animals. Two modifications to that expression: $(\alpha\, G + \beta\, A_{22})^{-1} - A_{22}^{-1}$ and $\tau\,(0.95\, G + 0.05\, A_{22}^{-1} - \omega\, A_{22}^{-1}$ were investigated with regard to accuracy and scale of genomic predictions. While the first is equivalent to assuming a genomic and polygenic effect for genotyped animals, the second is equivalent to assuming a double prior for the additive effect. Data included final scores recorded from 1955 to 2009 for 6.2 million Holsteins, pedigrees for 10.5 million animals, and SNP50 genotypes for 6,508 bulls. Analyses used a repeatability animal model. Comparisons involved R^2 and regression coefficients (REG) based on 2004 predictions of young bulls and their 2009 daughter deviations. REG below 1.0 indicate inflation of genomic predictions. The initial expression yielded $R^2 = 0.41$ and REG = 0.75. With the first modification, varying α from 0.6 to 1.2 decreased R^2 less than 0.01 and decreased REG from 0.81 to 0.71. Increasing β from 0 to 0.6 decreased the R^2 and REG by 0.02 or less. With the second modification, varying τ from 0.6 to 1.5 increased R^2 by about 0.02 and increased REG by 0.02 ($\omega = 0$) to 0.15 ($\omega = 1.0$). Decreasing ω from 1.0 to 0 decreased the R^2 by 0.03 and increased REG from 0.2 ($\tau = 1$) to 0.3 ($\tau = 0$). Parameters $\tau = 1.5$ and $\omega = 0.4$ yielded $R^2 = 0.40$ and REG = 1.0. While the scale of G (parameters α and τ) has a small effect on R^2 and REG, matrix G as used here is about 50% too large. The scale of A_{22}^{-1} (parameter ω), which is associated with parental index based on genotyped bulls, has a large impact on inflation of genomic predictions.

Key Words: genomic relationships, single-step evaluation, inflation

617 Improved reliability approximation for genomic evaluations in the United States. G. R. Wiggans* and P. M. VanRaden, *Animal Improvement Programs Laboratory, ARS, USDA*, *Beltsville, MD*.

For genomic evaluations, the time required to calculate the inverse of the coefficient matrix for the mixed-model equations increases cubically as the number of genotyped animals increases, and an approximation became necessary for estimating US evaluation reliabilities. The original approximation method used the same contribution to reliability from genomics for all animals. That method was improved by using a weighted sum of the genomic relationships of an animal with predictor animals (ΣG_W), which allowed for individual animal differences. Because calculation time for the genomic relationship matrix only increases quadratically and is routinely available, the sum of relationships of an animal with predictor animals can be obtained. Those relationships were weighted by reliability of the traditional evaluation after removing the contribution to reliability from parent average by first converting both reliabilities to daughter equivalents (DE). Reliabilities from August 2009, the last genomic evaluation for which the coefficient matrix was inverted, were decomposed to extract the genomic contribution in terms of DE calculated with an error-to-sire variance ratio of 14. Of 28,047 genotyped Holsteins, 8,353 bulls and 3,559 cows had genomic evaluations and 16,135 animals did not. Regression of DE on ΣG_W was calculated for those 3 groups. Goodness of fit was assessed by plotting predicted values against mean DE for ΣG_W groups, where groups were by 10. A straight line through the origin provided a good fit except for low ΣG_W. A floor of 30 DE was adopted to improve evaluation accuracy for animals with low ΣG_W. The slope was 0.0584 for evaluated bulls, 0.0557 for evaluated cows, and 0.0506 for animals without evaluations. The higher slope for bulls resulted in a higher reliability for the same ΣG_W. The improved approximation method increased accuracy of genomic reliabilities, particularly when comparing animals with different countries of origin and bulls with only genomic evaluations with progeny-test bulls.

Key Words: reliability, genomic evaluation, genomic relationships

618 Cow adjustments for genomic predictions of Holstein and Jersey bulls. G. R. Wiggans, T. A. Cooper*, and P. M. VanRaden, *Animal Improvement Programs Laboratory, ARS, USDA*, *Beltsville, MD*.

Genomic evaluations are calculated by using values that have been deregressed from traditional PTAs estimating single nucleotide polymorphism (SNP) effects. Previous research indicates that including cow genomic data to calculate SNP effects does not increase reliabilities of genomic evaluations of yield traits. Upward bias in traditional PTA of genotyped cows may be the reason for this. The direct genomic value (DGV) is the sum of an animal's SNP effects. It should be consistent with traditional PTA and is for bulls. For cows, however, the traditional PTA is higher. To make the cow PTA more like those of the bulls for the yield traits (milk, fat and protein), mean and variance adjustments were calculated. Evaluations were stratified by reliability so cow PTA could be adjusted to be similar to bulls with the same reliability. The variance adjustment was the SD of deregressed Mendelian sampling within reliability group for bulls divided by the value for cows. The mean adjustment is the difference between bull and cow evaluations

after variance adjustment. Deregressed Mendelian sampling values were adjusted, and then the deregression was reversed to obtain the corrected PTA. To determine gains in reliabilities, predictions were made for bulls with current evaluations that did not have evaluations in August 2006. The predicted values were compared with the bull's actual evaluation from January 2010. For Holstein bulls, predictions using cows' adjusted data were 2.5, 2.8 and 2.1 points higher than those from data without adjustment for milk, fat and protein respectively. Jersey bulls also benefit from cow adjustments with an increase in gains in reliability over parent average of 3.9 points for milk, 5.6 points for fat and 3.5 points for protein. Brown Swiss adjustments could not be evaluated due to low numbers of genotyped cows. Genomic evaluations for Holsteins and Jerseys will be more accurate by better using the information from cows.

Key Words: genomics, prediction, evaluation

619 Investigating bull dam bias in national genetic evaluations. F. Canavesi* and R. Finocchiaro, *Associazione Nazionale Allevatori Frisona Italiana*, *Cremona, Italy*.

Parent averages (PA) are used in combination with direct genomic values to predict genomic breeding values (GEBV). Studies conducted in Germany (2009) showed that classic PA making use of sire and dam EBV deviates from expected contribution to the EBV of sons. This is due to overestimation of bull dams for production traits if compared with a trait like somatic cell score where selection and commercial interests play a minor role. The objective of this study was to investigate the relationship between PAs and realized EBVs in the Italian genetic evaluation system for progeny test bulls. A total of around 800 EBV of bulls born between 2001 and 2003 were used to analyze the relationship between their EBV in January 2010 and their PA in 2004 for production, conformation and somatic cells traits. Regression coefficients of sire and dam, EBV used to predict realized 2010 EBV were examined. Results show that both production and conformation traits deviates from expected values while somatic cell count are close to expected contribution of 0.50 for both EBVs of sire and dam respectively. In agreement with the German study the use of male pedigree information resulted in values close to expected and therefore would be the preferred choice in the prediction of GEBV.

Key Words: parent average, future predictions, bulldam bias

620 Gains in reliability from combining subsets of 500, 5,000, 50,000 or 500,000 genetic markers. P. M. VanRaden and M. E. Tooker*, *Animal Improvement Programs Laboratory, ARS, USDA*, *Beltsville, MD*.

More genetic markers can increase both reliability and cost of genomic selection. Fewer markers can be used to trace chromosome segments within a population once identified by high-density haplotyping. Combinations of marker densities can improve reliability at lower cost. As of January 2010, 33,414 North American Holsteins had been genotyped for 50,000 genetic markers. Genotypes for 500,000 markers were simulated using pedigree data for this same population. Linkage was introduced among base alleles to make correlations among simulated genotypes similar to actual. Reduced subsets were examined using every 10th, 100th, or 1000th marker. In marker regression models, polygenic variance was 70, 30, 10, and 0% of genetic variance with 500, 5,000, 50,000 and 500,000 markers, respectively. Respective reliabilities obtained as squared correlations of estimated and true breeding values averaged across 5 replicates were 39.4, 70.2, 82.6, and 84.0% for 14,061 young bull predictions. At highest density, one processor required 2.5 d to complete 150 iterations for the 5 replicates. A mixed-density data set had 500,000 markers genotyped for 3,515 young bulls and 3,883 bulls with > 90% reliability and 50,000 markers genotyped for the remaining 26,016 animals. This data set had 70% missing genotypes; however, after imputing from haplotypes, only 4% of genotypes were missing, and average reliability was 83.1%. Two other mixed-density data sets had 50,000 markers for cows and progeny-tested bulls but only 5,000 or 500 markers for young animals. Reliabilities averaged 79.6% for young animals if 5,000 markers were genotyped and the other 45,000 imputed. At 500-marker density, inheritance probability was computed for each marker instead of simply assigning either parental haplotype; reliabilities averaged 70.3% when young animals were genotyped for 500 markers and both parents were genotyped for 50,000. Very high marker density can increase reliability slightly (1.4%), whereas low marker density allows breeders to apply cost-effective genomic selection to many more animals.

Key Words: reliability, marker density, genomic evaluation

621 Accuracy of direct genomic values derived from imputed single nucleotide polymorphism genotypes in Jersey cattle. K. A. Weigel*[1], G. de los Campos[1], A. I. Vazquez[1], G. J. M. Rosa[1], D. Gianola[1], and C. P. Van Tassell[2], [1]*University of Wisconsin*, *Madison,* [2]*USDA-ARS*, *Beltsville, MD*.

The objective of the present study was to evaluate the predictive ability of direct genomic values for economically important dairy traits when genotypes at some single nucleotide polymorphism (SNP) loci were imputed, rather than measured directly. Genotypic data consisted of 42,552 SNP genotypes for each of 1,762 Jersey sires. Phenotypic data consisted of predicted transmitting abilities (PTA) for milk yield, protein percentage, and daughter pregnancy rate from May 2006 for 1,446 sires in the training set and from April 2009 for 316 sires in the testing set. The SNP effects were estimated using the Bayesian least absolute selection and shrinkage operator (LASSO) with data of sires in the training set, and direct genomic values (DGV) for sires in the testing set were computed by multiplying these estimates by corresponding genotype dosages for sires in the testing set. The average correlation across traits between DGV (before progeny testing) and PTA (after progeny testing) for sires in the testing set was 70.6% when all 42,552 SNP genotypes were used. When genotypes for 93.1, 96.6, 98.3, or 99.1% of loci were masked and subsequently imputed, mean correlations between DGV and PTA were 68.5, 64.8, 54.8, or 43.5%, respectively. When genotypes were also masked and imputed for a random 50% of sires in the training set, mean correlations between DGV and PTA were 65.7, 63.2, 53.9, or 49.5%, respectively. Results of this study indicate that a low density chip comprised of 3,000 equally spaced SNPs can provide approximately 95% of the predictive ability observed with the BovineSNP50 Beadchip (Illumina, Inc., San Diego, CA), but if fewer than 1,500 SNP are genotyped the accuracy of DGV may be limited by errors in the imputed genotypes of selection candidates.

Key Words: genomics, imputation, Jersey

622 Filling in missing genotypes using haplotypes. P. M. VanRaden*[1], J. R. O'Connell[2], G. R. Wiggans[1], and K. A. Weigel[3], [1]*Animal Improvement Programs Laboratory, ARS, USDA*, *Beltsville, MD,* [2]*University of Maryland School of Medicine*, *Baltimore,* [3]*University of Wisconsin*, *Madison*.

Unknown genotypes can be made known (imputed) from observed genotypes at the same or nearby loci of relatives using pedigree haplotyping, or from matching allele patterns (regardless of pedigree) using population haplotyping. Fortran program findhap.f90 was designed to

combine population and pedigree haplotyping. Each chromosome was divided into segments of about 100 markers each. Each genotype was matched to the list of currently known haplotypes sorted from most to least frequent for efficiency. If a match was found (no conflicting homozygote), any remaining unknown alleles in the found haplotype were imputed from homozygous genotypes. The individual's second haplotype was obtained by subtracting its first from its genotype, and the second was checked against remaining haplotypes. If no match was found, the new genotype (or haplotype) was added to the list. After completing population haplotyping, pedigrees were examined to resolve conflicts between parent and progeny haplotypes, locate crossovers that created new haplotypes, and impute haplotypes of nongenotyped ancestors from their genotyped descendants. One processor took 2 h to find haplotypes for 43,385 actual markers of 33,414 Holsteins. For the same population, time increased only to 2.5 h with 500,000 simulated markers but with 500 markers per segment. Computing time increased much less than linearly because most haplotypes were excluded as not matching after just the first few markers. Genotype storage required 13 GB for 500,000 markers, but haplotype storage required only 2.5 GB. Shared haplotypes were stored just once, and only index numbers were stored for individuals instead of full haplotypes. Paternal alleles were determined correctly for 95% of heterozygous markers, and linkage was determined correctly for 98% of adjacent pairs of heterozygous markers in simulated data. Population haplotyping correctly filled 95% of missing high density marker genotypes. Pedigree haplotyping can fill missing genotypes efficiently for nongenotyped ancestors or progeny with lower marker density.

Key Words: haplotyping, marker density, imputation

623 Use of haplotypes to predict selection limits and Mendelian sampling. J. B. Cole*, *Animal Improvement Programs Laboratory, ARS, USDA*, *Beltsville, MD*.

Limits to selection and Mendelian sampling terms can be calculated using haplotypes, which are sums of individual additive effects on a chromosome. Haplotypes were imputed for 43,385 actual markers of 3,765 Jerseys using the Fortran program findhap.f90, which combines population and pedigree haplotyping methods. Longer chromosomes had more distinct haplotypes, ranging from 7,287 for *Bos taurus* autosome 1 (BTA) to 2,460 for the X chromosome. This is expected because longer chromosomes undergo recombination more often than shorter ones. Mendelian sampling (MS) variances were calculated for genotyped animals as the sum of squared haplotype differences for each chromosome in the genome. The distribution of MS variances had a heavy right tail (skewness = 0.276), with a mean of 49,290 ± 13,981. Genotypes for each chromosome were constructed from pairwise combinations among the top 5% of haplotypes based on the sum of marker effects for lifetime net merit (NM) for each chromosome. Correlations among raw and adjusted values in the top group ranged from 0.897 on BTA12 to 0.998 on the X chromosome. Selection of the best unadjusted haplotypes for each chromosome results in an animal with an EBV of +$5,243 for NM. Adjusting for inbreeding resulted in a slightly lower EBV of +$4,496. Haplotype values were adjusted to account for changes in homozygosity by adding or subtracting 6% of an additive genetic standard deviation per 1% decrease or increase in homozygosity. The top Jersey bull, ALL LYNNS RESTORE VERNON-ET (29JE03647), had an EBV NM of +$1,180 in the January 2010 evaluation. For 11 chromosomes (BTA 4, 9, 13, 15, 20, 21, 22, 25, 26, 28, and X) the best genotype after adjusting for inbreeding consisted of 2 copies of the same haplotype. Differences between the best and poorest haplotypes ranged from a maximum of $65 for BTA1 to a minimum of $12 for BTAX. Selecting animals rather than chromosomes may result in slower progress, but limits may be the same because most chromosomes will become homozygous with either strategy. Selection on functions of MS could be used to change variances in later generations.

Key Words: genetic gain, haplotyping, mendelian sampling

Dairy Foods Symposium: Towards a Mechanistic Understanding of Probiotic Function in Man and Animals

624 Application of "omic" tools to understanding probiotic action. T. R. Klaenhammer*[1,2], [1]*North Carolina State University*, *Raleigh,* [2]*Southeast Dairy Foods Research Center*, *Raleigh, NC*.

Lactic acid bacteria are associated with various plant and animal niches and play a key role in the production of fermented dairy foods and beverages, with some species also exerting probiotic properties. As generally recognized as safe (GRAS) organisms, they have been orally ingested safely by humans over the centuries, often at levels exceeding 100 million per gram of food. Genome sequencing of ~30 LAB and probiotic species has revealed a path of evolution toward specialized habitats that are nutritionally rich. Comparative genomic analyses of lactobacilli occupying either food/dairy systems, or the intestinal tract (probiotic species), have identified both conserved and unique gene sets important for food/dairy fermentations, but recently have also identified key genes likely involved in functional roles that impact health. Functional genomic analyses using "omic" technologies have identified systems responsible for acid and bile tolerance, prebiotic utilization and revealed several cell surface proteins and structures on probiotic microbes that interact with host epithelial and immunomodulatory cells. Among these are lipoteichoic acids, surface layer proteins, and mucus binding proteins. Alteration of the cell surface display of such structures can dramatically alter dendritic cell binding and cytokine signaling and promote inflammatory or anti-inflammatory responses. Employing genomic tools for gene cloning, expression, and inactivation, the field is uniquely positioned to investigate mechanisms through which probiotic microbes interact with the intestinal mucosa, compete with pathogens and impact health.

Key Words: probiotic, lactic acid bacteria, genomics

625 The gastrointestinal microbiome and probiotics: Effects on intestinal physiology and mucosal inflammation. J. Versalovic*, *Baylor College of Medicine*, *Houston, TX*.

The human gastrointestinal microbiome is composed of many bacterial species that may affect signaling pathways in intestinal epithelial cells, stem cell compartments and mucosal immune cells. Differences in microbial composition may affect the intestinal mucosa in terms of effects on cell proliferation, apoptosis, antibody and cytokine production, and cell migration. Direct effects by microbial and probiotics-derived signals on specific mammalian cell signaling pathways may explain mechanisms of mucosal immunity. The gut microbiome may affect the biology of innate and adaptive immune responses in the gut mucosa. Specific components of the microbiome may have net anti-inflammatory or pro-inflammatory effects, and the relative balance of microbes may result in different patterns of mucosal inflammation. Differences in patterns of inflammation and immune responses to the gut microbiome and probiotics may determine, in part, differences in the risk of immune-mediated disorders and infections of the gastrointestinal tract.

626 An evolutionary link between bifidobacterial probiotics and milk. D. Mills*, *University of California*, *Davis*.

Bifidobacteria are commonly used as probiotics in dairy foods. Select bifidobacterial species are also early colonizers of the breast-fed infant colon, however the mechanism for this enrichment is unclear. We have previously shown that *Bifidobacterium longum* ssp. *infantis* is a prototypical bifidobacterial species that can readily utilize human milk oligosaccharides as a sole carbon source. Mass spectrometry-based glycoprofiling has revealed that numerous *B. infantis* strains preferentially consume small mass oligosaccharides, abundant in both human and bovine milks. Genome sequencing showed that *B. infantis* possesses a bias toward genes required to utilize mammalian-derived carbohydrates. Many of these genomic features encode enzymes that are active on milk oligosaccharides including a novel 40-kb region dedicated to oligosaccharide utilization. Biochemical and molecular characterization of the encoded glycosidases and transport proteins have further resolved the mechanism by which *B. infantis* selectively imports and catabolizes milk oligosaccharides. Expression studies indicate that many of these key functions are only induced during growth on milk oligosaccharides and not expressed during growth on other prebiotics. In addition, key cell surface oligosaccharide binding proteins in *B. infantis* bind both milk oligosaccharides and epithelial cell surface glycans. Moreover, growth on milk oligosaccharides results in significant increases in binding of *B. infantis* to intestinal cells in vitro. Additional sequencing of numerous *B. infantis* genomes has confirmed that these features are common among the *infantis* subspecies and likely constitute a competitive colonization strategy employed by these unique bifidobacteria. Through detailed characterization of the molecular mechanisms responsible for bifidobacterial enrichment in the gastrointestinal tract of breast fed infants, these studies provide a conceptual framework for enhancement of probiotic persistence and host-interaction through delivery in animal milks.

Key Words: probiotics, milk oligosaccharides, bifidobacteria

627 Assessing and maintaining probiotics in food. T. Hornbaek*, *Chr. Hansen A/S*, *Hoersholm, Denmark*.

Dairy products, and specifically yogurt-like products, form the largest segment by far in the market for probiotic foods. Dairy products are excellent vehicles for delivering useful probiotic bacteria such as Bifidobacteria and introducing them into the gastrointestinal tract. Increased consumer awareness of the health benefits of probiotics has led to numerous new probiotic product launches both in the market for fermented milk products as well as other food categories. In the development of new probiotic food products, there are several factors to consider including: 1) the documentation of the probiotic strain; 2) the ability to produce the probiotic strain in large scale; and 3) successful application in the food product. This presentation will focus on the last aspect: how to obtain successful probiotic food applications. Challenges with respect to sensory impact and survival of probiotics in different food applications will be discussed. Recent work will be presented to illustrate various ways of increasing probiotic cell counts and stability in dairy as well as non-dairy applications. Ways to circumvent the lack of important nutrients and the potential negative effect of different processing conditions will be discussed, also in relation to the use of adjunct cultures.

Without having bio-markers related to probiotic effects, the best way to ensure the probiotic properties of a food product is by measuring probiotic cell counts throughout shelf life. Our newest findings will be presented on the correlation between traditional plate counting methods and novel probiotic cell count methods such as qPCR and flow cytometry. Furthermore, a dynamic, multi-compartmental model system will be presented which provides the ability to estimate survival rates of probiotics delivered in different food vehicles on their way through the stomach and small intestine.

Key Words: probiotic, food, survival

628 Translating the science into efficacy claims on probiotic or prebiotic products in the US market. M. E. Sanders*, *Dairy & Food Culture Technologies*, *Centennial, CO*.

The US marketplace is home to an increasing number of food products labeled "probiotic" or "prebiotic." Although the scientific definitions of these terms are clear, they lack legal definition in the US. Responsible companies seek scientific substantiation for claims. Translating science into product claims starts with conducting research on endpoints that are compatible with the category of product. A product claiming to cure, treat, mitigate or prevent disease is a drug, not a food. Claims stating the effect of the product on the normal structure or function of the human body (structure/function claim), or on reducing the risk of a diet-related, chronic disease (health claim) are allowed for food. However, many studies comprising the body of research on probiotics and prebiotics would be considered drug studies by the FDA, and therefore would not be suitable as primary substantiation for a structure/function claim. Endpoints such as prevention of allergy, reducing the incidence of intestinal or respiratory infections among healthy children or managing symptoms of irritable bowel syndrome are seen by the FDA as drug uses. Securing public funding to conduct such research might trigger a request to file an Investigational New Drug Application with the FDA. Such a process – especially for a study recruiting healthy subjects - seems like an unnecessary burden for researchers with no intention to market a drug. Endpoints such as modulation of immune system function and alteration of colonizing microbiota fall under the structure/function claim rubric, but the consumer benefit from such endpoints is not always obvious. The arena of crafting "truthful and not misleading" product claims that accurately reflect scientific substantiation is a challenge. In addition to compliance with regulatory statutes, claims are scrutinized by other audiences, such as: consumers, healthcare professionals, media professionals, consumer watchdog organizations, advertising watchdog organizations (e.g., the National Advertising Division of the Better Business Bureau), and litigious elements in society.

Key Words: probiotic, prebiotic, claims

629 Strategic application of direct-fed microbials to livestock for growth efficiency and production. E. Davis* and T. Rehberger, *Dansico*, *Waukesha, WI.*

The establishment of the commensal microbiota in the gastrointestinal tract of the neonate is the impetus for the development of a functional immune system, with ramifications on metabolic functions related to subsequent growth in later production stages. The administration of probiotics, termed direct-fed microbials (DFM) when delivered to livestock, affords an opportunity to dictate a portion of the microbial consortia and thereby exert a positive influence on production efficiency and health. With the use of culture-independent molecular techniques, microbial diversity in the intestinal tract of neonatal pigs has been assessed and members of the intestinal microbial population identified that were positively correlated to specific immune cell phenotypes and growth performance traits. The administration of a *Bacillus*-based DFM to sows enhanced specific *Lactobacillus* populations in piglets at 3 and 10 d of age compared with pigs born to unsupplemented sows, with differences also observed in nutrient composition and immune cell phenotypes within colostrum, piglet growth, and immune cell populations in the gastrointestinal tracts of piglets. Although early delivery of a DFM may be ideal to influence early microbial colonization, administration of microorganisms in later production stages can still elicit improvements in production efficiency. Administration of *Propionibacterium* strain P169 to dairy cows during late gestation and early lactation altered ruminal metabolism toward increased propionate, resulting in increased milk production without increasing DMI. Host-microbial interactions during early post-natal development and in later production stages indicate that strategic applications of DFM to livestock can positively impact growth efficiency and production.

Key Words: probiotics, swine, cattle

Forages and Pastures: Environmental Impact of Forage-Based Livestock Production Systems

630 Compatibility of beef cattle management with multiple use values on western rangelands. T. DelCurto* and P. Kennedy, *Eastern Oregon Agricultural Research Center, Union Station, Oregon State University*, *Union*.

Beef cattle production in the western United States is dependent on systematic approaches that maintain the biological diversity of native rangelands. In addition, the continued use of these rangelands may depend on our ability to demonstrate that domestic livestock production can be compatible with multiple uses that not only include native vegetation/wildlife diversity, but also focus on water quality, fisheries, and recreation/esthetic values. The purpose of this paper is to quantify research that has evaluated the impact of beef cattle grazing on big game habitat, riparian areas critical to fish habitat, vegetation diversity, logging/grazing interactions, and, although information is limited, insect and bird diversity/abundance. Over 20 years of research will be summarized in respect to the interaction of beef cattle grazing and deer/elk big game herds in the Blue Mountains of Oregon. This research represents decades of collaborative research between the USDA FS Starkey Experimental Forest and Range and Oregon State University. In addition, research focused on the management of beef cattle relative to riparian areas that provide habitat to threatened and endanger fish will be discussed. Finally, a new generation of research will be discussed that uses a food web approach to enumerate the impact of beef cattle grazing on soils, vegetation, insects that feed on the vegetation, insects that prey on other insects, and ground nesting birds that need the vegetation for cover as well as use insects for their primary food sources. This type of research is difficult and often necessitates the need to develop multi-disciplinary and, in some cases, multi-agency teams. However, this type of research approach may be critical to addressing public concerns about the long-term sustainability of beef cattle production on western rangelands.

Key Words: beef cattle, rangelands, multiple use

631 Livestock grazing and endangered species habitat. G. S. Lewis*, C. A. Moffet, and J. B. Taylor, *USDA, ARS, U.S. Sheep Experiment Station*, *Dubois, ID*.

Livestock grazing can improve wildlife habitat, including critical habitat for species listed as endangered. However, that assertion presumes that appropriate and unbiased data have been used to define critical habitat; an appropriate recovery plan has been approved with clear and firm objectives that can be used to develop grazing strategies for habitat conservation; and legal challenges do not result in significant and frequent changes in the recovery plan. The Endangered Species Act (ESA) of 1973 defines endangered species as one that is "in danger of extinction throughout all or a significant portion of its range, and a threatened species as one that is "likely to become an endangered species within the foreseeable future." The ESA and amendments "provide a means whereby the ecosystems upon which endangered species and threatened species depend may be conserved, provide a program for the conservation of such endangered species and threatened species, and take such steps as may be appropriate to achieve the purposes of the treaties and conventions set forth" in the ESA, including "esthetic, ecological, educational, historical, recreational, and scientific value." Also, the ESA describes the process of listing species, determining critical habitat, developing a recovery plan, and delisting species. Nearly 1,900 species have been listed and <50 species have been delisted under the ESA. Even though strategic livestock grazing can benefit wildlife habitat, the scope and vagaries of the ESA and Federal judicial process, combined with institutional opinions of "antiagriculture" groups that livestock grazing is always detrimental, prevents scientists from conducting the well-designed research needed to develop site-specific livestock grazing plans for conserving endangered species habitat. Our presentation will include discussions of these issues and suggestions for how scientists can provide robust data for developing livestock grazing plans that will conserve endangered species habitat.

Key Words: Endangered Species Act, livestock grazing

632 Economic and environmental issues associated with confinement and pasture-based dairy systems. D. A. Clark*[1], S. F. Ledgard[2], P. Gregorini[1], and C. A. Rotz[3], [1]*DairyNZ*, *Hamilton, Waikato, New Zealand*, [2]*AgResearch*, *Hamilton, Waikato, New Zealand*, [3]*USDA-Agricultural Research Service*, *University Park, PA*.

Milk is produced in a continuum of dairy systems from full confinement to full pasture grazing. Climate, available feeds, and milk price: feed cost ratio influence the preferred system. All dairy systems have an environmental impact and inputs to maximize profit may lead to pollution levels unacceptable to society. There is vigorous debate concerning the trade-off between dairy farm profit and air and water quality impacts. Reasoned debate requires good information on the key production, economic and environmental parameters associated with different dairy systems and an agreement on the boundaries of each system. We provide a summary of literature on experiments and modeling of confinement and pasture-based dairy systems as a framework for future analysis and debate. There are few published experimental comparisons of confinement and pasture-based systems that account for both production and environmental parameters, so we make extensive use of modeling studies (e.g., life cycle assessment, Integrated Farm System Model, DairyNZ Whole Farm Model and OVERSEER). Where possible we use experimental data to evaluate model predictions. We compare a subset of possible dairy systems for both economic and environmental performance and identify areas of high sensitivity to factors such as input costs or environmental pollutants. Strengths and weaknesses of different systems are identified and we highlight opportunities for economic and environmental improvements by both component technologies and system redesign. Stored feed systems need to reduce their production costs and environmental footprint. Pasture-based systems need to reach the energy intake levels associated with TMR, and reduce the nitrate and N_2O losses associated with urine patches in grazed pasture. Dairy systems research must ensure that advances in animal and plant breeding lead to simultaneous economic and environmental benefits.

Key Words: dairy production systems, confinement feeding, grazing

633 Forages and livestock production with declining water resources and a changing agricultural industry. V. G. Allen*, C. P. Brown, R. L. Kellison, P. N. Johnson, and C. J. Zilverburg, *Texas Tech University, Lubbock*.

Agriculture is undergoing radical change driven by continued global population growth, a fossil fuel-based energy system, unstable economics and policies, depletion of natural resources, environmental concerns, and dependence on irrigation. Agriculture is the biggest single user of water, largely for irrigated crop production, and demands continue to

escalate. Urban expansion and conversion of prime agricultural land to non-agricultural uses force crop production into more marginal environments resulting in increased resource inputs to ensure production. Such inputs frequently include water for irrigation at non-sustainable rates of use. The semi-arid Texas High Plains is one of the most intensive agricultural areas in the US and is a model for factors driving change. Agriculture conservatively accounts for over 40% of the regional economy but depends heavily on water for irrigation from the Ogallala aquifer. Recharge is negligible, and water demand is expected to exceed supply within the next 10 to 20 years. About 30% of the cotton (*Gossypium hirsutum* L.) and 25% of the cattle on feed in the US are located here primarily in monoculture systems. Recently, the dairy industry and an emerging renewable fuel industry have entered this region placing increased demands on soil and water resources and influencing cropping decisions. Impending water depletion, evolving water policies and laws, and volatile commodity and input prices are contributing to destabilizing agriculture. A 10-year replicated comparison of an integrated crop/forage/beef stocker steer system and a monoculture cotton system demonstrated ($P < 0.05$) that the integrated system required about 25% less irrigation water, 40% less nitrogen fertilizer, improved soil organic carbon and microbial activity, reduced erosion, and was as profitable as the cotton monoculture. Monitoring of 27 producer systems in the Texas High Plains continues to demonstrate water conservation and economic opportunities through integrating forages and livestock into cropping systems but long-term field-scale systems research is essential. Lessons learned here have global significance.

Key Words: water, grazing systems, integrated systems

634 Pasture management strategies to minimize the impacts of grazing on water quality of surface water resources. J. R. Russell*[1], D. A. Bear[1], K. A. Schwarte[1], and M. M. Haan[2], [1]*Iowa State University*, *Ames,* [2]*Michigan State University*, *Hickory Corners*.

Sediment, nutrient, and pathogen loading of pasture streams result from stream bank erosion, direct manure deposition, and\or transport in precipitation runoff. Risks of loading streams with these pollutants may be increased by biotic and abiotic factors that encourage congregation of cattle near streams. Congregation of cattle near pasture streams may be discouraged by management practices that control the temporal\spatial distribution of grazing cattle. Restricting stream access of beef cows either to stabilized crossings in continuously stocked pastures or to riparian paddocks grazed to a minimum sward height of 10 cm in rotationally stocked pastures reduced the proportion of time that cattle spent in and within 33.5 m of the pasture streams by 81% in comparison to continuous stocking with unrestricted stream access. Providing off-stream water or shade may alter the temporal\spatial distribution of cattle in pastures, but efficacy of management practices to alter the distribution of grazing cattle is dependent on pasture size and shape and climatic conditions. The proportion of time that cattle spent in and within 30.5 m of a stream (streamside zone) in pastures with different areas was more highly related to the proportion of pasture area in the streamside zone than pasture shade distribution or botanical composition. In pastures with comparable areas, the proportion of time that cattle spent in the streamside zone was highly related to the proportion of total pasture shade in the streamside zone in the spring and fall, but not in the summer. Stream bank erosion and total coliform concentrations in stream water were not affected by stocking density or grazing management. Reducing pasture stocking density or restricting stream access to stabilized crossings or riparian paddocks limit the risk of sediment, nutrient, and pathogen loading of streams by reducing the proportion of bare and\or manure-covered ground and precipitation runoff in streamside zones.

Key Words: grazing, water quality, beef cattle

635 Evaluation of the NCAPG I442M locus, a major gene for bovine prenatal growth, for effects on postnatal development compared to a disruptive mutation in the myostatin encoding gene GDF8. C. Kuehn*, P. Widmann, R. Pfuhl, and R. Weikard, *Leibniz Institute for Farm Animal Biology (FBN)*, *Dummerstorf, Germany*.

Recently, we identified the I442M mutation in the bovine non-structural maintenance of chromosomes condensin I complex, subunit G (NCAPG) gene affecting bovine prenatal growth in an F2 resource population. Due to consistent application of embryo transfer during generation of the resource population, the direct genetic background of divergent postnatal growth dissected from putatively persistent maternal allelic effects could be addressed. In addition to the NCAPG I442M locus, also the disrupting mutation Q204X of the growth differentiation factor 8 (GDF8) segregated in our resource population. Thus, the effects of both loci could be evaluated on an identical genetic background. For our study, male calves were fed a milk replacer/hay/concentrate diet until d 121 followed by a semi ad libitum feed ration of concentrates and chaffed hay. Body weight was recorded monthly until 18 mo of age. All P0, F1 and F2 individuals were genotyped for NCAPG I442M and GDF8 Q204X. Association analyses were performed with a single locus and a 2 locus model fitting a fixed effect of the year of birth, an additive genetic SNP effect and an infinitesimal polygenic animal effect. The NCAPG 442M allele that had been associated with increased birth weight, showed a significant effect ($P = 0.0001$) increasing body weight at 18 mo of age. The locus explained 9.3% of the variance in the model. The effect of the loss-of-function allele GDF8 204X on body weight was also significant ($P = 0.006$). The difference between alleles amounted to 25.4 kg (std. err. 6.34 kg) for NCAPG I442M and 30.0 kg (std. err 12.5 kg) for GDF8 Q204X, respectively. For the 2-locus model, effects of essentially the same magnitude were obtained. In conclusion, both, the NCAPG I442M locus and the GDF8 Q204X locus, exhibit significant, independent effects on postnatal growth.

Key Words: postnatal growth, cattle, NCAPG

636 Maternal nutrition differentially influenced gene expression responsible for fetal bovine adipocyte development. T. D. Jennings*, K. R. Underwood, A. E. Wertz-Lutz, and A. D. Weaver, *South Dakota State University*, *Brookings*.

Maternal nutrition during mid-late gestation influences adipose development in the fetus of various species, however bovine research is limited. The objective of this experiment was to determine the effects of maternal nutrition on the expression of genes in bovine fetal tissues. Genes of interest were selected because each has been demonstrated previously to influence body composition. Twenty-two Angus cross-bred heifers (BW = 527.73 ± 8.3 kg) were assigned randomly to 3 dietary treatments. Maternal dietary treatments were formulated and intake was controlled to provide 150% (HIGH; n = 7), 100% (INT; n = 7), and 80% (LOW; n = 8) of maintenance energy requirements for growing pregnant heifers. Heifers received dietary treatment from d 85 to d 180 of gestation, at which time fetuses were removed via cesarean section and muscle, subcutaneous fat, and liver samples were collected. At trial initiation, dam BW was similar among treatment groups. Final BW was lowest for the LOW dams ($P < 0.05$), however final BW for INT and HIGH were similar. Ribfat thickness increased in the HIGH treatment group compared with LOW and INT dams ($P < 0.05$). Thus, dam growth was influenced by diet during the treatment period, however dietary treatment did not influence fetal weight, crown rump length, or liver weight. Preadipocyte factor-1 showed increased expression in fetal LM ($P < 0.05$) of HIGH fetuses as compared with INT and LOW. Peroxisome proliferator-activated receptor gamma and C/EBPα did not differ as a result of dietary treatment. However, LOW fetuses showed increased C/EBPβ expression as compared with INT ($P < 0.05$). Collectively these results suggest that fetal growth characteristics are not affected by maternal nutritional manipulation during mid-gestation in beef cows. However, differences in expression of fetal genes regulating adipose tissue growth and development could lead to differences in composition of growth and warrants further investigation.

Key Words: adipose tissue, beef cattle, fetal programming

637 Lipid accumulation and fibrosis in skeletal muscle of offspring born to obese dams. X. Yan*[1], Y. Huang[1], M. J. Zhu[1], N. M. Long[1], A. B. Uthlaut[1], R. J. McCormick[1], S. P. Ford[1], P. W. Nathanielsz[2], and M. Du[1], [1]*Department of Animal Science, University of Wyoming*, *Laramie,* [2]*University of Texas Health Science Center*, *San Antonio*.

Enhancing adipogenesis in muscle increases intramuscular adipocytes, while increasing fibrogenesis would affect meat tenderness. The objective was to evaluate the effects of maternal obesity on the intramuscular fat and collagen content of offspring muscle. Multiparous ewes (Rambouillet/Columbia cross) were fed a control diet (100% energy requirement, Con, n = 8) or an obesogenic diet (150% energy requirement, OB, n = 9) from 2-mo before pregnancy to parturition. Then, offspring lambs were fed commercial feeds to 22 mo old. The Longissimus dorsi (LD) muscle (2g) was biopsied at the left 12th rib for histochemical examination, mRNA and protein expression analyses and collagen content assessment. Mean ± standard errors of means are reported. No difference was observed in maternal body weight (68.3 ± 2.9 kg vs. 71.6 ± 3.2 in Con and OB) or body condition score (4.9 ± 0.4 in Con and 5.0 ± 0.3 in OB) before dietary treatments. Following 2 mo treatment (before mating), both maternal body weight (73.1 ± 4.0 vs.108.8 ± 3.1 in Con and OB, $P < 0.05$) and maternal body condition score (4.9 ± 0.3 vs. 8.6 ± 0.2, $P < 0.05$) were higher on OB compared with Con diet. More intramuscular adipocytes were observed in OB offspring muscle compared with Con muscle; the mRNA expression of peroxisome proliferator-activated receptor (PPAR) γ, an adipocyte marker, was 33.6 ± 15.6% higher ($P < 0.05$) in OB, and the protein content was 51.1 ± 5.1% greater ($P < 0.05$), consistent with the 32.1 ± 9.8% higher intramuscular triglyceride content in OB compared with Con muscle ($P < 0.05$). The mRNA and protein contents of fatty acid transport protein 1 (FATP1) were increased in OB group by 61.8 ± 24.8% and 40.8 ± 9.3% ($P < 0.05$) respectively. We also detected 39.4 ± 8.8% higher mRNA expression for fatty acid translocase (FAT)/CD36 ($P < 0.05$). In addition, 50.6 ± 15.3% higher collagen content was detected in OB compared with Con offspring muscle ($P < 0.05$). In conclusion, maternal obesity increases intramuscular fat and collagen contents in offspring muscle, which results in changes of skeletal muscle composition and might affect the quality of resulting meat.

Key Words: maternal obesity, collagen, muscle

638 Enhanced transforming growth factor β (TGF-β) signaling and fibrogenesis in ovine fetal skeletal muscle of obese dams at late gestation. Y. Huang*[1], X. Yan[1], M. J. Zhu[1], R. J. McCormick[1], S. P. Ford[1], P. W. Nathanielsz[2], and M. Du[1], [1]*Department of Animal Science, University of Wyoming*, *Laramie,* [2]*University of Texas Health Science Center*, *San Antonio*.

Maternal obesity is increasing at an alarming rate. The objective was to evaluate the effect of maternal obesity on fibrogenesis in fetal skeletal muscle at late gestation when ovine fetal muscle matures. Non-pregnant ewes were assigned to a control diet (Con, fed 100% of NRC nutrient recommendations, n = 6) or obesogenic diet (OB) fed 150% of NRC recommendations, n = 6) from 60 d before conception, and fetal semitendenosus (St) muscle was sampled at 135 d of gestation (term 148 d). The total concentration and the area of collagen in the cross-sections of muscle increased by 27.0 ± 6.0% ($P < 0.05$) and 105.1 ± 5.9% ($P = 0.05$) in OB compared with Con group. The expression of precursor TGF-β was 177.3 ± 47.6% higher ($P < 0.05$) in OB fetal muscle. The concentration of phospho-p38 was 74.7 ± 23.6% higher ($P < 0.05$) in OB group. An increase of 327.9 ± 168.0% ($P < 0.05$) and 188.9 ± 82.1% ($P < 0.05$) respectively for the mRNA expression of Smad7 and fibronectin was observed in OB compared with Con samples. In addition, enzymes involved in collagen synthesis, including lysyl oxidase, lysyl hydroxylase 2b and prolyl 4-hydroxylase α1 were increased by 350.2% ± 90.0% ($P < 0.05$), 236. Five ± 25.2% ($P < 0.05$) and 82.0 ± 36.2% ($P = 0.05$) respectively in OB muscle. In conclusion, maternal obesity enhanced fibrogenesis in fetal muscle at late gestation which was associated with upregulation of TGF-β/p38 signaling pathway. Because muscle fibrosis is a hallmark of aging, enhanced fibrogenesis at such an early stage of development is expected to negatively affect the properties of offspring muscle.

Key Words: collagen, TGF, muscle

639 Up-regulation of nutrient transporters in the placenta of nutrient restricted pregnant ewes. Y. Ma*[1], M. J. Zhu[1], P. W. Nathanielsz[2], and S. P. Ford[1], [1]*Center for the Study of Fetal Programming, Univ. of Wyoming*, *Laramie,* [2]*Center for Pregnancy and Newborn Research, Univ. of Texas Health Sciences Center*, *San Antonio*.

In sheep, maternal:fetal exchange occurs in placentomes, comprised of uterine caruncular and placental cotyledonary (COT) tissues. Glucose transporters (GLUT) and fatty acids transporters (FATP) in COT deliver glucose and long chain fatty acids (LCFA) to the fetal compartment. We have reported that fetuses from ewes fed to 50% NRC recommendations from 28 to 78 d of gestation (dGA; nutrient restricted, NR) weighed ~30% less than fetuses gestated by control ewes (C, 100% of NRC) at 78dGA. In contrast, NR fetuses exhibited a marked increase of LCFA storage in their lung, liver and muscle. When NR ewes were re-alimented to a C diet from 78dGA, their fetuses exhibited weights similar to C fetuses by 135dGA. COT tissue collected on 78 and 135 dGA was used to investigate GLUT and FATP systems via Realtime PCR and Western blot. Ewes assigned to C (n = 5) and NR (n = 6) groups were necropsied on 78dGA, while 6 C and 7 NR-realimented ewes were fed the C diet from 78 to 135dGA before necropsy. At 78dGA, COT GLUT1 mRNA and protein levels were greater ($P < 0.05$) in NR than C ewes. Similarly, COT FATP4 mRNA and protein levels were greater ($P < 0.05$ and $P = 0.06$, respectively), and CD36 mRNA and Protein levels tended to be greater ($P = 0.06$) in NR versus C ewes. At135dGA, COT FATP4 mRNA and protein levels tended to remain elevated ($P = 0.06$ and $P = 0.09$, respectively) in NR-realimented versus C ewes. CD36 and GLUT3 protein levels also tended to remain elevated ($P = 0.08$ and $P < 0.05$, respectively) in NR-realimented versus C ewes on 135dGA. The increased COT GLUT and FATP expression in NR versus C ewes at 78dGA is consistent with increased placental efforts to increase maternal nutrient transfer to the fetus. The continued elevation in COT GLUT3, FATP4 and CD36 expression after realimentation of NR ewes, would facilitate delivery of the increased blood levels of maternal nutrient to the fetus, accelerating its growth, and possibly causing metabolic problems in postnatal life.

Key Words: maternal nutrient restriction, placental nutrient transport, sheep

640 Effect of grouping calves post-weaning according to pre-grouping feed intake on animal performance. C. M. Matuk*[1], M. Chahine[1], A. Bach[2,3], B. Ozer[1], M. E. de Haro Martí[3], J. B. Glaze Jr.[1], T. Fife[1], and M. Nelson[1], [1]*University of Idaho*, *Twin Falls*, [2]*IRTA*, *Caldes de Montbui, Spain*, [3]*ICREA*, *Barcelona, Spain*, [4]*University of Idaho*, *Gooding*.

The effect of grouping calves post-weaning according to pre-grouping feed intake on animal performance was evaluated using 752 replacement Holstein calves raised on a large operation in southern Idaho. In 4 different periods, individual feed intake was recorded 4 times a week during the last 3 wk that calves were individually hutched (56 d of age). Calves were classified as ′high eaters′ (highest feeding level quartile) and ′low eaters′ (lowest feeding level quartile). When leaving the individual hutches in each period, calves formed 6 groups: 20 animals randomly chosen without considering their level of feed intake (Control), 20 calves within the highest quartile of feed intake during the 3 wk prior leaving the hutches (HH), 20 within the lowest quartile (LL), 5 calves from the lowest and 15 from highest feeding level (LHH), 15 calves from the lowest and 5 from highest feeding level (LLH), and 10 calves from the highest and 10 from lowest feeding level (HL). Thus, out of 752 initially-tracked heifers, 480 heifers were chosen to form the 20 groups (6 groups per period) that were studied. Pen feed intake was recorded during the first 4 wk after grouping. After grouping, calves received a TMR composed of 95% starter and 5% alfalfa. Final weight was recorded at the end of the 12 wk of study. Pen was the experimental unit. Data were analyzed using a mixed-effects model with repeated measures accounting for the random effect of period and pen and the fixed effects of treatment, intake level class, time of measurements, and their 2-way interaction. Average DMI after grouping was greatest ($P < 0.05$) in HH (2.24 kg/d) and HHL (2.15 kg/d) followed by HL (2.07 kg/d), Control (2.06 kg/d), LLH (1.92 kg/d) and LL (1.77 kg/d). Similarly, ADG was greatest ($P < 0.05$) in HH (694 g/d) and HHL (658 g/d) than in HL (584 g/d), LLH (571 g/d), Control (546 g/d), and LL (531 g/d). The coefficient of variation of final BW (at 84 d of age) was lowest ($P < 0.05$) for HH (9.3%) and LL (11.7%), followed by Control (12.9%), LLH (15.8%), HHL (13.5%), and HL (17%). Grouping calves according to pre-weaning intake improves overall animal performance and diminishes variation.

Key Words: calves, heifers, intake

641 Evaluation of serum protein-based arrival formula and serum protein (Gammulin) on growth, morbidity, and mortality of stressed dairy calves. A. Pineda*[1], J. K. Drackley[1], and J. M. Campbell[2], [1]*University of Illinois*, *Urbana,* [2]*APC, Inc.*, *Ankeny, IA*.

Appropriate nutrition is a crucial factor to decrease morbidity and mortality of pre-weaning dairy calves. Several nutritional additives are available that may help to achieve this goal; however, their effectiveness is uncertain. The objective of this study was to evaluate a serum protein-based arrival formula (AF) and use of a commercial serum protein supplement (G; Gammulin, APC Inc.) in milk replacer for stressed (transport, cold) male calves on performance, morbidity, and mortality. Ninety-three male Holstein calves were stratified by arrival BW and plasma protein, and then randomly assigned to 1 of 4 treatment groups: Treatment A = AF, milk replacer without G (n = 22); Treatment B =

control electrolyte, milk replacer without G (n = 25); Treatment C = AF, milk replacer with G (n = 22); and Treatment D = control electrolyte, milk replacer with G (n = 24). At arrival, calves were fed either AF or a control electrolyte solution. At the next feeding, all calves received either a commercial calf milk replacer (20% CP, and 20% fat; no G supplementation) or the same milk replacer supplemented with G (50 g/d during the first 14 d only). Feed offered and refused was recorded daily. Calf health was assessed by daily assignment of scour and respiratory scores. Body weight, withers height, body length, heart girth, hip height, and hip width were measured weekly. Calves remained in the experiment until d 56. Data were analyzed using the MIXED procedure of SAS (v. 9.2). Results indicated that, during the first 2 wk of dietary treatment, calves fed AF had significantly greater hearth girth ($P = 0.05$) and body length ($P = 0.03$), while G supplementation resulted in greater BW ($P = 0.05$). In addition, a significant ($P = 0.03$) interaction of G × week was observed for ADG. Mortality was greater ($P = 0.007$) for calves that did not receive G. Addition of a serum protein product improved early growth and decreased mortality in transported male calves.

Key Words: calves, serum protein, Gammulin

642 The effect of maternal exercise on gestating gilts on neonatal piglet organ weight. E. K. Harris*, K. A. Vonnahme, J. D. Kirsch, J. D. Magolski, T. L. Neville, and E. P. Berg, *North Dakota State University*, *Fargo*.

To determine the effects of maternal exercise of gestating gilts on fetal piglet development and growth, Yorkshire gilts (n = 8), bred to a common boar, were placed in individual gestation stalls at d 30 of gestation. Treatments were assigned and initiated at d 40 of gestation. Exercise gilts (EX) were housed in individual gestation stalls but were individually exercised 3 times per week for 30 min until d 105 of gestation. Control gilts (CON) remained in gestation stalls for the duration of gestation. All farrowings were attended. Within 12 h of completion of farrowing, the lightest (LWT) and heaviest (HWT) male and female from each litter, excluding piglets <800 g, were selected for necropsy. Adrenal glands, brain, digesta, heart, kidneys, intestines, liver, lung, pancreas, spleen, stomach, gonads, semimembranosus (SM) and semitendinosus (ST) were dissected and weighed. Organ weights (g) and organ weight/live BW (g/g) were analyzed by PROC MIXED. Live weight of necropsied piglets was greater in offspring from EX gilts ($P = 0.03$; 1282.06 and 1698.70 ± 125.40 g). Piglets from EX gilts had larger adrenal glands (g) ($P < 0.01$), kidneys (g) ($P < 0.01$), liver (g) ($P < 0.01$), and stomach (g) ($P < 0.01$) than CON gilts. Piglets from EX gilts had a tendency ($P < 0.10$) to have more digesta (g), heavier hearts (g), intestines (g), spleen (g), and SM (g/g). The brain and pancreas were the only organs not affected by treatment. Treatment by weight interaction occurred in liver (g/g) ($P = 0.05$), ovaries (g) ($P = 0.02$), and uterus (g/g) ($P < 0.01$). Light weight EX offspring had larger liver (g/g) ($P < 0.001$) compared with LWT CON offspring but were not different compared with HWT CON and EX treatments. LWT CON livers were also smaller than HWT EX ($P = 0.01$) but not different than HWT CON livers. Ovaries (g) were lightest in gilts from LWT CON gilts compared with all other treatment groups ($P < 0.05$). Light weight CON offspring had heavier uteri (g/g) compared with all other treatment groups ($P < 0.05$). Maternal activity during mid to late gestation influenced the developmental composition of the neonate.

Key Words: neonatal offspring, organ weights, pigs

643 Changes in gene expression during pituitary morphogenesis and organogenesis in embryonic chicks. M. Proszkowiec-Weglarz*, S. E. Higgins, and T. E. Porter, *University of Maryland, Department of Animal and Avian Sciences*, *College Park*.

The anterior pituitary gland (AP) plays an important role in the regulation of many physiological processes in vertebrates. Formation of Rathke's pouch (RP), the precursor of the AP, involves invagination of the oral ectoderm (OE) and a multi-step process regulated by cell interactions, signaling pathways and transcription factors. In contrast to mammals, the molecular mechanisms underlying development of the AP in birds are poorly understood. Thus, the aim of this study was to evaluate tissue-specific gene expression patterns in the developing chicken AP. OE/RP and the adjacent neuroectoderm (NE) were collected by laser capture microdissection from 60 paraffin-embedded chicken embryos at 12-h intervals from embryonic day (e) 2.5 to e7 (n = 3 replicates). After RNA isolation and amplification, quantitative real-time PCR was performed to determine RP- and NE-specific gene expression. RP was formed by invagination of OE around e2.5, and by e6-e6.5 RP lost its connection with the oral cavity and proliferated to form the AP. Among genes involved in early pituitary organogenesis, *Pitx1*, *Pitx2* and *Hesx1* showed high expression at e2.5 in RP that decreased during development ($P < 0.05$). Expression of pituitary cell lineage specification and differentiation genes (*Pit1* and *Tbx19*) increased gradually, reaching the highest level by e7 and e6.5 in RP, respectively ($P < 0.05$). *Alpha-GSU*, encoding a common glycoprotein subunit of gonadotropins and thyrotropin, showed increasing mRNA expression from e4 ($P < 0.05$). *BMP4*, *BMP2*, *Wnt5a*, *Isl1* and *Noggin* were expressed in both RP and NE, while *Nkx2.1* showed NE-specific expression during AP formation. Taken together, we present a gene expression profile of the developing AP in the chicken. Our results will be helpful in better understanding the functional development of this gland, which is critical for controlling animal growth, reproduction, metabolism, and stress responses.

Key Words: Rathke's pouch and neuroectoderm, pituitary development, chicken embryo

644 Effects of in ovo feeding of carbohydrates and arginine on the energy metabolism, protein status and perinatal growth in Pekin ducks. M. Tangara*, W. Chen, F. R. Huang, and P. Jian, *Laboratory of Animal Molecular Nutrition, Department of Animal Nutrition and Feed Science, Huazhong Agricultural University*, *Wuhan, Hubei, P. R. China*.

The objective of the present study was to determine the effects of in ovo feeding of exogenous nutrients on the glycogen reserves, protein status and early growth of Pekin ducks. To this end, based on randomized completely block design, 750 fertile eggs were divided into following 5 groups of 150 eggs: 1) Uninjected; 2) 0.35% sodium chloride (NaCl); 3) 2.5% sucrose + 3% maltose (CHO); 4) 0.22% arginine (Arg); and 5) 2.5% sucrose + 3% maltose + 0.22% arginine (CHO+Arg). At 23 d of incubation, 1.2 mL of each solution was injected into amniotic fluid of each group using a 22-gauge needle. Ten eggs/ducklings per treatment were sampled at 25 d of incubation, hatch, 3 and 7d of age to determine liver and muscle glycogen, glucose-6-phosphatase (G6P) activity and different protein expression including S6K1 (S6 kinase1), phosphorylated S6K1 and phosphorylated adenosine monophosphate-activated protein kinase (AMPK) using iodine reduction test, colorimetric oxidase test and Western blot, respectively. Maximal hatchability was found in the group ($P < 0.05$) fed with CHO+Arg (94%) followed in order by Arg (90%), CHO (89%), uninjected control (85%) and NaCl (80%). All the ovo fed ducklings improved BW at hatch, 3, 7, 14, 21, 28 and 35 d of age related to uninjected ($P < 0.05$). Arg and CHO+Arg had significantly enhanced the liver glycogen by 188% and 249%, respectively at hatch ($P < 0.01$) compared with that of uninjected group.

CHO and CHO+Arg significantly increased muscle glycogen level ($P < 0.01$) by 22% and 42%, respectively at 25 d of incubation over the uninjected group. CHO and Arg had significantly decreased ($P < 0.01$) G6P by 41% and 30%, respectively at 25 d of incubation, whereas NaCl and CHO+Arg increased G6P by 30% and 20%, respectively at hatch in comparison with the uninjected group ($P < 0.01$). At 25 d of incubation, hatch, 3 and 7d posthatch, greater values of S6K1 and S6 phosphorylation were observed in duck embryos and neonates fed with Arg and CHO+Arg. The activation of AMPK was also detected in the group fed with Arg and CHO+Arg. The present results indicated that in ovo feeding CHO and Arg may improve glycogen storage and muscle protein deposition in ducks

Key Words: in ovo feeding, energy, protein, metabolism, growth, ducks

645 The effect of induced moisture loss on embryonic development of pekin ducks. C. Noonan* and M. S. Lilburn, *Ohio State University/OARDC*, *Wooster*.

Moisture loss in commercial Pekin duck eggs during incubation is often variable and accelerated moisture loss may contribute to excessive hatchling dehydration and adversely effect later developing systems such as the intestine. Two experiments were conducted to determine the effect of induced moisture loss on embryonic development. In both experiments, commercial duck eggs were individually weighed at set. At 12 d, all eggs were reweighed and randomly allocated to one of 4 treatments consisting of 0, 1, 2, or 3 holes (Experiment 1; n = 40 per treatment) or 0, 1 or 2 holes (Experiment 2; n = 120 per treatment). The holes (<1 mm) were drilled above the air sac. All eggs were reweighed at approximately 2-d intervals. All data was analyzed by ANOVA using the PROC Mixed program (SAS Inc.) and least squares means were separated using LSD. In Experiment 1, there were no differences in initial egg wt or moisture loss (4.67%; $P > 0.05$) at 12 d. On D 14 and all sample days thereafter, there were incremental increases in moisture loss with each additional hole ($P < 0.01$). At D 19, the range was 7.35% (0-hole) to 20.86% (3-hole) and the experiment was terminated. In Experiment 2, the range was from 5.32% (0-hole) to 7.34% (2-hole) on D 14 ($P < 0.01$) and 8.03% (0-hole) to 15.15% (2-hole) on D 19. On Day 20, a sample of embryos from each treatment (n = 25) was broken out for embryo weight determination. Wet embryo weight was heavier ($P < 0.01$) in the 1-hole treatment (36.7 g) compared with the 0-hole (33.9 g) and 2- hole (31.8 g) treatments. The same pattern was observed for dry embryo weight. There was a progressive decrease in hatch weight ($P < 0.05$) as moisture loss increased (0-hole, 55.3 g; 1-hole, 53.6 g; 2-hole, 52.3 g) but no effects on intestinal measures (villus height; crypt depth). In conclusion, major differences in moisture loss during incubation in Pekin duck embryos have only a small effect on body weight or physiological status at hatch.

Key Words: Pekin, embryo, incubation

646 Bone development of three breed crosses of broilers is affected by incubation profiles. E. O. Oviedo-Rondón*, M. J. Wineland, C. M. Ashwell, and P. R. Ferket, *North Carolina State University*, *Raleigh*.

Genetics, maternal nutrition, and incubation conditions affect bone development in broilers. One experiment was conducted to observe epigenetic effects of 2 incubation temperature profiles on bone development in 3 groups of broilers (A, B, C) differing in genetic background and maternal nutrition. Group A was the final cross of this strain; and B and C were the progeny of the male line either feed restricted or with no feed restriction. The first incubation profile followed standard (SS) temperatures to maintain eggshell temperature (EST) at 37.5°C. The second profile (LH) was similar to what one observes when eggs are in a multi-stage incubation system, the first 7 d EST was maintained at 36.5°C EST, during the second 7 d at 37.5°C EST and the remaining days at 39°C EST. At hatch, a random sample of 8 chicks per treatment were collected, weighed, sacrificed, and residual yolk determined. Both legs were dissected and shank and femur weights, lengths, and thickness were obtained. Relative asymmetry and weight relative to BW without yolk (%) of each leg section were calculated, and bone density estimated as g/mm. A total of 288 chicks were randomly placed in 48 battery cages and raised until 21 d. Bones were collected again at 14 and 21 d and similar parameters evaluated. Data were analyzed as a 2x3 factorial design considering incubation profiles and genetic strain as main factors. No consistent interactions were observed. Chickens from C group were heavier than B chickens only at hatch. The B group had the shortest bones and the lowest femur density. The C group was heavier at 14 d, but no other effects of epigenetics were observed. The LH profile reduced yolk absorption, and weight, length, width and density of all bones at hatch. Similar effects of incubation were observed at 14 and 21 d of age. The LH profile caused shorter bones, with lower density, and higher asymmetry independently of the genetic group. These results indicated that incubation profiles may have more importance on bone development than the genetic background, and the epigenetic effects of parental feed restriction were only observed at hatch.

Key Words: bone development, incubation, epigenetics

647 Effect of in ovo selenium injection on chick embryo viability and tissue selenium levels. L. M. Macalintal*, A. H. Cantor, A. J. Pescatore, M. J. Ford, H. D. Gillespie, J. L. Pierce, K. A. Dawson, and R. F. Power, *Alltech-University of Kentucky Nutrition Research Alliance*, *Lexington*.

The effect of injecting graded levels of selenium (Se) as selenomethionine (SeMet) or sodium selenite (Na_2SeO_3) into the yolk of incubating eggs on embryo viability and liver Se levels was studied. Fertile eggs were obtained from white shell laying hens (Hy-Line W-36) that were fed a low Se corn-soybean meal diet. On Day 10 of incubation, eggs were candled to ensure embryo viability. The shell surface was disinfected with alcohol and a small hole was drilled over the air cell. The yolk of each of 30 eggs per treatment was then injected with 0.1 mL of a phosphate buffered saline solution providing 0, 2.5, 5, 10 or 20 µg Se as either SeMet or Na_2SeO_3. In a control group of eggs holes were drilled in the shell, but no injection was administered. The holes were sealed with glue and eggs were returned to the incubator. On Day 20 of incubation, eggs were candled to determine viability. Viable embryos were then killed to obtain tissue samples. Liver samples were analyzed for Se using fluorometric analysis following digestion in nitric and perchloric acids. Embryo viability values for the non-injected eggs and eggs injected with buffer without Se were 100% and 94%, respectively. Viability values for eggs injected with 2.5, 5, 10 and 20 µg Se as SeMet were 97, 94, 90 and 83%, respectively, while the respective values for eggs treated with Na_2SeO_3 were 87, 94, 74 and 87%. Injecting graded doses of Se resulted in linear increases ($P < 0.001$) in liver Se. However, the regression coefficient for Na_2SeO_3 was greater than that for SeMet (0.059 vs. 0.014). The results indicate that in ovo injection of Se as SeMet or Na_2SeO_3 at levels up to 20 µg does not have a detrimental effect on embryo viability. The effects of the SeMet and Na_2SeO_3 on liver Se concentrations suggests that the compounds are metabolized differently by the chick embryo.

Key Words: in ovo injection, selenium, embryo viability

Immunology and Pathology: Poultry Immunology and Diseases

648 Testosterone exposure alters embryonic bursal gene expression in chicken lines selected for differential antibody response. R. L. Taylor, Jr.*[1], T. Burks[1], C. Timmerman[2], P. B. Siegel[3], and C. M. Ashwell[2], [1]*University of New Hampshire*, *Durham,* [2]*North Carolina State University*, *Raleigh,* [3]*Virginia Tech*, *Blacksburg*.

Chicken B cells mature in the bursa of Fabricius (BF) microenvironment producing antibody diversity through their V-gene repertoire. Testosterone propionate (TP) exposure on d 3 of incubation severely impairs BF development, elevates IgM, lowers IgG and causes bursal epithelial cell proliferation. From a common founder population, White Leghorn lines selected for high (HAS) or low (LAS) antibody produced 5 d after a 0.25% SRBC suspension (0.1 mL) injected intravenously, have a several fold difference in anti-SRBC antibody titer. Eggs from the 34th selected generation were dipped in a 2% TP ethanol solution or ethanol alone for treatment and control groups, respectively. We examined gene expression in bursal tissue collected from 4 embryos of each line and treatment (HAS, HAS TP, LAS, LAS TP) at 15, 18, and 21 d of incubation. Tissue samples were held in RNALater at −80 C until RNA was extracted followed by reverse transcription to cDNA. Individual cDNA samples, labeled indirectly with Cy3 or Cy5 fluorescent dyes, were hybridized including a dye swap to a 320 gene focused microarray. Each gene, represented by a 70-mer oligonucleotide, was spotted 12 times in a single array enhancing sensitivity to detect sample group differences. Fluorescent intensity data were transformed via log2, normalized by weighted regression, and analyzed by a mixed-model ANOVA. Pathway, process and networks were evaluated using the Metacore database. Growth hormone (GH), growth hormone receptor (GHR), thyroid hormone receptor α, and hemoglobin rho expression was higher in Line LAS controls than Line HAS controls. TP treatment in Line LAS elevated GH and GHR genes as well as interleukin(IL)-1 whereas Line HAS TP embryos had higher fibroblast growth factor 1 and endothelin receptor expression. Network analysis identified biomarkers associated with pathways for immune response IL-1, immune response NK2g, and developmental growth hormone signaling. Real-time PCR confirmed gene expression differences found on the microarray.

Key Words: immune response, microarray, bursa of Fabricius

649 Limiting dilution studies to detect avian influenza viruses from questionable allantoic fluid samples. T. V. Dormitorio* and J. J. Giambrone, *Auburn University*, *Auburn, AL*.

Detection of avian influenza viruses (AIV) from wild birds can be complicated when there is the presence of other hemagglutinating agents, including some avian adenoviruses, mycoplasma, Newcastle disease virus (NDV), and other paramyxoviruses (APMV). Moreover, dual isolations of influenza virus and APMVs are not unusual. Limiting dilution studies were conducted using fecal swab samples collected from wild birds, which were determined to be AIV positive by real-time RT-PCR (rRT-PCR), but had high crossing point (Cp) values (>32). The NVSL failed to isolate AIV from 2 of these samples, but instead they reported the presence of APMV-1 and APMV-4. Results showed that AIV positive samples, with high Cp, had either AIV, APMV, or both. The effect of egg passage on AIV detection by rRT-PCR had lowered Cp, indicating that there was an increase in the detectable virus. When there was a mixed infection, several dilutions and passages were needed to separate the viruses. Moreover, the presence of APMVs may have interfered with AIV detection, and thereby produced false positive AIV rRT-PCR results.

Key Words: avian influenza virus, avian paramyxovirus, real-time RTPCR

650 Development and characterization of mouse monoclonal antibodies reactive with chicken CD80. S.-H. Lee*[1], H. Lillehoj[1], M.-S. Park[1], K.-W. Lee[1], C. Baldwin[2], D. Tompkins[2], B. Wagner[3], U. Babu[4], and E. Del Cacho[5], [1]*Animal and Natural Resources Institute, ARS-USDA*, *Beltsville, MD,* [2]*University of Massachusetts*, *Amherst,* [3]*Cornell University*, *Ithaca, NY,* [4]*Food and Drug Administration*, *Laurel, MD,* [5]*University of Zaragoza*, *Zaragoza, Spain*.

The CD80 (B7.1) is a molecule found on monocytes providing a signal necessary for T cell activation and interferon-γ production. The characteristics of this molecule have been studied in human, swine, ovine, feline, and canine. However, information about CD80 and its antibodies (Abs) in chicken has not been reported. To develop immune reagents for chicken CD80 (chCD80), we have immunized mice with recombinant chCD80, and hybridomas producing monoclonal Abs against chCD80 were produced. Recombinant chCD80/IgG4 fusion protein was expressed in mammalian cells and chCD80 was purified and used to immunize mice. In this study, 158 hybridomas were screened and 3 mAbs with high binding specificity against chCD80-transfected cells were selected by flow cytometric analysis. Western blot showed a 80 kDa protein against chCD80. Monoclonal Abs to chCD80 showed staining of chicken macrophage cell line (HD11), bursa, and spleen. Taken together, mouse monoclonal antibodies specific for chicken CD80 have been developed and these immune reagents will be useful tools to analyze CD80 activity during infections and to do basic and applied research for poultry.

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Key Words: chickens, CD80, monoclonal antibody

651 Suppressive properties of chicken CD25$^+$ cells during lipopolysaccharide injection. R. Shanmugasundaram[1,2] and R. K. Selvaraj*[1,2], [1]*Ohio Agricultural Research and Development Center*, *Wooster,* [2]*The Ohio State University*, *Wooster*.

Suppressive properties of splenic chicken CD25$^+$ cells were evaluated during in vivo lipopolysaccharide (LPS) injection. One-week-old chickens were injected with 0 or 100 μg of LPS/kg body weight. Spleen CD4+8–25+ cell percentage increased from 8% to 24% at 4 d post-LPS injection. Spleen CD4+8–25+ cell percentage decreased to 11% at 5 d post-LPS challenge, but remained greater than the 0 μg LPS control group until 12 d post-LPS injection. Suppressive properties of CD25$^+$ cells were determined by naïve cell proliferation suppression assay. At CD25$^+$:T responder cell ratio of 1:1, CD4+8–25+ cells collected at 5 and 12 d after 100μg LPS injection were suppressive while CD4+8–25+ cells collected at 2 d after 100 μg LPS injection were not suppressive. CD4+8–25+ cells collected at 5d after LPS injection had a greater suppressive potential in the 100 μg LPS group than CD4+8–25+ cells from the 0μg LPS group. At 5 d post LPS injection, CD4+8–25+ cells from 100 μg LPS injection were suppressive at CD25$^+$:T responder ratio of 0.25:1, while those from 0 μg LPS injection were suppressive only at Treg:T responder ratio of 1:1, but not at 0.25:1. It could be concluded that in vivo LPS treatment alters the suppressive properties of chicken CD25$^+$ cells.

Key Words: T regulatory, suppression, LPS

652 Expression profile of cytokines in cecal tonsils of broiler chicks challenged with *Clostridium perfringens*. Y. O. Fasina*[1], H. S. Lillehoj[2], M. S. Park[2], and D. E. Conner[1], [1]*Auburn University*, *Auburn, AL*, [2]*USDA-ARS-ANRI-APDL*, *Beltsville, MD*.

Necrotic enteritis is an economically important enteric disease of poultry that is caused by *Clostridium perfringens* (CP). Understanding the role of cytokines in modulating intestinal innate immune response to CP will facilitate the design of effective non-antibiotic control measures such as vaccines. An experiment was conducted to determine the effect of CP infection on the expression of selected T helper type 1 (Th1 - inflammation-inducing) and T helper type 2 (Th2 - antibody-inducing) cytokines in the cecal tonsils of broiler chicks. Chicks (400) obtained from a commercial hatchery were randomly assigned to 4 treatments. Treatment 1 (CX) consisted of chicks fed unmedicated corn-soybean meal (SBM) diet. Treatment 2 (MX) consisted of chicks fed corn-SBM basal into which bacitracin methylene disalicylate antibiotic was added at 0.055g/kg. Treatments 3 (PCX) and 4 (PMX) consisted of chicks fed diets similar to those given to CX and MX, respectively, and were additionally challenged with 3.5 mL of CP inoculum (10^8 CFU/mL) on d 14, 15, and 16 of experiment. At 1 and 7 d post-challenge, intestinal CP levels were estimated. Cecal tonsils were also collected and subjected to quantitative reverse transcriptase-polymerase chain reaction (qRT-PCR) to determine the expression levels of cytokine genes. From results, PCX and PCM (3.04 to 3.68 $\log_{10}$ CFU/mL) had higher CP levels ($P < 0.05$) compared with control CX and MX (1.12 to 1.70 $\log_{10}$ CFU/mL), thus confirming an established infection in PCX and PCM chicks. RT-PCR results showed upregulation of genes of several Th1/proinflammatory cytokines (interleukin [IL]-1β, IL-12, and lipopolysaccharide-induced TNF-associated factor], and to a lesser extent Th2 cytokines such as IL-13 in PCX and PCM ($P < 0.05$), compared with control CX and MX. There was no difference in anti-inflammatory IL-10 among treatments. It was concluded that cytokine response to CP infection in the cecal tonsil is more of a Th1 type which promotes cell-mediated immunity.

Key Words: *Clostridium perfringens*, cytokines, broiler chickens

653 Gel spray as a viable method to apply a coccidia vaccine to chickens. G. F. Mathis*[1], E. H. Lee[2], T. Cosstick[2], and B. Lumpkins[1], [1]*Southern Poultry Research, Inc.*, *Athens, GA,* [2]*Vetech Laboratories, Inc.*, *Guelph, Ontario, Canada*.

On day of hatch, chicks are routinely administered uniformly low doses of live coccidia oocysts to aid in the development of immunity against coccidiosis. Two studies were conducted to examine the novel approach of using a spray gel to orally deliver the oocysts to the chicks through mutual preening. In both studies, chicks were vaccinated with Immucox, a coccidia vaccine. In study 1, on d 21 chicks were individually weighed and challenged with field isolates of *Eimeria* (*E. acervulina* (EA), *E. maxima* (EM), *E. tenella* (ET), or *E. necatrix* (EN)). Individual bird weights and coccidia lesion scores were recorded on d 26 (6 d post challenge). EA, EM, ET, and EN lesion scores were significantly lower (greater than 1.5 score reduction for each species) and weight gain during the challenge period was significantly better than non-vaccinated challenged and equal to the non-vaccinated, non-challenged controls. Study 2 examined performance of non-vaccinated non-challenged, non-vaccinated challenged and Gel sprayed challenged. To represent a natural coccidiosis challenge, on d 28 all birds in the challenge groups were orally dosed with a mixture of EA, EM, and ET. Feed conversion and weight gain were determined on d 21 and at market weight (d 42). On d 21, weight gain was not significantly different among treatments. There was significantly higher feed conversion in the gel spray treatment birds than the non-vaccinated treatment birds. On d 42, gel spray treatment birds had significantly better feed conversion (1.859) and average live weight (1.985 kg) than non-vaccinated challenged (1.954 and 1.857 kg, respectively). However, the gel sprayed birds had significantly lower performance than the non-vaccinated non-challenged birds. Efficacy of the gel spray vaccination was indicated by the reduction in lesion scores and improvements in performance when compared with those of the non-vaccinated challenged control.

Key Words: coccidia, vaccine, chicken

654 A mixture of capsicum and turmeric oleoresins improve performance of vaccinated broilers challenged or not with coccidiosis. V. Brito*[1], C. Moynat[2], A. Casarin[3], M. Forat[3], and D. Bravo[2], [1]*Euronutec*, *Querétaro, Mexico*, [2]*Pancosma*, *Geneva, Switzerland*, [3]*Instituto Internacional de Investigacion Animal*, *Mexico*.

Capsicum (CA) and turmeric (TU) positively impact innate immunity. Their combination should improve performance of birds. Vaccines induce acquired immunity and are efficient in case of challenge. So combining CA, TU and vaccination should improve performance of birds infected by *Eimeria*. The objective was to evaluate the effect of a mixture of CA and TU oleoresins (PF = Proflora/XT 6986) on performance of vaccinated broilers challenged with coccidiosis, and non-challenged non-vaccinated birds. One-day-old broilers were allotted to the following treatments (48 birds × 10 cages/treatment), doses in ppm, with Bacitracin (BA), Nicarbazin (NI), Salinomycin (SA). T1b and T1a acted as positive controls either challenged or not (T1a = 125 NI + 55 BA from d1 to 28, 125 NI + 55 BA from d29 to 52; T1b = T1a + challenge to Eimeria spp. at d14). T2a tested the effect of PF on non vaccinated and non challenged birds (T2a = 50 PF from d1 to 42, 100 PF from d42 to 52). T2b tested the effect of PF on vaccinated and challenged birds (T2b = T2a + coccidiosis vaccine at d1 and challenge to *Eimeria* sp. at d14). BW, BWG and FCR were recorded. Data were analyzed using GLM procedure of SAS. Pre-challenge, T2a and T2b performed better ($P < 0.01$) than T1a and T1b for BWG (+8.2%), FCR (−5.5%) and BW at d14 (+6.9%), showing the positive effect of stimulating innate immunity on performance. T2a and T2b had similar ($P > 0.1$) BWG, FCR and BW, confirming that vaccination was not affecting performance without challenge. After d14, T2a and T2b exhibited same BWG, FCR and final BW ($P > 0.7$), as well as T1a and T1b ($P > 0.5$). This demonstrated that PF with vaccination can maintain the performance of challenged birds at the same level as non challenged birds. Finally, BW in T2a and T2b was 3.7% higher than in T1a and T1b ($P < 0.03$), suggesting that using PF during the whole growing period improved final BW of birds.

Key Words: essential oils, coccidiosis, vaccination

655 Cinnamaldehyde and a blend of capsicum and turmeric oleoresins improve performance of vaccinated broilers subject to coccidiosis. C. Moynat*[1], V. Brito[2], A. Casarin[3], M. Forat[3], and D. Bravo[1], [1]*Pancosma*, *Geneva, Switzerland*, [2]*Euronutec*, *Queretaro, Mexico*, [3]*Instituto Internacional de Investigacion Animal*, *Mexico*.

Cinnamaldehyde (CI), capsicum (CA) and turmeric (TU) positively impact innate immunity. The combination of these 3 products should positively affect immunity and improve performance of birds infected by *Eimeria*. The objective was to evaluate the effect of a mixture of CA and TU oleoresins (PF1 = Proflora / XT 6986) and a product with CI (PF2 = Proflora Plus / XT 6987) on performance of vaccinated broilers challenged with coccidiosis. Broilers vaccinated against coccidiosis at d 1 were allotted to 5 treatments and challenged at d 14 with *Eimeria* sp. (40 birds * 12 cages/treatment). The treatments were set as follow,

doses expressed in ppm, with Bacitracin (BA), Nicarbazin (NI), Salinomycin (SA): T1 = un-supplemented. For starter diet (d 1 to 14): T2 = 55 BA; T3 = 100 PF1; T4 = 100 PF1 + 10 PF2; T5 = 10 PF2. For grower diet (d 15 to 42): T2 = 55 BA + 50 NI + 30 SA; T3 = 100 PF1 + 50 NI + 30 SA; T4 = 100 PF1 + 5 PF2 + 30 SA; T5 = 100 PF1 + 10 PF2 + 30 SA. For finisher diet (d 43 to 52): T2 = 55 BA + 50 NI + 30 SA; T3 = 100 PF1 + 50 NI + 30 SA; T4 = 100 PF1 + 2.5 PF2 + 30 SA; T5 = 100 PF1 + 5 PF2 + 30 SA. BW, BWG and FCR were recorded. Data were analyzed using GLM procedure of SAS. Pre-challenge, there was no difference between treatments in BW, BWG, FCR ($P > 0.1$). Post-challenge, FCR of T1 was deteriorated (+4.3%, $P < 0.01$) showing the positive impact of supplementations on vaccinated birds subject to coccidiosis. No difference between supplementations was observed for FCR ($P > 0.1$). Final BW of T1 was lower ($P < 0.01$) than T2 (−4.2%), T3 (−4.8%) and T4 (−16.4%), and tended to be lower than T5 ($P = 0.08$). A higher inclusion of PF2 post-challenge is not beneficial for the supplementation program. These results show that a mixture of CA and TU oleoresins alone or combined with adequate doses of CI can be used with vaccination to maintain broiler performance.

Key Words: essential oils, cocciodiosis, vaccination

656 Ileal and cecal microbial populations and coccidia infection in broilers given probiotics and essential oil blends. M. E. Hume*[1], E. O. Oviedo-Rondón[2], N. A. Barbosa[2,3], N. K. Sakomura[3], M. C. Jenkins[4], and S. E. Dowd[5], [1]*USDA, ARS, FFSRU*, *College Station, TX*, [2]*Department of Poultry Science, North Carolina State University*, *Raleigh*, [3]*Universidade Estadual Paulista*, *UNESP-Jaboticabal, Brazil*, [4]*Animal Parasitic Diseases Laboratory, USDA, ARS*, *Beltsville, MD*, [5]*Research and Testing Laboratories, Medical Biofilm Research Institute*, *Lubbock, TX*.

A protective digestive microflora helps prevent and reduce broiler infection and colonization by enteropathogens. Some feed additives (FA) promote healthy and protective microbial populations (MP) and could be used as alternatives to antibiotic growth promoters. In the current experiment, broilers fed corn-soybean meal diets with inclusion of 5% DDGS and supplemented with essential oil (EO) blends and probiotics were infected with mixed *Eimeria* spp. to determine effects of these FA and *Eimeria* infection on ileal and cecal MP. The 8 treatments (Trt) included 4 controls: Uninfected-Unmedicated (UU), Unmedicated-Infected (UI), BMD+Coban as positive control (PC), and ionophore (Coban) as negative control (NC). The 4 Trt included FA: 2 probiotics, BC30, and Calsporin; and 2 EO, Crina POULTRY Plus (CPP) and Crina PoultryAF (CPF). Day-old male Ross broilers were raised to 14 d and inoculated at 15 d with *E. acervulina*, *E. maxima*, and *E. tenella*. Ileal and cecal samples were collected at 14 and 22 d (7 d post-infection). Digesta DNA was PCR-amplified at the 16S rDNA V3 region and analyzed by denaturing gradient gel electrophoresis (DGGE) to generate % similarity coefficients (%SC) on band pattern dendrograms. Coccidia infection, probiotic, and EO changed MP from those seen in UU ilea. Treatment with CPF greatly altered cecal MP. UU ilea MP had about 60%SC to those in other treatment groups. While CPF cecal MP at pre-challenge had 77.7%SC with other groups, there was a decreased to 54%SC at post-challenge. There were expected changes in pre- and post-challenge ileal and cecal MP, respectively, with CPF having the greatest treatment effect on digestive MP.

Key Words: coccidia, probiotic, essential oil

657 Effect of microbial-nutrition interaction on chicken immune system after the early administration of probiotic with organic acids in young chicks. J. C. Rodriguez-Lecompte*[1], J. Brady[1], G. Camelo-Jaimes[2], S. Sharif[3], G. Crow[1], G. O. Ramirez-Yañez[1], W. Guenter[1], and J. D. House[1], [1]*University of Manitoba*, *Winnipeg, Manitoba, Canada*, [2]*ADYZYME*, *Bogota, Cundinamarca, Colombia*, [3]*University of Guelph*, *Guelph, Ontario, Canada*.

The present study was conducted to characterize the effect of *Lactobacillus acidophilus*, *Streptococcus faecium*, and *Saccharomyces cerevisiae* and organic acids (e.g., sorbic acid and citric acid) on intestinal morphology, immunological parameters, and nutritional associated-genes. One-day old chicks were randomly allocated to one of 3 treatments: treatment 1 (T1) consisting of chicks not receiving either probiotic or organic acids; chicks in treatment 2 (T2) orally received probiotics and organic acids for 7 consecutive d; and treatment 3 (T3) chicks receiving probiotics and organic acids for 14 consecutive d. The study lasted 21 d. On d 11 and 21 (4 and 7 d after finishing T2 and T3 respectively), intestinal sections from duodenum (distal), jejunum (proximal to Meckel's diverticulum), ileum (proximal to ileo-cecal junction), and cecal tonsils were collected and analyzed by histology, reverse transcriptase-polymerase chain reaction (RT-PCR), and quantitative RT-PCR. T2 and T3 decreased ($P < 0.05$) villous height and width, crypt depth in the jejunum area during the first 7 d. At d 21, T3 affected increasing crypt depth and the number of goblet cells/mm2 in the jejunum and ileum area ($P < 0.05$). Regardless of the treatment at d 0, 11 and 21, there was only avian β-defensin (AvBD)3 mRNA expression in the crop, proventriculus, duodenum, jejunum, ileum, cecal tonsil and bursa; however, cathelicidin B1 was present in the bursa in all treatments after d 7. Interestingly, AvAng4 was not affected either by treatment or time. In the ileum area, only mRNA levels of interleukin (IL)-10 and IL-12 were affected by T2 and T3 at d 22 ($P < 0.05$). In cecal tonsils, IL-6 and IL-12 were affected by T2 and T3 at d 11 ($P < 0.05$); however, there was a significant downregulation of IL-12 and upregulation of interferon-γ at d 22 ($P < 0.05$). GHR and GHSR mRNA expression was detected in all the groups at d 11 and d 22. In conclusion, probiotic and organic acid effects on chick's intestine include triggering sensor molecules of the innate immune system, which may produce antimicrobial proteins and peptides.

Key Words: probiotic, defensin, cytokines

658 Probiotic, prebiotic and yeast supplementation in broiler diets from 1 to 42 days of age: 2. Immune response and slaughter traits. H. M. Safaa*[1], S. A. Riad[1], F. R. Mohamed[1], S. S. Siam[2], and H. A. El-Minshawy[3], [1]*Animal Production Department, Faculty of Agriculture, Cairo University*, *Giza 12613, Giza, Egypt*, [2]*Breeding Department, Animal Production Research Institute*, *Dokki, Giza, Egypt*, [3]*Ministry of Agriculture*, *Dokki, Giza, Egypt*.

A total of 630 Arbor Acres broiler chicks at one-day old was used to study the effect of probiotic, prebiotic and/or yeast supplementation on the immune response and slaughter traits. Chicks were divided randomly into 6 treatments and housed at deep litter in an open house system. The 6 treatments, each replicated 3 times (35 chicks/replicate), were as follows: T1 (control; chicks fed corn-soy basal diet), and the other treatments diets were supplemented with 1g probiotic/kg diet as *Lactobacillus acidophilus* (T2), 1g yeast/kg diet as *Saccharomyces cerevisiae* ($5x10^{12}$ CFU/g; T3), 1g prebiotic/kg diet as mannan-oligosaccharide (T4), 1g probiotic+1g prebiotic/kg diet (T5), or 1g yeast+1g prebiotic/kg diet (T6). Basal diet contained 23.1% CP and 3,103 kcal AME/kg for the starter diet (0–21 d) and 20.0% CP and 3,207 kcal AME/kg for the finisher diet (21–42 d). Results indicated that, all biological additives increased the total count of white blood cells, the antibody titer against sheep red blood cells and the relative weights of immune organs (bursa, spleen and thymus) at 42 d. However, heterophils/lymphocytes ratio was

not affected by any treatment. In addition, carcass, giblets and edible relative weights at 42 d of age were improved by using the biological feed additives. For all traits, the best values were obtained in T6 followed by T5. It could be recommended from this study to supplement the biological additives to broiler diet from 0 to 42 d of age as mentioned above because it improves the broiler immunity and slaughter traits.

Key Words: probiotic, prebiotic, yeast, broiler immune response, slaughter traits

659 Forage concentration and dried distillers grains with solubles in diets for lactating dairy cows. S. D. Ranathunga*, K. F. Kalscheur, A. R. Hippen, and D. J. Schingoethe, *South Dakota State University*, *Brookings*.

The objective of this study was to investigate the effects of concentrations of forages and dried distillers grains with solubles (DDGS) on production of lactating dairy cows. Twelve Holstein cows were assigned randomly to replicated 4 × 4 Latin squares in a 2 × 2 factorial arrangement of treatments. Diets were formulated containing low forage (LF; 41% of diet DM) or high forage (HF; 60% of diet DM) and DDGS at 0 or 18% of diet DM. Forage consisted of 80% corn silage and 20% alfalfa hay (DM basis). Ground corn and soybean feeds were partially replaced by DDGS from 0% DDGS diets to formulate 18% DDGS diets. Average DMI was not affected by diets (Table 1). Milk yield was greater when cows were fed LF compared with HF regardless of the addition of DDGS (43.3 vs. 41.5 kg/d). Milk fat concentration (3.03 vs. 3.38%) were lesser for cows fed LF compared with HF, whereas protein concentration (3.11 vs. 2.98%) and yield (1.34 vs. 1.24 kg/d) were greater for cows fed LF compared with HF. Yields of fat, total solids (TS), and 4% fat-corrected milk (FCM) were not affected by diets. Cows fed HF had greater feed efficiency FCM/DMI) compared with cows fed LF (1.50 vs. 1.43). Overall, there were no interactions of forage and DDGS for any of the measures. Results suggest that the concentration of forage in diets influences the performance of cows, but not the addition of DDGS. Consequently, partially replacing starch from ground corn and protein from soybean feeds with DDGS at either 41 or 60% of forage in the diet did not affect the production of lactating dairy cows.

Table 1.

	Low forage		High forage			
Item	0DDGS	18DDGS	0DDGS	18DDGS	SE	Pa
DMI, kg/d	25.6	26.1	25.1	25.1	0.56	NS
Milk, kg/d	42.8	43.7	41.7	41.2	1.31	F
Fat, %	3.07	2.99	3.42	3.34	0.25	F
Protein, %	3.09	3.13	3.00	2.96	0.05	F
Fat, kg/d	1.30	1.30	1.43	1.37	0.08	NS
Protein, kg/d	1.32	1.36	1.25	1.22	0.04	F
TS, kg/d	5.17	5.26	5.12	4.96	0.15	NS
4% FCM, kg/d	36.6	37.0	38.1	37.0	1.32	NS
FCM/DMI	1.43	1.42	1.52	1.48	0.04	F

F = Forage effect ($P < 0.05$); NS = No significant effect of forage, DDGS levels, and forage*DDGS interaction.

Key Words: distillers grains, starch, forage

660 In vitro effects of *Escherichia coli* lipopolysaccharide on the function and gene expression of neutrophils isolated from the blood of dairy cows. X. S. Revelo* and M. R. Waldron, *University of Missouri*, *Columbia*.

The objective of this study was to investigate the effects of *Escherichia coli* lipopolysaccharide (LPS) on the function and gene expression of bovine neutrophils (PMNL). PMNL from midlactation cows (161 ± 15 d postpartum; n = 7) were incubated with 0, 1, 25 and 50 μg/mL of LPS for 120 min and the generation of reactive oxygen species (ROS), PMNL extracellular traps (NETs), chemotaxis and killing of *Staphylococcus aureus* were determined. Incubation with 25 μg/mL of LPS increased intracellular ROS by 79% in non-mitogen-stimulated PMNL whereas 50 μg/mL of LPS enhanced intracellular ROS in non-stimulated and stimulated PMNL by 184 and 145%, respectively. Non-stimulated PMNL incubated with 25 and 50 μg/mL of LPS both had a 105% increase in NETs. LPS had no effect on subsequent PMNL chemotaxis or killing of *S. aureus*. To examine the effect of LPS on the expression of genes involved in PMNL function, mRNA was purified from PMNL isolated from midlactation (143 ± 5.6 d postpartum; n = 5) and early lactation cows (7 ± 0 d postpartum; n = 5), after a 120-min incubation with 0 or 50 μg/mL of LPS. Amounts of interleukin-8 (IL-8), tumor necrosis-α (TNF-α), bactericidal/permeability-increasing protein (BPI), myeloperoxidase (MPO), superoxide dismutase (SOD), cytosolic NADPH oxidase (p67-phox), flavocytochrome *b* (p22-phox), histone H2A.1 (H2A.1) and histone H2B-like (H2B) mRNA were determined by real-time quantitative reverse transcription PCR. LPS increased IL-8, TNF-α and SOD mRNA expression in PMNL isolated from all cows (7.9, 21.5 and 2.1 fold change relative to β-actin, respectively) whereas only PMNL collected from midlactation cows had higher p67-phox and flavocytochrome mRNA expression when incubated with LPS (2.10 and 2.06 fold change relative to β-actin, respectively). LPS had no effect on MPO, H2A.1 and H2B mRNA levels. These results suggest that LPS primes the neutrophils toward enhanced immunity by increasing the generation of ROS and expression of NETs along with elevated expression of genes encoding inflammatory mediators and enzymes involved in the production of ROS.

Key Words: neutrophils, lipopolysaccharide, reactive oxygen species

661 Expression analysis of genes of sialic acid metabolism in transition and late lactation Holstein cows using microarrays and RNA sequencing. S. Wickramasinghe*, S. Hua, G. Rincon, A. Islas-Trejo, C. B. Lebrilla, and J. F. Medrano, *University of California, Davis*.

Recent studies on sialylated milk oligosaccharides demonstrated beneficial effects to the suckling neonate. However, the concentrations of sialylated oligosaccharides are low in cow milk and it is important to identify a genetic strategy to optimize the content of sialylated oligosaccharides because cow milk based formula is the first choice as a substitute for human breast milk. The objective of this project was to identify and characterize the genes involved in sialic acid (Sia) metabolic pathways in milk in transition and late lactation cows. Expression analysis of genes in Sia metabolism was conducted by microarrays and RNA-sequencing (RNaseq) in milk cell samples collected from Holstein cows. Gene expression results from microarrays and RNaseq were in good agreement. However, RNaseq offered a larger dynamic range and provided a detailed characterization of genes by identifying alternative splice forms and abundant single nucleotide polymorphisms. Twenty genes in Sia metabolic pathway had low or medium levels of expression in milk and were categorized as genes involved in Sia synthesis, conjugation, transport and breakdown. Eighteen genes showed increased levels of expression in late lactation. ST8SIA1 which regulates synthesis of GD3, the most abundant ganglioside in early lactation showed a higher expression in transition milk, and ST35Gal5 that regulates synthesis of GM3, a prominent ganglioside in late lactation, had high expression in late lactation milk. Among the genes in conjugation, α-2,3-sialyltransferases showed higher levels of expression at the 2 stages of lactation than α-2,6-sialyltransferases, that is characteristically more active in human milk. Sialidases and Sia transporters showed a higher activity in late lactation milk indicating an increase in synthesis and breakdown of sialylconjugates in late lactation. These findings agree with published research on bovine milk oligosaccharide profiles and

variation in type and amount of sialylconjugates, and provide a detailed characterization of the expression of genes determining oligosaccharide content in cow′ milk.

Key Words: milk, sialic acid, gene expression

662 Incidence and risk factors of bovine respiratory disease in dairy heifer calves in Ontario and Minnesota. C. Windeyer*[1], S. J. LeBlanc[1], K. D. Lissemore[1], D. C. Hodgins[1], S. M. Godden[2], and K. E. Leslie[1], [1]*University of Guelph*, *Guelph, ON, Canada*, [2]*University of Minnesota*, *St Paul*.

Bovine respiratory disease (BRD) during calfhood has substantial impacts on the growth, survival and profitability of replacement heifers. One objective of this study was to evaluate risk factors for BRD in dairy heifers until 4 mo of age. A total of 2882 heifer calves from 15 herds in Ontario and 4 herds in Minnesota were examined at 1–7, 15–21, 35–42, and 84–112 d of age. Height, weight and body temperature were measured and health scores assigned using a standardized system. Serum total protein was assessed to evaluate passive transfer, with values less 5.2 g/dL considered failure of passive transfer (FPT). Farm personnel maintained birth, treatment and death records. Mortality was 2.9% overall (4.4% in Ontario and 1.5% in Minnesota) with herd mortality risk ranging from 0 to 9.5%. FPT occurred in 11.3% of calves, but varied by farm (0 to 53.5%). In Ontario, 19.1% of calves had FPT compared with 4.1% of calves from the herds in Minnesota. Overall, 19.4% of calves were treated for BRD (range: 0 to 36.7%). Mean age at first diagnosis was 33 d. Similar proportions of calves were treated for BRD in Ontario (21.9%) and Minnesota (17.1%). Significant risk factors as determined by a generalized linear mixed model for BRD were FPT, season of birth and assistance at calving, controlling for clustering by farm. Calves with FPT had 1.9 times (CI: 1.4–2.7) the odds of BRD compared with calves with successful passive transfer. Odds ratios of BRD for calves born in winter versus fall and summer, and spring versus summer were 2.1 (CI: 1.2–3.5), 2.7 (CI: 1.7–4.2), 2.1 (CI: 1.5–3.0), respectively. Assistance at calving increased a calf's odds of BRD 1.6 times (CI: 1.0–2.7). FPT, season of birth and assistance at calving significantly affect the odds of BRD. The age of onset of BRD may be earlier than traditionally expected. The variation by farm in FPT, incidence of BRD and mortality warrants further investigation.

Key Words: calf, respiratory disease, passive transfer

663 Effect of antibiotic treatment at post-weaning movement and BRD on growth at multiple time points in commercial dairy calves. A. L. Stanton*[1], S. J. LeBlanc[1], D. Kelton[1], S. T. Millman[2], J. Wormuth[3], and K. E. Leslie[1], [1]*University of Guelph*, *Guelph, Ontario, Canada*, [2]*Iowa State University*, *Ames,* [3]*CY Heifer Farm*, *Elba, NY*.

Bovine respiratory disease (BRD) is common following weaning and movement of calves from individual to group housing. The objective was to evaluate the effects of single injection of tulathromycin administered at post-weaning grouping of calves, and the effect of BRD in the 60 d following grouping on the growth of dairy calves at multiple time points. The study was conducted at a custom heifer raising facility in New York State. 1,367 weaned dairy calves were randomly assigned to receive either tulathromycin (TUL) or oxytetracycline (TET), once at the time of first movement to group housing. The incidence of BRD was 8% and 13% in the TUL and TET groups. A total of 248 heifers were identified and treated for BRD in the 60 d following movement. Post-weaning BRD events were recorded by trained barn staff. Weights and heights were measured at strategic points throughout the growing period based on movement through the facility. On average, calves were 56 d of age at enrollment and were re-weighed at 98, 180, 271 and 381 d of age. The effect of BRD and experimental treatment on the ADG of calves that were retained in the herd (n = 1,271) was evaluated between each time period using a mixed model, controlling for source farm and enrollment cohort. Between 56 and 98 days of age, TUL calves had an ADG of 0.90 ± 0.02 kg/day compared to TET calves with an ADG of 0.82 ± 0.02 kg/day ($P < 0.001$). After 98 days of age, there was no difference in ADG. However, the initial advantage in ADG resulted in TUL calves weighing 3.7 kg more than TET calves at 180 days ($P < 0.05$). Calves with BRD in the 60 days following enrollment gained 0.15 ± 0.02, 0.06 ± 0.01 and 0.03 ± 0.01 kg/day less than non-BRD calves between 56 and 98, 98 and 180, and 180 and 270 days of age, respectively. BRD did not have a significant effect on ADG after 270 days of age. At 381days of age BRD calves weighed 18kg less than non-BRD calves ($P < 0.001$).
In this population of calves, who remained in the herd for over a year, BRD in the 60 days following first movement to group housing continued to affect the ADG until 9 months of age.

Key Words: respiratory disease, dairy heifers, tulathromycin

664 Effects of glucose and essential amino acids on phosphorylation of signaling proteins for protein synthesis in bovine mammary epithelial cells. J. A. D. R. N. Appuhamy*[1], J. Escobar[2], and M. D. Hanigan[1], [1]*Department of Dairy Science, Virginia Polytechnic Institute and State University*, *Blacksburg,* [2]*Department of Animal and Poultry Sciences, Virginia Polytechnic Institute and State University*, *Blacksburg*.

Protein synthesis responds to nutrient signals such as amino acids and energy supply which involve AMP-activated protein kinase (AMPK), tuberous sclerosis complex 2 (TSC2), mammalian target of rapamycine (mTOR), ribosomal protein S6 (rpS6), and eukaryotic elongation factor 2 (eEF2). Increasing phosphorylation (PhS) of AMPK, TSC2, and eEF2 impair protein synthesis while increasing PhS of mTOR and rpS6 stimulate it. Our objective was to investigate the individual and interactive effects of essential amino acids (EAA) and glucose on PhS of AMPK, TSC2, eEF2, mTOR and rpS6 in MAC-T cells. Cells were deprived of serum, EAA, and glucose overnight and then incubated in complete or EAA-deprived DMEM/F12 with and without glucose (3.51 g/L) in a 2 × 2 factorial design for 1 h. Cell lysates were subjected to Western immunoblotting with antibodies against total and phosphorylated mTOR (Ser2448), rpS6 (Ser235/236), eEF2 (Thr56), AMPK (Thr172), and TSC2 (Thr1462). The PhS of each signaling protein was determined as a ratio of the phosphorylated to total forms. Glucose and EAA deprivations increased ($P < 0.10$) PhS of TSC2 (47 and 85%) and AMPK (29 and 28%), and reduced ($P < 0.01$) PhS of rpS6 (31 and 58%). Deprivation of EAA alone reduced ($P = 0.02$) PhS of mTOR by 31% and increased ($P = 0.01$) PhS of eEF2 by 20%. Interactive effects between glucose and EAA for PhS of AMPK, TSC2, and eEF2 were significant ($P < 0.06$) but that for mTOR and rpS6 were non-significant ($P > 0.51$). Glucose and EAA availability appear to synergistically modulate PhS of AMPK, TSC2 and eEF2. Regulation of rpS6 by EAA appears to be mediated by mTOR (Ser2448), but regulation by glucose occurred through an alternative mechanism in MAC-T cells. The effects of EAA on mTOR and rpS6 and the effects of glucose on rpS6 are supportive of independent effects of energy and EAA on protein synthesis.

Key Words: energy, amino acid, cellular signal

665 Prevention of *Mycobacterium avium* ssp. *paratuberculosis* (MAP) infection in Balb/c mice by feeding probiotic *Lactobacillus acidophilus* NP-51. M. A. Osman*[1], J. R. Stabel[2], J. M. Hostetter[3], D. S Nettleton[4], and D. C. Beitz1,5, [1]*Department of Animal Science, Iowa State University*, *Ames,* [2]*US Department of Agriculture, ARS, National Animal Disease Center*, *Ames, IA,* [3]*Department of Veterinary Pathology, Iowa State University*, *Ames,* [4]*Department of Statistics, Iowa State University*, *Ames,* [5]*Department of Biochemistry, Biophysics, and Molecular Biology, Iowa State University*, *Ames*.

The objective of this study was to examine effects of feeding *Lactobacillus acidophilus* strain NP51 to mice challenged with *Mycobacterium avium* ssp. *paratuberculosis* (MAP), the causative agent of Johne's disease. We hypothesized that feeding NP51 would increase Th-1 responses and decrease progression of MAP infection in mice. Thus, Balb/c mice were randomized to treatment groups in a factorial design including mice either fed heat-killed or viable NP51and challenged with either heat-killed or viable MAP. Mice were fed 1×10^6 CFU of either heat-killed or viable NP51·mice^{-1}·day^{-1} along with normal mouse chow until the end of the study. On d 45, mice were challenged with 1×10^8 CFU of heat-killed or viable MAP injected intraperitoneally. Ten mice from each group were killed on d 45, 90, 135, and 180. At each sampling period, tissues were excised from mice and cultured for MAP. Splenocytes were cultured in vitro with either MAP antigen or concanavalin A and examined for proliferation of T cells subpopulations. Overall, feeding NP51 to mice (either heat-killed or viable) significantly increased the frequency of CD8+ cytotoxic T cells in spleens of mice infected with viable MAP. Most importantly, MAP burden was decreased in the mesenteric lymph nodes, livers, and spleens of mice fed the NP51 compared with the MAP-infected controls on d 135. These results suggest that feeding NP51 modifies the immune responses and prevents progression of MAP infection in Balb/c in mice.

Supported in part by the Nutrition Physiology Corp.

Key Words: MAP, Johne's disease, *Lactobacillus acidophilus*

666 Effects of varying DCAD and Na:K on production, rumen and urine parameters in lactating dairy cows. K. E. Cowles* and M. R. Murphy, *University of Illinois*, *Urbana*.

Six multiparous Holstein cows, fitted with rumen cannulas, averaging 122 ± 31 d in milk were randomly assigned to 6 treatments allocated in an equiradial (pentagonal) second-order response surface design with a center point to examine the effects of dietary cation-anion difference (DCAD) and Na:K on lactating dairy cows. Replication of treatments within a 6 × 6 Latin square minimized the potential effects of outliers and allowed a surface covering a 3 × 3 matrix of DCAD and Na:K combinations to be examined. Ranges in DCAD and Na:K were chosen to be equally spaced on logarithmic scales; tripling each time from 0.25 for the former, and 1.5-fold each time from 25 mEq/100 g DM for the latter. The response surface was centered on a molar Na:K of 0.75 (0.60% Na and 1.37% K in DM) and a DCAD of 37.5 mEq/100 g of DM. The other 5 treatments were: 1.63, 50.0 (Na:K, DCAD); 0.46, 53.8; 0.25, 35.2; 0.63, 25.1; and 2.00, 31.2. Percentages of Na and K in DM of the TMR for vertices of the pentagon were calculated as 1.05, 1.10; 0.56, 2.08; 0.27, 1.84; 0.44, 1.17; and 0.84, 0.72. Diets were based on corn silage and corn-based grain mix. The Na:K ratios were varied with $NaHCO_3$ and K_2CO_3. Periods were 14 d. Daily feed intake of each cow was recorded during each period; samples of feed and orts were collected daily. Milk production was measured daily; samples were collected weekly and analyzed for components. Rumen and urine samples were collected and analyzed for pH on the last 3 d of each period. The MIXED procedure of SAS was used for ANOVA. There were no response surface effects of treatment on milk production and components, and DMI ($P < 0.05$). A linear relationship ($r^2 = 0.15$, $P < 0.022$) between mean rumen pH and mean urine was found. A quadratic effect of Na:K ($P < 0.01$) and interaction of DCAD ($P < 0.003$) indicated that urine pH was maximal (8.24 or above) at high DCAD and low Na:K. Linear ($P < 0.05$) and quadratic effects ($P < 0.05$) of DCAD on rumen pH were indicated. In conclusion, relationships exist among rumen pH and urine pH. Urine pH was maximized when diets had high DCAD and low Na:K. Rumen pH responded quadratically to DCAD.

Key Words: DCAD, rumen pH, urine pH

667 Increased AME and growth performance in broiler chicks fed a high DDGS diet supplemented with a mixture of NSPase. H. B. Lee*, K. L. Price, M. D. Utt, and J. Escobar, *Virginia Polytechnic Institute and State University*, *Blacksburg*.

High-fiber content of distillers dried grains with soluble (DDGS) is partially responsible for its low ME, which may be increased with dietary inclusion of non-starch polysaccharidase (NSPase). Broiler chicks (7-d-old, 6 chicks/pen, 6–7 pens/diet) were randomly allotted to 4 treatments with free access to feed and water. Corn and DDGS (20%) diets were supplemented or not with a proprietary mixture of NSPase. DDGS diets were formulated to be deficient only in ME (90% of corn diets). In wk 2, average weekly weight gain (AWG), gain:feed, and apparent ME (AME) of the chicks receiving corn diets were higher ($P < 0.001$) than DDGS diets. DDGS+NSPase increased ($P < 0.08$) AME by 9.4% but had no effect on AWG. In wk 3, AWG and gain:feed were higher ($P < 0.001$) in chicks receiving corn diets compared with DDGS diets. NSPase inclusion improved ($P < 0.04$) AWG in both corn (312 vs. 338 g) and DDGS (262 vs. 283 g) diets. DDGS+NSPase increased ($P < 0.007$) AME by 11.7%, which made this diet comparable in energy to both corn diets. However, AWG of chicks fed DDGS+NSPase was lower ($P < 0.005$) than chicks eating the corn diets, regardless of NSPase inclusion. The main effect of NSPase inclusion during the 2-wk assay was an increase in standardized ileal digestibility (SID) of all amino acids ($P < 0.003$). Overall energy restriction reduced SID of Pro, Leu, Phe, and Ala ($P < 0.05$). Regardless of diet, age increased ($P < 0.05$) amino acid SID except for Ser, His, Thr, Val, and Ala. Results indicate the ability of a mixture of NSPase to increase AME of ME-deficient diets containing 20% DDGS. Further, a lag in AWG response at equal AME suggests a metabolic adaptation in birds to the use the reducing sugars freed by NSPase for growth.

Key Words: non-starch polysaccharidase, apparent metabolizabe energy, amino acid standardized ileal digestibility

668 Effects of heat treating soybean meal and DDGS on ileal amino acid digestibility in broilers. A. Helmbrecht*[1], H. Kluth[2], A. Lemme[1], M. S. Redshaw[1], and M. Rodehutscord[3], [1]*Evonik Degussa GmbH*, *Hanau, Germany*, [2]*University Halle-Wittenberg*, *Halle-Wittenberg, Germany*, [3]*University Hohenheim*, *Stuttgart, Germany*.

The objective was to study effects of extreme feed conditioning on ileal amino acid (AA) digestibility of protein sources in broilers. Soybean meal (SBM) and corn DDGS were subjected to heat (135°C) in combination with steam in an autoclave system for 20 or 40 min. Each of the untreated and treated ingredients was included at 0, 10 or 20% into a basal diet at the expense of corn starch. Ileal AA digestibility both of SBM and of DDGS were finally calculated by linear regression analysis resulting in digestibility coefficients which are independent of endogenous losses. Ileal AA digestibility was studied in 2 experiments utilizing 3-week-old broilers and using TiO_2 as the indigestible marker. Each dietary treatment was allocated to 6 pens of 10 birds each. Feeds and water were offered for ad libitum intake for 5 d. For SBM, the 20-min heat treatment caused a significant reduction in digestibility of all AA, and the 40-min treatment caused a further significant reduction in digestibility for 6 out of 17 AA studied ($P < 0.001$). Mean digestibility of Arg, His, Ile, Leu, Lys, Met, Phe, Thr, Trp and Val wa reduced from 82% (control) to 68% (20 min) and 62% (40 min). For DDGS the treatment effects were not as great as for SBM. However, the mean digestibility of the aforementioned AA was 85% (control), 80% (20 min) and 79% (40 min). The effect of 20-min treatment of DDGS was significant for 11 out of 17 AA studied ($P < 0.001$). It was concluded that extreme conditions in feed conditioning will reduce AA digestibility greatly. The magnitude of the effect depends on the origin of the protein in the diet.

Key Words: amino acid digestibility, broiler, heat treatment

669 High dietary inclusion of dried distillers grains with solubles in broiler chick rations in combination with AllzymeSSF enzyme—Effects on yield and endogenous enzyme levels. M. K. Masa'deh*[1], C. A. Fassbinder-Orth[2], and S. E. Scheideler[1], [1]*University of Nebraska-Lincoln*, *Lincoln,* [2]*Creighton University*, *Omaha, NE*.

A study was conducted to test the effects of feeding high levels of dried distillers grains with solubles (DDGS) in combination with AllzymeSSF enzyme on production parameters and endogenous enzyme activity in broiler chicks. 480 d-old broiler chicks were divided into 8 diets (15 chicks per pen) with 4 replicate pens from day-old to 43 d. Chicks were fed 4 DDGS levels (0, 10.0, 20.0, or 30.0%) and 2 levels of the enzyme AllzymeSSF (0, or 0.02%) having activities of phytase, protease, pentosanase, pectinase, cellulase, beta-glucanase, and amylase in 4 × 2 factorial design. All diets were formulated to be isocaloric and isonitrogenous with the enzyme treatments replacing 75 kcal/kg ME, 0.1% Ca, and 0.1 P. All diets were fed a phase-feeding program, starter (0–15 d), grower (15–30 d), and finisher (30–43 d). At 43 d, 2 birds per pen were selected for yield %, parts yields and enzyme activities of amylase, maltase, aminopeptidase, trypsin and chymotrypsin from intestinal and pancreatic tissues. The dietary enzyme by DDGS interaction was not different ($P > 0.05$) for production parameters, mortality, yield % and tissue enzyme activities. Percent carcass yield ($P > 0.05$) was no different between treatments. Parts yield were not affected ($P > 0.05$) by dietary treatments except for breast yield as a % of carcass wt ($P < 0.05$) with the highest yield for broiler fed 10% DDGS. Endogenous enzyme activity levels in the intestine and pancreas were not different ($P > 0.05$) between DDGS levels. However, AllzymeSSF enzyme increased endogenous amylase activity ($P < 0.1$) in the enzyme treatments compared with non-enzyme treatment. In summary, feeding DDGS at higher levels, up to 30% in combination with AllzymeSSF enzyme, did not negatively affect production parameters or % yield compared with the basal diet. Exogenous enzyme supplementation appears to positively influence endogenous enzyme activity. Feeding DDGS at 30% had an economical benefit on average of $60/ton compare with the basal diet (0% DDGS). In addition, feeding the AllzymeSSF enzyme has an economical benefit of $14/ton.

Key Words: DDGS, AllzymeSSF, amylase

670 Effect of exogenous enzyme supplementation on performance and carcass characteristics of broilers fed distillers dried grains with solubles (DDGS). B. Jung*[1], A. B. Batal[1], and R. Mitchell[2], [1]*University of Georgia*, *Athens,* [2]*Perdue Farms, Inc.*, *Salisbury, MD*.

An experiment was conducted to determine the effect of supplementing with exogenous enzymes on performance, gastrointestinal tract weights and carcass characteristics of broilers fed diets containing distillers dried grains with soluble (DDGS). In a 3 × 2 factorial design 1,920 one-day-old male Heritage broilers were randomly assigned to the 6 dietary treatments; Corn-soybean meal (SBM), Corn-SBM + Hemicell, Corn-SBM + Avizyme 1510, 12% DDGS, 12% DDGS+ Hemicell, and 12% DDGS+

Avizyme 1510. Eight replicate pens containing 40 chicks were fed each experimental diet from 0 to 50 d of age. The diets were formulated to be isocaloric and isonitrogenous and to meet the bird′s digestible amino acid requirements. Performance was evaluated at 14, 21, 36 and 50 d of age, gastrointestinal tract weights were measured at 21 and 50 d of age, and carcass characteristics were measured at 51 d of age. From 0 to 36 d of age the inclusion of 12% DDGS in the diets decreased ($P < 0.05$) BW gain and feed efficiency (gain: feed). The supplementation of enzymes (Hemicell and Avyzime) to the corn-SBM and 12% DDGS diets increased ($P < 0.05$) BW gain and feed efficiency. The birds fed the diets with DDGS had significant heavier ($P < 0.05$) relative proventriculus and small intestinal weights, but the supplementation with enzymes did not affect the relative gastrointestinal tract weights at 21 d of age. There was no interaction between DDGS and enzymes on performance and gastrointestinal tract weights. The carcass data are being conducted. Careful consideration should be given when 12% DDGS is fed to broilers due to negative effects on performance and the addition of enzymes to the DDGS diets may overcome this negative effect.

Key Words: distillers dried grains with solubles (DDGS), broilers, performance

671 Effects of varying levels of DDGS on broiler growth and intestinal content characteristics at 28 days post-hatch. R. E. Loar II*, J. R. Donaldson, and A. Corzo, *Mississippi State University*, *MS*.

A study comprised as a factorial arrangement of treatments consisted of a starter (0 vs. 8%) and grower (0, 7.5, 15, 22.5, 30%) feed phases with various DDGS inclusion levels that served as the factors evaluated. 1,350 Ross × Ross 708 male chicks were placed in floor pens (15 birds/pen) and randomly assigned to a starter phase diet from placement until 14 d of age, and subsequently a grower phase diet (14–28 d). Birds were collectively weighed at d 0, 14 and 28 d. Feed consumption and mortality were monitored throughout the study. At the conclusion of the grower phase, the cecal contents from one randomly selected bird were analyzed for *Clostridium perfringens* and *Escherichia coli* growth through both selective media and real-time PCR. Two additional birds were randomly selected from each pen, their liver weights determined, and their ileal contents measured for viscosity. Our results indicated that DDGS levels had no effects during the starter phase. Birds exhibited a linear decrease in BW gain ($P < 0.0001$) and liver relative weight ($P < 0.0004$) as dietary DDGS were increased in the grower phase. Feed conversion and mortality were unaffected by DDGS grower phase level. A DDGS starter × grower phase interaction ($P < 0.05$) was observed for feed consumption during the grower phase, where birds that consumed no DDGS during the starter phase exhibited a decrease in feed consumption at 22.5 and 30%, while birds that received 8% DDGS during the starter phase were unaffected by DDGS during the grower phase. Broilers were unaffected by DDGS grower phase levels for ileal viscosity, and cecal *C. perfringens* and *E. coli* concentrations. Results from this study suggest that young broilers remain susceptible to high levels of DDGS inclusion during the 14 to 28 d feeding period.

Key Words: DDGS, broiler, PCR

672 Effect of distillers dried grains with solubles and enzyme supplementation on production performance and egg quality of laying hens through 36 weeks of egg production. P. Rossi*, A. J. Pescatore, A. H. Cantor, J. L. Pierce, T. Ao, L. M. Macalintal, M. J. Ford, W. D. King, and H. D. Gillespie, *Alltech-University of Kentucky Nutrition Research Alliance*, *Lexington*

The effects of diets containing 15 or 23% distillers dried grains with solubles (DDGS) with and without a naturally occurring enzyme complex (Allzyme SSF, Alltech Inc., Nicholasville, KY) on performance and egg quality of laying hens was evaluated during 36 weeks of production. At 17 weeks of age, 420 Hy-Line W-36 hens were randomly assigned to 5 treatments with 7 replicate groups of 12 hens each. Treatments consisted of feeding the following diets: 1) positive control (corn-soybean meal), 2) 15% DDGS, 3) 15% DDGS + enzymes, 4) 23% DDGS, and 5) 23% DDGS + enzymes. Diets containing DDGS had reduced levels of ME (2800 vs. 2877 Kcal/kg), Ca (4.1 vs. 4.2%) and available P (0.17% for 15% DDGS or 0.2% for 23% DDGS vs. 0.29%), compared with the control diet. Six eggs were randomly collected from each replicate every 4 weeks to determine egg quality. Feed intake was significantly ($P < 0.05$) decreased by DDGS during wk 9–12, 17–20 and 25–28. During the 36 weeks of production Allzyme SSF reduced feed intake by 2.6 g/hen/d. Hen-day production was lower for DDGS + enzymes during wk 29–32. There was no effect of treatments on feed efficiency. Egg weight at wk 8, 12, 16 and 20 and shell weight at wk 12 were decreased by 23% DDGS. The diet with 15% DDGS + enzymes increased yolk weight at wk 12 and 16 and % yolk at wk 16. Albumen weight was significantly increased by 15% DDGS at wk 8 and 16. Hens fed 15 or 23% DDGS +/− enzymes, had lower yolk lightness (L*) vs. hens fed the control diet. Hens fed 23% DDGS had higher yolk redness (a*) and yellowness (b*) values vs. hens fed 15% DDGS or the control diet, indicating a darker yolk color. The current study suggests that DDGS can be included in the diet up to 23% with minimal effects on performance and egg quality and can be used to improve yolk color. Using Allzyme SSF in DDGS diets with lower nutrient density can reduce feed intake. Feeding diets with 15% DDGS plus Allzyme SSF increased yolk weight and percent yolk.

Key Words: DDGS, yolk color, egg quality

673 Effects of high concentrations of distillers dried grains with solubles on long-term laying hen performance. J. Green*, D. U. Ahn, and M. E. Persia, *Iowa State University*, *Ames*.

A 28-week study was conducted with 240 Hy-Line W-36 laying hens to investigate the effects of long-term feeding of high concentrations of corn distillers dried grain with solubles (DDGS) on hen performance (egg production, feed intake). The experimental treatments consisted of 10 replicate groups of 6 hens housed in 2 hens per cage in 3 consecutive cages. The 4 dietary treatments consisted of increasing percentage of DDGS (0, 17%, 35%, and 50%) formulated into a corn-soybean meal (SBM) based diet. The DDGS were obtained from a local ethanol plant and all diets were formulated to be isocaloric and to meet or exceed industry based nutrient requirements. Crude protein content of the diets was allowed to increase with increasing dietary concentrations of DDGS. Hens were secured from a local commercial facility at 72 weeks of age after having gone through a molt period. Hens were started on 12 h of light with a half-hour increase weekly until hens reached 16 h of light daily. Hens were fed corn-SBM diets for 2 weeks before being stair-stepped up to 50% DDGS diets after a 2-week adjustment period to higher DDGS diets. Egg production and mortality data were collected and recorded daily, feed intake and egg production were analyzed weekly, while body weight gain was determined monthly. After 24 of 28 weeks on the 0, 17, 35 and 50% DDGS diets, total egg production was 89.2, 84.0, 86.8 and 63.5%, respectively. Feed intake for this period mirrored egg production at 104.1, 101.7, 105.4, and 91.6 g of feed intake per hen per day for the 0, 17, 35 and 50% DDGS diets, respectively. The reduction in feed intake and egg production with the 50% DDGS diet is most likely due to a methionine deficiency. Longer

term laying hen performance is possible with diets formulated to contain higher concentrations of dietary DDGS, but care must be taken to ensure adequate amino acid utilization when including this highly variable feed ingredient into laying hen diets.

Key Words: laying hen, DDGS, egg production

674 Effects of high concentrations of dried distillers grains with solubles on intestinal structure and nutrient and endotoxin transport of laying hens. K Gudenkauf*, M Jeffrey, N. K Gabler, D. U Ahn, and M. E Persia, *Iowa State University*, *Ames*.

The objective of this research is to determine the effects of high concentrations of dried distillers grains with soluble (DDGS) on nutrient and endotoxin transport of laying hens. Second-cycle laying hens were fed corn-soybean meal based diets containing either 0 or 50% DDGS for one month. Both diets were formulated to meet minimum total amino acid requirements regardless of crude protein content and equal energy concentrations. Eight hens per dietary treatment were sacrificed and intestinal tissue samples were collected from the duodenum loop (duodenum) and the midpoint between Meckel's diverticulum and the ilio-cecal junction (ileum). Fresh segments of ileum were collected and mounted in modified Ussing chambers to measure mucosal to serosal glucose, glutamine, phosphate, lysine, and methionine (met) transport rates. The changes in electro-physiology for each tissue were calculated after each nutrient challenge. Furthermore, permeability and tight junction integrity were also assessed by measuring the transepithelial electrical resistance (TEER). Statistical analysis was carried out using ANOVA. In general, nutrient transport was unaltered by diet although met transport rate tended to be increased by the 50% DDGS diet (P = 0.10), likely due to met deficiency in the 50% DDGS diet. No differences were noted in TEER. Lastly, ileal and colon samples were also mounted in modified Ussing chambers and mucosal to serosal endotoxin transport rates were determined using fluorescein isothiocyanate labeled lipopolysaccharide. The diet did not alter ileum endotoxin transport, but the 50% DDGS diets resulted in a significant decrease in colon endotoxin transport ($P \leq 0.05$). These data may indicate that the increased fiber in the DDGS diet is stimulating colon health resulting in decreased endotoxin transport.

Key Words: DDGS, laying hen, endotoxin transport

675 Effects of extruding DDGS at high and low temperatures on nutritional value of diets for nursery pigs. S. M. Williams*, J. D. Hancock, S. Issa, C. B. Paulk, and T. L. Gugle, *Kansas State University*, *Manhattan*.

A total of 224 nursery pigs (112 barrows and 112 gilts with an average initial BW of 8.4 kg) were used in a 21-d experiment to determine the effects of extrusion processing on the nutritional value of DDGS. The pigs were weaned, blocked by weight, and allotted by sex and ancestry with 7 pigs/pen and 8 pens/treatment. All pigs were fed a common diet for 11 d post weaning and the experimental treatments for the next 21 d. Treatments were a corn-soybean meal-based control and 3 diets formulated with 30% DDGS. For the DDGS treatments, the DDGS were not extruded, extruded with the barrel configured for processing cereal grain (to generate less shear and temperature rise), and extruded with the barrel configured for processing soybeans (to generate more shear and temperature rise). Orthogonal contrasts were used to separate treatment means with comparisons of: 1) the control vs. DDGS treatments; 2) untreated DDGS vs. extruded DDGS; and 3) low shear vs. high shear extrusion of the DDGS. For d 0 to 21, ADG and ADFI were greater for pigs fed the corn-soy control compared with pigs fed the DDGS treatments ($P < 0.02$). Extruding the DDGS did not affect ADG or G:F ($P > 0.11$) and there were no differences in growth performance among pigs fed the DDGS extruded with low- vs. high shear ($P > 0.2$). Overall, ADG was 526, 507, 472, and 493 g/d, ADFI was 784, 741, 682, and 707 g/d, and G:F was 671, 684, 692, and 697 g/kg. Our results indicate that feeding nursery pigs diets with 30% DDGS decreased ADG and ADFI with no affect on G:F. Extruding the DDGS did not ameliorate this loss in performance in nursery pigs.

Key Words: nursery pigs, DDGS, extrusion

676 Belly firmness and bacon quality from finishing pigs fed DDGS with various withdrawal times and with added tallow. M. C. Ulery*[1], G. L. Cromwell[1], G. Rentfrow[1], M. D. Lindemann[1], and M. J. Azain[2], [1]*University of Kentucky*, *Lexington,* [2]*University of Georgia*, *Athens*.

An experiment involving 168 pigs (6 reps of 3 or 5 pigs/pen) was conducted to evaluate belly firmness and bacon quality of pigs fed a high level of DDGS followed by varying withdrawal periods before slaughter, and to see if adding a more saturated fat (tallow) to diets containing DDGS would alter belly firmness and bacon quality. Treatments (Trt) were (1) a corn-soy diet or (2) a diet with 45% DDGS fed to term (121 kg) or removed during the final 2, 4, or 6 wk (Trt 3, 4, 5). Trt 6 and 7 were the same as 1 and 2 except 5% tallow was added. Belly flex measures (Abstr. 159, Midwest Section ASAS, 2010) indicated that bellies were softer in pigs fed DDGS, but firmness increased linearly ($P < 0.01$) with increased withdrawal time; tallow addition did not improve firmness. Backfat (inner and outer) and belly fat were analyzed for FA. PUFA (mean of the 3 fat depots) increased when DDGS was fed ($P < 0.01$), and the changes were moderated (linear, $P < 0.01$) with DDGS withdrawal time (Trt 1–5: 12.6, 24.9, 21.6, 18.8, 17.0% of total FA). Iodine values (IV) followed similar trends (62.0, 78.2, 74.1, 69.7, 67.7). Tallow addition had little effect on PUFA (Trt 6–7: 13.4, 23.3%) and IV (66.5, 78.7), particularly in pigs fed DDGS. Bellies from 3 reps were pumped with brine, smoked, and sliced (9 slices/2.54 cm) at a commercial plant. Bacon slices (10/slab) were scored for shatter; fried and scored for distortion, cook loss, and shrink; and evaluated by an 8-member trained sensory panel. DDGS inclusion did not affect bacon yield but it improved shatter scores ($P < 0.01$). Greater distortion, cooking loss, and shrink ($P < 0.05$) occurred in fried bacon from pigs fed DDGS with withdrawal time having no effect. Tenderness and flavor of bacon was not affected by DDGS. Tallow did not consistent affect any of the measures. The results indicate that withdrawal of a high level of DDGS from the finishing diet for 6 wk partially restores belly firmness, but addition of a harder fat does not overcome softer bellies. Except for an improvement in shatter scores and increased cooking loss, most of the other traits and eating quality of bacon were not affected by DDGS.

Key Words: pig, DDGS, bacon

677 Effects of co-products inclusion on growth performance and carcass characteristics of grower-finisher pigs. R. Jha*[1], J. K. Htoo[2], M. G. Young[3], E. Beltranena[1,4], and R. T. Zijlstra[1], [1]*University of Alberta*, *Edmonton, AB, Canada*, [2]*Evonik Degussa GmbH*, *Hanau, Germany*, [3]*Gowans Feed Consulting*, *Wainwright, AB, Canada*, [4]*Alberta Agriculture and Rural Development*, *Edmonton, AB, Canada*.

Using co-products (Co-P) while balancing on the basis of NE and standardized ileal digestible (SID) AA provides opportunities to reduce pig feed costs. In a completely randomized design, effects of increasing (from 2.0 to 12.5, 25.0, 37.5 and 50.0%) levels of Co-P (identical ratio of co-extruded flaxseed and field pea, canola meal, wheat/corn

DDGS (1.5:1.0:2.5) on growth performance, carcass quality, and feed cost indices were evaluated. Diet 6 supplemented SID AA 10% above the 37.5% Co-P diet to overcome potential ADFI reductions. In total, 1056 pigs (initial BW 29.5 kg) were fed 1 of 6 isocaloric and iso-lysinic dietary regimens in 4 phases (2.40, 2.35, 2.30, and 2.30 Mcal NE/kg and 3.96, 3.62, 3.22, and 2.83 g SID Lys/Mcal NE for d 0 to 19, d 20 to 38, d 39 to 56, and d 57 to 97, respectively) with 22 pigs per pens and 8 pen replicates per regimen. After slaughter at constant BW (118 to 120 kg), carcasses were characterized for all pigs. During the entire 97 d, increasing Co-P did not affect ADFI (2.90 kg), ADG, (1.01 kg) and G:F (0.35). For d 0 to 56, feeding 50% Co-P diet but not at or below 37.5% Co-P inclusions, reduced ($P < 0.05$) ADG and ADFI, however, G:F was not affected. Increasing dietary Co-P levels decreased ($P < 0.05$) dressing percentage and loin depth, but carcass weight was not affected. Increasing Co-P from 2 to 50% decreased ($P < 0.01$) feed cost/unit BW gain by 7%. Supplementing extra 10% SID AA to 37.5% Co-P did not affect performance, increased ($P < 0.01$) carcass lean, but decreased ($P < 0.01$) dressing percentage and backfat compared with 37.5% Co-P diet, indicating that dietary AA supply did not limit BW gain. In conclusion, using feed formulation to balance for identical NE and SID AA content, Co-P can be included up to 50% in grower-finisher pig diets to reduce feed costs without affecting growth performance.

Key Words: carcass quality, co-products, pig

678 Effects of dietary crude protein and inclusion of co-products on growth performance and carcass characteristics of grower-finisher pigs. R. T. Zijlstra*[1], R. Jha[1], M. G. Young[2], J. F. Patience[3], E. Beltranena[1,4], and J. K. Htoo[5], [1]*University of Alberta*, *Edmonton, AB, Canada*, [2]*Gowans Feed Consulting*, *Wainwright, AB, Canada*, [3]*Iowa State University*, *Ames,* [4]*Alberta Agriculture and Rural Development*, *Edmonton, AB, Canada*, [5]*Evonik Degussa GmbH*, *Hanau, Germany*.

The use of supplemental AA and co-products (Co-P) provide opportunities to reduce feed costs. Co-extruded flax-field pea Co-P may also enhance pork ω-3 fatty acid content, especially α-linolenic acid, and thereby add pork value attributes. In a 2 × 3 factorial arrangement, effects of 2 levels of dietary CP (N-CP: normal, without restriction) and reduced CP (R-CP: 3%-unit reduction in CP plus supplemental AA), and 3 levels of Co-P (low, without Co-P; medium, 30% Co-P; and high, 40 to 50% Co-P) on growth, carcass, and feed cost indices were explored. In total, 1056 pigs (initial BW 35.4 kg) were fed 1 of 6 isocaloric (2.40 Mcal NE/kg) and iso-lysinic (SID Lys:NE (g/Mcal); 4.00, d 0 to 25; 3.63, d 26 to 50; 3.25, d 51 to 71; 2.92, d 72 until end) diet regimens, in pens of 22 pigs for 8 pens per regimen. At slaughter (118 kg BW), the carcass was characterized for all pigs and jowl fat was sampled on 2 pigs per pen. Overall (d 0 to 86), increasing Co-P decreased ($P < 0.001$) ADFI and consequently ADG, and BW at d 86, but did not alter G:F. Decreasing CP did not affect ADG, ADFI, and G:F. Increasing dietary Co-P at the highest level increased ($P < 0.001$) jowl α-linolenic acid by 82%, decreased ($P < 0.001$) carcass weight and backfat, and reduced ($P < 0.001$) feed cost/unit BW gain by 15%. Decreasing CP did not affect jowl α-linolenic acid content, loin depth, and feed costs, but increased ($P < 0.01$) backfat content. In conclusion, increasing dietary Co-P above 30% may reduce growth performance of pigs via reduced ADFI, but will drastically reduce feed costs while enhancing carcass ω-3 fatty acid profile.

Key Words: co-product, omega-3 fatty acid, pig

679 Effects of dbcAMP on the proliferation, differentiation and adipogenesis-related genes of porcine adipocytes. L. Wang*[1,2], Z. Y. Jiang[1], Y. C. Lin[1], X. Y. Ma[1], and X. G. Lei[2], [1]*Institute of Animal Science, Guangdong Academy of Agricultural Sciences*, *Guangzhou, Guangdong, China*, [2]*Department of Animal Science, Cornell University*, *Ithaca, NY*.

We investigated the roles of dbcAMP (N^6, 2′-O-dibutyryl adenosine 3′, 5′ cyclic monophosphate) on adipogenesis of porcine adipocytes. Adipocytes were derived from freshly dissected back subcutaneous fat of 7-d Duroc × (Large White × Landrace) crossbred pig and incubated for 1d to 6d in DMEM/F12 media containing 10% fetal bovine serum and dbcAMP (0, 0.001, 0.01, 0.1, 1, 10, 100 and 1000 μmol/L). The proliferation and differentiation of adipocytes were measured by the MTT assay and Oil Red O staining, respectively. The mRNA expression of peroxisome proliferator-activated receptor γ_2 (PPARγ_2), adipocyte fatty acid binding protein (A-FABP) and CCAAT/enhancer binding protein α (C/EBPα) were measured by semiquantitative RT-PCR using β-actin as an internal standard. All data were analyzed by ANOVA using the GLM procedure of SAS 8.2. Supplementation with dbcAMP inhibited porcine preadipocytes proliferation in a dose-dependent manner with significance ($P < 0.05$) reached at 1000 μmol/L. The differentiation of porcine preadipocytes changed quadratically with increasing concentration of dbcAMP, and minimal differentiation at 0.1 or 1 μmol/L ($P < 0.05$). PPARγ_2 and A-FABP mRNA expression were decreased significantly ($P < 0.05$) by supplementation with 1000 μmol/L dbcAMP, while C/EBPα mRNA expression was unchanged. Above-mentioned results indicated dbcAMP supplementation in porcine preadipocytes inhibited proliferation and differentiation.

Key Words: dbcAMP, adipocytes, adipogenesis

680 DbcAMP increased lean percentage and protein deposition in finishing pigs. Z. Y. Jiang, L. Wang*, Y. C. Lin, C. T. Zheng, and X. Y. Ma, *Institute of Animal Science, Guangdong Academy of Agricultural Sciences*, *Guangzhou, Guangdong, China*.

This study was conducted to investigate the effects of dbcAMP (N^6, 2′-O-dibutyryl adenosine 3′, 5′ cyclic monophosphate) on growth performance and muscle growth in finishing pigs. Seventy-two Duroc × (Landrace × Large White) barrows (57.3 ± 0.6 kg) were randomly allotted to 3 treatments with 6 replicate pens (4 pigs per pen). The pigs were fed corn-soybean diets containing 0 (control), 10 and 20 mg/kg dbcAMP (purity, 98%), respectively, and allowed ad libitum access to feed and water, until the final slaughter weight of approximately 90 kg. Lean percentage was calculated by dissecting lean, fat and bone. Cryostat sections were stained with hematoxylin and eosin to determine fiber diameter and density of longissimus dorsi muscle (LDM). The concentration of cAMP (3′, 5′-cyclic adenosine monophosphate) and activities of cAMP dependent protein kinase A, adenylate cyclase (AC) in LDM were measured by ELISA. The mRNA expression of myogenic determinative factor (MyoD), myostatin, α-actin and myosin heavy chain (MHC) were measured by semiquantitative RT-PCR using β-actin as an internal standard. All data were analyzed by ANOVA using the GLM procedure of SAS 8.2. The ADG were 808, 836 and 832 g/d separately, but there were no significant differences among treatments ($P > 0.05$). Lean percentage in pigs fed 10 mg/kg dbcAMP was 5.64% greater ($P < 0.05$). No difference in fat percentage, bone weight percentage and in fiber density of LDM were detected ($P > 0.05$) among treatments. Compared with the control, fiber diameter of LDM tended to increase 8.61 ~26.17% ($P = 0.06$). Supplementation with 10 mg/kg dbcAMP elevated significantly AC activity, and MyoD, α-actin, MHC mRNA expression in LDM ($P < 0.05$). These results indicated that supplementation with dbcAMP in the diet could promote muscle growth and increase protein deposition in finishing pigs.

Key Words: dbcAMP, protein deposition, finishing pigs

681 The impact of dietary long chain fatty acids on bone and cartilage in swine. C. I. O'Connor-Robison*[1], J. D. Spencer[2], and M. W. Orth[1], [1]*Michigan State University*, *East Lansing,* [2]*JBS United, Inc.*, *Sheridan, IN*.

Dietary long chain polyunsaturated fatty acids (LCPUFA) including arachidonic acid (AA), eicosapentaenoic acid (EPA) and docosahexaenoic acid (DHA) can regulate the production of certain inflammatory mediators. The objective of this study was to characterize the effects of dietary LCPUFA on cartilage fatty acids and bone density and morphology. Sows and gilts were fed either control corn/soybean meal based diets, or the control diet supplemented with 1.0% protected LCPUFA from Fertilium (JBS United, Sheridan, IN). Sows had completed an average of 5.5 parities while gilts reached an average BW of 111 kg at time of slaughter. The cartilage was biopsied from the right and left humeral-ulnar joints of 14 sows (7/trt) and 16 gilts (8/trt) within 30 h of slaughter for fatty acid analysis. The right fused radius/ulna was saved for analysis via computerized topography (CT). Cartilage was pulverized in a freezer mill then fatty acids were extracted, methylated, and analyzed by GLC. Bones were cleaned and then analyzed with CT where 1 cm slices were acquired through the distal radius, central radius, and proximal ulna. Cortical width and density were measured and trabecular density was measured at the distal radius. Sows fed LCPUFA had increased DHA ($P < 0.01$), decreased C20:1 ($P < 0.01$), and an overall decrease in the omega-6 to omega-3 ratio ($P < 0.05$) in cartilage. Gilts fed LCPUFA had increased EPA ($P < 0.10$), DHA ($P < 0.01$), C22:1 ($P < 0.01$), and C22:5 ($P < 0.10$) in cartilage. CT scans of the radius/ulna from gilts revealed no differences for cortical width and bone density. Sows fed LCPUFA had greater cortical width of the proximal ulna ($P < 0.05$) and decreased cortical width of the distal radius ($P < 0.05$). Although the LCPUFA diet did increase omega-3 incorporation into chondrocytes the biological significance is unclear since concentrations of AA were at least 9-fold higher than EPA or DHA. Also, bone density was not affected by a LCPUFA enriched diet. Changes in cortical width were interesting but cannot be explained at this time. Thus, if omega-3 fatty acids can mitigate inflammation in joints, the benefit would likely be the result of systemic changes in inflammatory mediators.

Key Words: swine, omega-3, cartilage

682 Cannabinoid receptor type 1 (CB1) antagonist, SR141716 suppresses hepatic carnitine palmitoyltransferase 1 (CPT1) gene expression in rat. T. Wu*, Z. Yuan, and Y. Wang, *Institution of Feed Science*, *Hangzhou, Zhejiang province, China*.

SR141716 is the antagonist of cannabinoid receptor type 1 (CB1). The study was conducted to investigate the effects of SR141716 on body weight gain, hepatic fat deposit and carnitine palmitoyltransferase 1 (CPT1) expression in obese Sprague-Dawley (SD) rats induced by high fat diet (HFD). Twenty-four SD rats were randomly allocated to 3 groups: the normal diet (ND) as control group, the high fat diet (HFD) and SR141716 treated HFD-diet (SFD) animals as experimental

groups. Plasma was collected immediately for following plasma indexes determination. Liver samples were flash frozen in liquid nitrogen and stored at –80°C until use for following experiments. Compared with the ND group, HFD significantly increased the body weight gain (ND: 158.5 ± 4.14g, HFD: 173.8 ± 2.58g, $P \leq 0.05$), total viscera fat pad (ND: 2.38 ± 0.14 g/100g BW, HFD: 2.52 ± 0.11 g/100g BW, $P \leq 0.05$) and hepatic triglyceride (TG) (ND: 5.74 ± 0.58 mg/100g tissue, HFD: 10.71 ± 1.05 mg/100g tissue, $P \leq 0.05$) in rats, while SR141716 significantly suppressed these effects (154.6 ± 5.96g; 2.04 ± 0.10g/100g BW; 7.76 ± 0.52mg/100g tissue, $P \leq 0.05$). Furthermore, hepatic CPT1 mRNA level was significant decreased by HFD (24.78%, $P \leq 0.05$). Hepatic CPT1 and PPARgamma mRNA level were significantly suppressed by SR141716 accompanied with a decrease in expression of CB1 mRNA (19.52%, $P \leq 0.05$). The results indicated that SR141716 can significantly suppress the excess hepatic adipose deposit induced by HFD in rats. During this process, the pivotal role of CB1 in hepatic fat deposit may be due to modulation of CPT1 expression through PPARgamma. However, the accurate mechanism remains to be elucidated in the future.

Key Words: SR141716, Hepatic fat deposition, CPT1

683 Is the effect of dietary energy levels on feed intake of broiler chickens affected by bird age? M. Cho*[1], R. L. Payne[2], and H. L. Classen[1], [1]*Department of Animal and Poultry Science, University of Saskatchewan*, *Saskatoon, Saskatchewan, Canada*, [2]*Evonik-Degussa Corporation*, *Kennesaw, GA*.

It is historically known that chickens are able to adjust their feed intake according to the dietary energy content. However, broiler chickens may not be able to adjust their feed intake due to intense genetic selection and/or limited gut capacity at a young age. Hence, 2 experiments were conducted to clarify the relationship between dietary energy level and feed intake in broiler chickens and how it is affected by bird age. Trial 1 was conducted to determine the AME of Western Canadian feedstuffs using 5 and 21 d old broilers. Differences were found between 5 and 21 d old chickens for AMEn of some ingredients and therefore the determined values were used to formulate diets for trial 2 using age appropriate values. Trial 2 was conducted to investigate the effect of age on the feed intake response of broiler fed diets with a range in dietary energy content (2700, 2833, 2966 and 3100 kcal/kg). Diets in this energy range were fed for the entire experiment (SGF), for the grower and finisher periods (GF) or only in the finisher period. (F). Starter, grower and finisher diets were fed from 0 to10, 11 to 25 and 26 to 35 d, respectively. Amino acid levels in diets met or exceeded the primary breeder recommended values. Overall, birds did not adjust their feed intake based on the energy level of the diet. Switching from 3100 kcal/kg diets to lower energy had no impact on feed intake when started at the grower phase. A similar switch at the finisher phase caused a temporary (25 to 30 d) decrease in feed intake and consequently growth rate. Growth rate of birds fed the 2700 kcal/kg diet was lower than other treatments. The data suggest that modern broilers do not or cannot change feed intake in response to dietary energy when dietary amino acid requirements are met and this response is relatively consistent through-out the broiler growth period.

Key Words: nutrient density, poultry nutrition, AME

684 Estimation of net energy values of feedstuffs by simulation of biochemical reactions in broiler chicks. S. Cerrate* and C. Coon, *University of Arkansas*, *Fayetteville*.

A computer program is proposed which simulates energy metabolism in the growing broiler chicken for the estimation of net energy (NE) values of feedstuffs. This approach is based on a quasi-steady-state system which measures reactants and products in major metabolic pathways for carbohydrates, protein and fats. The input variables were digestible carbohydrates, amino acids and fatty acids and the output variables were 1) estimated net energy needs for maintenance and 2) net energy for tissue gain. Adenosine triphosphate was used to quantify the energy from chemical reactions obtained from oxidative metabolism of nutrients and then utilized for maintenance and gain by anabolic reactions. Simulations of a basal diet and 10 experimental diets (basal + feedstuff), were formulated to estimate their NE values. For each diet an estimation of NE value was simulated and then calculated for each feedstuff. The simulated NE values for each feed ingredient were compared with determined NE values of feedstuffs reported by past studies. A high correlation was observed between simulated and determined NE values for feed ingredients. The data indicates that the proposal model can be used to predict net energy values of feed ingredients.

Key Words: broiler, net energy, biochemical reactions

685 Energy determination of corn co-products fed to broiler chicks from fifteen to twenty-four days of age and use of composition analysis to predict AME_n. S. J. Rochell*[1], B. J. Kerr[2], and W. A. Dozier, III[1], [1]*Auburn University*, *Auburn, AL*, [2]*USDA-ARS Agroecosystems Research Unit*, *Ames, IA*.

Fifteen co-products collected from various wet and dry milling plants were fed to broiler chicks to determine AME_n and to generate an equation to predict AME_n based upon each ingredient′s chemical composition. Co-products included: DDGS (6), high protein dried distillers grain (HP-DDG) (2), dehydrated corn germ (2), corn germ meal, corn bran, corn gluten meal, corn gluten feed, and dehulled degermed corn. A control diet was fed containing corn, soybean meal, dextrose (15%), dicalcium phosphate, limestone, salt, vitamins, and trace minerals. Test diets were formulated by mixing the control diet with 15% of a co-product at the expense of dextrose. Nineteen hundred and 20 Ross × Ross 708 chicks (10 per pen; 5 males and 5 females) were randomly assigned to 15 dietary treatments (12 replicate pens). Broilers were fed experimental diets from 15 to 22 d of age followed by a 48 h total excreta collection period. Ingredients were analyzed for GE, CP, DM, crude fat, crude fiber, ash, total dietary fiber, NDF, and ADF, and hemicellulose was determined by difference. Gross energy was determined on the feed and excreta to calculate AME_n for each ingredient. The corn-soybean meal portion of the basal diet averaged 3,037 kcal AME_n/kg DM, with dextrose having an assumed value of 3,640 kcal/kg DM. For the 6 samples of DDGS, AME_n ranged from 2,146 to 3,098 kcal/ kg DM, averaging 2,676 kcal/ kg DM. The AME_n values for dehydrated corn germ, corn germ meal, HP-DDG, corn gluten meal, corn gluten feed, corn bran, and dehulled, degermed corn were 3,308, 1,991, 2,820, 3,182, 1,746, 3,030, and 3,442 kcal/kg DM, respectively. Stepwise regression resulted in the equation: AME_n, kcal/kg DM = 3,517 + (46.02 × % crude fat, DM basis) – (82.47 × % ash, DM basis) – (33.27 × % hemicellulose, DM basis) ($R^2 = 0.89$; SEM = 191; $P \leq 0.01$). These results determined that wide variability exists among corn co-products produced from dry and wet milling plants, and that the best predictors of AME_n are crude fat, ash, and hemicellulose.

Key Words: corn co-products, metabolizable energy, chicks

686 Apparent metabolizable energy (AME_n) content and standardized ileal amino acids digestibility of wheat, wheat-corn and corn distillers dried grains with solubles (DDGS) for broilers. A.

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In Exp. 1, the apparent metabolizable energy (AME_n) contents of 2 samples of wheat distillers dried grains with solubles (DDGS), 3 samples of wheat-corn DDGS, and 3 samples of corn DDGS were determined. A total of 225 broiler chickens were assigned to 9 dietary treatments, each consisting of 5 pens of 5 birds each, and were fed a basal starter diet or the basal diet plus 30% of DDGS from 14 to 19 d of age. All diets contained titanium dioxide (0.3%) as an indigestible marker. On average and in comparison with corn DDGS, wheat DDGS had lower AME_n content (2,872 vs. 3,177 kcal/kg DM) which is a reflection of its lower fat (4.5 vs. 10.7% DM) and carbohydrate (7.1 vs. 10.5% DM), including residual starch (1.6 vs. 6.6% DM), contents. The wheat-corn DDGS samples had intermediate values for AME_n contents which averaged 2,975 kcal/kg DM. As blending of wheat and corn is a common practice in bio-ethanol production in western Canada, a prediction equation for energy availability was developed and demonstrated a strong relationship between the amount of wheat and corn grain used and the AME_n content ($R^2 = 0.95$). The AME_n values corresponded well with the TME_n values, which averaged 3,160 for wheat DDGS, 3,238 for wheat-corn DDGS, and 3,488 kcal/kg DM for corn DDGS. In Exp. 2, the standardized ileal digestibility (SID) of amino acids (AA) was determined for 2 wheat DDGS, 6 wheat-corn DDGS and 4 corn DDGS samples. A nitrogen-free diet was used to determine endogenous AA losses. The SID values averaged 59.0, 59.6 and 62.7% for Lys; 82.7, 79.8 and 82.7% for Arg, and 70.6, 64.4 and 68.3% for Thr, respectively, for wheat, wheat-corn and corn DDGS ($P > 0.05$). The SID for Met was lower ($P < 0.05$) in wheat-corn DDGS (73.3%) compared with wheat DDGS (81.2%) or corn DDGS (81.3%). Overall, there was no conclusive relationship between the SID of amino acids and the type of DDGS used.

Key Words: DDGS, AME_n, amino acid digestibility

687 Use of the precision-fed rooster TME assay and chick AME assay to quantify the energy value of Nutridense corn. T. Loeffler*, D. A. Neves, and A. B. Batal, *University of Georgia*, *Athens*.

To determine the energy value of Nutridense corn, 2 precision-fed rooster TME assays and 2 conventional chick AME digestibility trials were conducted. The TME and AME values were compared within each experiment for both the Nutridense corn and the control corn, and the same experimental design was used for each study. The rooster assays were traditional precision-fed rooster assays in which 10 birds per diet were fasted for 24 h, crop intubated with 35 g of the test diet containing 92.25% control corn or 92.25% Nutridense corn, and excreta was then collected for 48 h. For the chick studies, 288 one-day-old Cobb 500 by product male broiler chicks were placed in Petersime battery brooders with raised wire floors. There were 12 replications of 12 chicks per replication assigned to the 2 corn diets. Chicks were fed a standard corn-soybean meal starter diet until 13 d of age, and on d 14, the chicks were allowed ad libitum access to the corn diet. Excreta were collected on d 17, dried, weighed, ground and analyzed for gross energy and crude protein. The determined AME values were 3.1% higher in study 1 (3096 vs. 3003 kcal/kg) and 2.3% higher in study 2 (2974 vs. 2907 kcal/kg) for the Nutridense as compared with the control corn. The determined TME values were also higher for the Nutridense corn as compared with the control corn; 2.2% increase (3463 vs. 3390 kcal/kg) and 1.2% increase (3446 vs. 3404 kcal/kg) for study 1 and 2, respectively. There was a larger difference in the ME values between the rooster TME and chick AME for study 1 than for study 2, but the Nutridense always had a higher ME than the control corn. Although the results for energy digestibility are not in agreement between the chicks and roosters in these studies, analysis of the data indicates that Nutridense corn has higher metabolizable energy than the control corn.

Key Words: Nutridense, corn, ME

688 Evaluation of energy digestibility among and within feedstuffs for swine using an in vitro digestibility technique. L. F. Wang*[1], P. R. Regmi[1], N. S. Ferguson[2], A. Pharazyn[2], and R. T. Zijlstra[1], [1]*University of Alberta*, *Edmonton, AB, Canada*, [2]*Nutreco Canada*, *Guelph, ON, Canada*.

The DE content of feedstuffs varies; thus, rapid and accurate evaluation of apparent total tract digestibility (ATTD) of energy is required for accurate swine feed formulation. Previously, a 3-step in vitro energy digestibility technique using pepsin, pancreatin and Viscozyme predicted ATTD of energy accurately among single samples of 8 feedstuffs ($R^2 = 0.97$). Within feedstuff variability was predicted well for grains and poorly for canola meal and corn DDGS. The objective was to expand the feedstuff matrix to multiple samples of corn, pulse crops, soybean meal and wheat; and to compare the accuracy of predicting ATTD of energy between in vitro digestibility and data from proximate analyses (fiber, ether extract, CP). The ATTD of energy was determined for 60 samples of 7 feedstuffs using 148 grower pigs with the indicator method. For multiple samples per feedstuff, in vitro energy digestibility was the best single predictor ($R^2 = 0.71$) compared with proximate analyses ($R^2 = 0.63$). Prediction accuracy of the in vitro technique was similar to using proximate analyses ($R^2 = 0.71$ vs. 0.75; SE of prediction [SEP] = 5.5 vs. 5.0; respectively). The prediction residuals from both methods were highly correlated (r = 0.88); the SEP for in vitro was highest for corn (5.1), then pulse (4.0), soybean meal (4.2), and lowest for wheat (1.3). Among feedstuffs, combining in vitro digestibility and proximate data reduced the error (SEP = 4.6). However, within feedstuff, the SEP of in vitro digestibility data was higher than for multiple chemical data (corn, 2.8 vs. 0.9; pulse crops, 2.6 vs. 1.7; soybean meal, 2.3 vs. 0.6; wheat, 1.4 vs. 0.1). In conclusion, in vitro energy digestibility and proximate analyses resulted in similar prediction accuracy for the ATTD of energy among feedstuffs. In contrast to grains, other feedstuffs revealed difficulty in achieving an accurate prediction of ATTD of energy within feedstuff using current procedure of in vitro energy digestibility.

Key Words: energy digestibility, in vitro, pig

689 The ontogeny of intestinal carbohydrate digestive, absorptive and nutrient sensing proteins in pigs. M. Al-Rammahi*[1], A. Moran[1], D. Batchelor[1], P. Sangild[2], C. Ionescu[3], D. Bravo[3], and S. Shirazi-Beechey[1], [1]*University of Liverpool*, *Liverpool, UK*, [2]*University of Copenhagen*, *Frederiksberg, Denmark*, [3]*Pancosma*, *Geneva, Switzerland*.

In the small intestine, dietary carbohydrate is hydrolysed ultimately by intestinal brush border membrane hydrolases, sucrase, lactase and maltase, to glucose, galactose and fructose. Glucose and galactose are transported across the luminal membrane of enterocytes by the Na^+/glucose cotransporter 1, SGLT1, which is upregulated by luminal sugars via the sweet taste receptor, T1R2/T1R3, expressed in enteroendocrine cells. Na^+-independent transporters, facilitate transport of fructose across the luminal membrane (GLUT5) and all 3 monosaccharides across the basolateral membrane (GLUT2). Aim: To determine the developmental profile of these key carbohydrate digestive-related gut functions in pigs before and after birth. Methods: Intestinal tissues were removed from pre-term (fetal age 105 d, n = 4), full-term (115 d, n = 4), suckling (15 d, n = 4) and weaned (28 d, n = 8) piglets following

euthanasia under ethical approval. Results: By immunohistochemistry, we showed presence of SGLT1 (on enterocytes luminal membrane), GLUT2 (on enterocytes basolateral membrane) and the glucose sensor (in enteroendocrine cells) both before and after birth; GLUT5 protein was only present after weaning. By functional assays and qPCR, we demonstrated highest expression of SGLT1 in weaned animals (on 60% carbohydrate diet). The expression level of SGLT1 was weaned > suckling > term > pre-term. A similar pattern of expression was observed for sucrase and maltase, while the developmental profile of lactase expression showed maximal levels in suckling animals. The presence of carbohydrate digestive/absorptive and nutrient sensing proteins in the intestine during pre-natal life indicates that a pre- programming of intestinal functions occurs before birth to prepare the gut for its post-natal functional demands. A better understanding of both ′hard wired′ and diet- induced functions of the gut in early life allows the design of rational and innovative approaches to formulate feed and feed additives to ensure the health and well-being of the young animal.

Key Words: gut development, sugar transporters, disaccharidases

690 Quality characteristics and fatty acid composition of eggs from hens fed *Camelina sativa* (camelina meal). R Kakani*[1], A Haq[1], J Fowler[1], E Murphy[2,3], T Rosenberger[3], M Berhow[4], and C. A. Bailey[1], [1]*Texas A&M University*, *College Station,* [2]*University of North Dakota*, *Grand Forks,* [3]*Agragen, LLC*, *Cincinnati, OH*, [4]*National Center for Agricultural Utilization Research, USDA*, *Peoria, IL*.

Camelina sativa or false flax is an oilseed producing plant rich in essential omega-3-fatty acids. Camelina meal is the by-product of oil extraction, and has a crude protein content (40%) similar to that of rapeseed meal. Camelina meal is a rich source of essential n-3 and n-6 fatty acids that can be incorporated in laying hen diets to enrich eggs with n-3 fatty acids. In this study, the effects of feeding camelina meal to commercial laying hens on egg production, egg quality characteristics and fatty acid composition of eggs was determined. Twenty-nine-week old Lohmann White Leghorn hens were randomly allocated to 3 dietary treatments (n = 25 per treatment) and data collected over a 12 week production period. All the treatment groups were fed a corn soy based experimental diets containing 0% (CON), 5% (CAM5) and 10% (CAM10) extruded camelina meal. Feed and water were offered ad libitum. There were no significant differences in % hen day egg production among the treatment groups. Egg weight was significantly lower in CAM5 (58 ± 4 g) relative to CON (60 ± 4 g), whereas no significant difference was detected between CAM10 (60 ± 5 g) and control. Egg shell strength (Instron) was significantly higher in CAM5 (5.0 ± 1.1 kg) and CAM10 (4.7 ± 1.1 kg) than in CON (4.5 ± 1.0 kg). Total cholesterol content in the yolk was unchanged between groups. Total egg n-3 fatty acid content was nearly doubled in CAM5 (117 ± 24 mg/yolk) and tripled in CAM10 (161 ± 20 mg/yolk) when compared with CON (60 ± 8 mg/yolk). The n-6 to n-3 ratio was significantly different between groups, 12.4 ± 0.8 (CON), 6.0 ± 0.2 (CAM5), and 4.3 ± 0.1 (CAM10). There were no detectable glucosinolates in the eggs of CAM5 and CAM10 treatment groups. Significant accretion of n-3 fatty acids was observed in the yolk of hens fed 5% and 10% camelina meal. These results indicate that camelina meal is a viable dietary source of n-3 fatty acids for poultry and its inclusion results in eggs enriched with n-3 fatty acids, including a 2.5-fold increase in DHA.
Funded by Great Plain Oil and Exploration

Key Words: camelina meal, egg quality characteristics, n-3 fatty acids

Nonruminant Nutrition Symposium: Models for Disease × Nutrition Evaluation and the Impact of Nutrition on Health, Disease, and/or Recovery

691 Possible nutritional interventions to improve intestinal health. J. Escobar*, M. A. Ponder, K. L. Price, and H. B. Lee, *Virginia Polytechnic Institute and State University*, *Blacksburg*.

In sick animals, the anorectic response is part of a series of complex but coordinated physiological and behavioral adaptations to recover from a disease episode. Thus, it is not surprising that animals appear to have a physiological preference for using endogenous nutrients over dietary supply, particularly during acute immune activation. Because survival and recovery have utmost nutritional priority, sick animals usually exhibit reduced growth performance, and nutritionists commonly rely on non-productive outcomes to determine the benefits of nutritional interventions. The effect supplementing diets with several nutrients and feed additives on intestinal health have been evaluated in various animal models using a wide variety of single immunological challenges. Our laboratory is currently using both *Salmonella*- and lipopolysaccharide-challenged pigs to determine how immune activation alters nutrient utilization as well as the contribution of prebiotic supplementation on intestinal health and recovery from an enteric infection. Results from our studies indicate increased amino acid catabolism during acute experimental sepsis and impaired amino acid digestibility during a bacterial infection of the gastrointestinal tract. Further, inclusion of a yeast-derived prebiotic in the diet of Salmonella-challenged pigs appears to improve fecal beneficial bacteria and intestinal morphology, which were associated with an enhanced growth performance during the recovery phase. The appropriateness of the animal model and the immune challenge, however, must be carefully considered when making intestinal health inferences of nutrients and supplements to be implemented in commercial animal production systems, which are usually affected by diseases of complex etiology.

Key Words: disease, intestine, amino acids

692 Challenge models to study foodborne pathogen transmission and test intervention strategies. P. Ebner*, *Purdue University*, *West Lafayette, IN*.

Foodborne illnesses are continually associated with the consumption of contaminated animal products (among other foods). As most of the more notable bacterial foodborne pathogens have reservoirs in at least one livestock species (e.g., *Campylobacter* in poultry, *Salmonella* in pork, *E. coli* O157:H7 in beef cattle), preharvest or on-farm intervention strategies aim to improve food safety by decreasing the amount and types of pathogens that animals bring with them into the processing facility. Various challenge models have been used in assessing the efficacy of these different strategies. Foodborne pathogen infection models present some special challenges as the organisms are, in many cases, among the normal microbiota of the animal. In addition, many of these organisms are seemingly ubiquitous within livestock facilities and are regularly isolated from the general environment. Such epidemiological factors should be taken into account when assessing the value of a certain infection model. Nutrition and management factors must also be taken under consideration with foodborne pathogen challenge models to varying degrees depending upon the organism. We have experimented with different models to study *Salmonella* infections in livestock. A major focus of our laboratory currently is the development of different methods to limit *Salmonella* infections associated with transport and lairage due to contaminated post-farm environments (e.g., contaminated trailers, crates or holding pens). Once a treatment has proven effective using a basic challenge such as co-inoculation, we usually progress to more complex models. As an example, we have simulated contaminated trailers or holding pens by inoculating small groups of seeder animals and then introducing unrelated treated and non-treated animals to the contaminated pen. These models, also used by other groups with *Salmonella* and other foodborne pathogens, attempt to more closely mimic the quantities and routes of exposure that the animal might encounter under a production setting in effort to better understand on-farm transmission and effectively reduce pre-processing pathogen loads in food animals.

Key Words: foodborne pathogens, *Salmonella*

693 Nutritional modulation of the gastrointestinal barrier and its role in gut health and disease. A. J. Moeser*, *North Carolina State University*, *Raleigh*.

Enteric disease is a major cause of mortality and production inefficiencies in swine. Environmental factors such as stress and nutrition have a profound influence on gut health and can triggers the onset of enteric disease but the mechanisms are poorly understood. Our studies have focused on elucidating how production stressors and nutritional factors influence the intestinal barrier, a critical line of defense against pathogens and antigens residing in the intestinal lumen. We have shown that stressors associated with current weaning practices have a deleterious impact on intestinal barrier function measured by increased intestinal permeability and mucosal inflammation. Furthermore, it was shown that weaning age is an important factor in determining the severity and duration of weaning-induced intestinal barrier dysfunction as incrementally increasing weaning age from 16 to 23 d of age led to graded improvements in post-weaning mucosal barrier function. Mechanisms underlying this weaning event were shown to be mediated through peripheral stress signaling pathways and innate immune cell dysfunction. Recent experiments with weaned pigs showed that early weaning exacerbated clinical disease and intestinal injury in response to an *E. coli* challenge. Furthermore, it was shown that increasing weaning age from 18 to 20 d of age ameliorated enteric disease *E. coli* challenged pigs. Given the important role of the intestinal barrier in gut health, we have begun studies investigating nutritional factors that can regulate the intestinal barrier. Beneficial results were shown with supplemental plasma protein into post-weaning diets specifically ameliorating a portion of the barrier dysfunction and intestinal inflammation and diarrhea that is associated with early weaning. In summary, the integrity of intestinal mucosal barrier is critical to pig health and can be influenced by production stress and nutrition. Identifying strategies to enhance intestinal barrier health in the pigs will be important to promote optimal pig health, performance, and well-being.

Key Words: intestine, stress, weaning

694 Is immunomodulation good? K. C. Klasing*, *University of California*, *Davis*.

Nutrients, pharmacological agents, and immunogens are often administered to animals for the purpose of immunomodulation, which is defined as shifting the immune systems response to pathogens or other triggers. The underlying principle is that the immune system can be improved by an informed intervention. Implicit in the idea of immunomodulation is that an animals immune system is mal-regulated or mal-designed as the result of improper genetics or environment and we know how to fix

it. Several examples of immunomodulation from the nutrition literature indicate that immunomodulation is situation dependent: improving disease resistance against some pathogens while impairing it against others. An understanding of the polarized response of the immune system in context of the optimal protective immune response helps explain this dichotomy. Pathogens often subvert the immune system to marshal a vigorous, yet counterproductive response. Modulation of the immune system in a more protective direction helps. However, this same immunomodulation may impair the protective response to other pathogens with different pathogenicity mechanisms. Thus, the value of immunomodulation appears to be context specific. When a single pathogen is dominant in a production system and the type of protective immune response is clearly understood, an immunomodulator that is known to shift the immune system in the protective direction is good for that pathogen; but not necessarily for others.

Key Words: nutrition, immunity, modulation

695 Functional characterization of folic acid transport in the intestine of the laying hen. G. B. Tactacan*, W. Guenter, and J. D. House, *University of Manitoba*, *Winnipeg, Manitoba, Canada*.

The deposition of dietary supplemented folic acid (FA) into the chicken egg is likely regulated by its absorption in the intestine. Therefore, factors affecting the intestinal transport of FA in the laying hen may influence the level of egg folate concentrations. To this end, a series of experiments using intestinal everted sacs were conducted to characterize the different aspects of the intestinal FA absorption process in laying hens. Effects of naturally occurring folate derivatives (5-methyl and 10-formyltetrahydrofolate) on FA absorption were also investigated. Folic acid absorption was measured based on the rate of uptake of ^{3}H-labeled FA in the everted sac from various segments of the small and large intestines. Folic acid concentration, incubation length, and pH condition were set to optimum before the performance of the uptake experiments. The distribution profile of FA transport along the intestine was highest in the upper half of the small intestine. Maximum uptake rate (nmol•100 g tissue^{-1}•min^{-1}) was observed in the jejunum (22.3 ± 2.0) and duodenum (20.6 ± 1.9) and decreased significantly ($P < 0.001$) in the ileum (15.3 ± 1.1) and cecum (9.3 ± 0.9). Transport characteristic of FA in the jejunum demonstrated a pattern of saturation, exhibiting decreased uptake rate with increased FA concentration. Transport increased proportionately ($P < 0.002$) between 0.0001 and 0.1 μM FA but showed a trend toward saturation in excess of 0.1 μM FA. Folic acid uptake in the jejunum showed greater transport at lower pH, exhibiting highest uptake at pH 5.5–6.0 but decreased ($P < 0.009$) at higher pH (7.5). Presence of 5-methyl and 10-formyltetrahydrofolate impeded FA uptake, reducing intestinal FA absorption by 21.9 and 14.9%, respectively, when added at concentrations ranging from 0 to 100 μM. Overall, these data indicated the presence of a FA transport system in the entire intestine of the laying hen. Uptake of FA in the cecum raises the likelihood of absorption of bacterial-derived folate.

Key Words: folic acid, everted sac, laying hen

696 Effect of choline, folacin and vitamin B_{12} on egg components and egg phospholipid composition in laying hens. P. Krishnan* and S. E. Scheideler, *University of Nebraska Lincoln*, *Lincoln*.

Choline, folacin and vitamin B_{12} are essential nutrients for all animals and a required dietary supplement for poultry. This study was designed to determine the effect of added choline, folacin and vitamin B_{12} to a corn-soy diet on egg production, egg quality and egg yolk phospholipid composition. A corn-soy basal diet was formulated with 2 levels supplemental choline (500 and 1000 ppm) 2 levels supplemental folacin (2 and 4 ppm) and 2 levels supplemental vitamin B_{12} (0.01 and 0.02 ppm) in a 2 × 2 × 2 factorial arrangement along with a control (no supplementation) group. The 9 experimental diets were arranged in a randomized complete block design with 6 replicate cages and 4 birds per cage for a total of 54 cages and fed for 6 wks. Percentage egg production, daily feed intake and body wt gain did not show any significant difference between experimental treatments as well as with the control. There was a significant ($P < 0.05$) effect of folacin on yolk wt with the wt. increasing at 2 ppm of folacin supplementation. Yolk wt also showed a significant ($P < 0.05$) 3 way interaction between choline, folacin and vitamin B_{12}. There was a significant difference in yolk wt between experimental treatments with the highest yolk wt being observed with choline, folacin and vitamin B_{12} at 1000, 2 and 0.01 ppm respectively. Albumen wt. showed a significant difference ($P < 0.05$) with choline and folacin supplementation with the values being higher at 1000 ppm of choline and 4 ppm of folacin. Phosphatidylcholine (PC) showed a significant increase ($P < 0.0001$) with added levels of choline, folacin or vitamin B_{12} with subsequent reduction in phosphatidylethanolamine (PE). The average value of PC (mg/g of egg yolk) at 500 and 1000 ppm of choline was 152.61 and 164.53 mg respectively. Similarly, the average values for PC at 2 and 4 ppm of folic acid and 0.01 and 0.02 ppm of vitamin B_{12} were 153.06, 164.07, 155.68 and 161.46 mg respectively. Results indicate that choline, folacin and vitamin B_{12} positively affect yolk wt. and egg yolk phospholipid composition in laying hens.

Key Words: choline, folacin, vitamin B_{12}

697 Effects of canthaxanthin and 25-hydroxycholecalciferol on reproductive aspects of roosters. A. P. Rosa*[1], P. Ferreira[1], A. Scher[1], R. P. Ribeiro[1], G. Farina[1], and J. O. B. Sorbara[2], [1]*Universidade Federal de Santa Maria - Animal Science Department - Poultry Laboratory*, *Santa Maria, RS, Brazil*, [2]*DSM Nutritional Products*, *São Paulo, SP, Brazil*.

Avian spermatozoa are characterized by high concentrations of fatty acids within their phospholipids and are susceptible to lipid peroxidation considered a problem in poultry reproduction. Antioxidant system is based on interactions of various antioxidants and the carotenoids are an essential part of that system. Among the carotenoids, canthaxanthin is characterized by its relatively high antioxidant activity. 25-OH-D3 (25-hydroxycholecalciferol) is an intermediary between the vitamin D3 and the active form of this vitamin. The aim of the present study was to evaluate the effects on the reproductive performance and seminal characteristics of roosters, fed diets with ROVIMIX MaxiChick (6 ppm Cantaxantina + 69 μg/kg of diet 25-OH-D3). This experiment was conducted at the Poultry Laboratory of Animal Science Dept. at The Federal University of Santa Maria-Brazil. Forty White Plymouth Rock roosters from 40 to 59 weeks of age were used. The males were submitted to T1 = control diet or T2 = control diet + MaxiChick. A completely randomized design was used with 2 treatments with 20 repetitions (one male each). The experimental phase was divided into 5 periods of 28 d. The parameters evaluated were: body weight and feed intake, motility, vigor score, sperm concentration and morphological anomalies. The data were transformed to adjustment the normality and then they were subjected to ANOVA. The differences between treatments were compared by Duncan test at 10% significance level. The addition of ROVIMIX MaxiChick in the diet improved the sperm concentration from 4.40 to 5.91*10^{8}/ml ($P = 0.0001$), motility improved from 91.40 to 92.80 ($P = 0.0071$) and sperm vigor score from 4.38 to 4.57 ($P = 0.0296$) and contributed to reduce the morphological anomalies from 21.90 to 16.70% in the semen ($P = 0.0001$).

Key Words: vitamin, D3, reproduction

698 Supplementation of canthaxanthin and 25-OH-D_3 to broiler breeders diet on broiler chick hatchery parameters and egg yolk TBARS. A. P. Rosa*[1], A. Scher[1], L. Boemo[1], T. N. N. Vieira[1], J. A. G. Ferreira Jr.[1], and J. O. B. Sorbara[2], [1]*Universidade Federal de Santa Maria - Animal Science Department - Poultry Laboratory*, *Santa Maria, RS, Brazil*, [2]*DSM Nutritional Products*, *São Paulo, SP, Brazil*.

The objective of this study was to determine the effect of the supplementation of Rovimix MaxiChick to broiler breeders diet on hatchery parameters and the antioxidant potential. The experiment was carried

out at The Federal University of Santa Maria, Brazil. Twenty incubations were carried out with eggs from 360 females Cobb 500 with 45 weeks of age. The experimental design was in a CRD with 2 treatments, control and Control + Rovimix MaxiChick (6ppm canthaxanthin + 69mcg/kg of diet 25-OH-D3) and 6 replicates of 30 females and 3 males each. The eggs were incubated following standard incubation procedures, and at 21 d the hatchability parameters were assessed. To evaluate the antioxidant potential of Rovimix MaxiChick, eggs were stored at 0, 4, 8 and 12 d. After storage period the yolk was collected for TBARS analysis. During incubation yolks or viteline sacs of embryos were collected at 0, 7, 14 and 18 d of incubation for TBARS analysis. When MaxiChick were supplemented, Hatchability improved from 83.03% to 87.35% ($P < 0.0001$); Hatchability of fertile eggs improved from 91.30 to 93.97 ($P < 0.0001$); Fertility improved from 90.94% to 92.95% ($P = 0.0017$); Total Embryo Mortality during incubation reduced from 5.46% to 3.46% ($P = 0.0002$). TBARS (MDA mg1 protein) of egg yolks during different storage time reduced from 13.53 to 10.82 ($P = 0.0355$); from 20.87 to 15.04 ($P < 0.0001$); from 20.73 to 12.96 ($P < 0.0001$); and from 28.97 to 20.90 ($P < 0.0001$) at 0, 4, 8 and 12 d of storage, respectively. TBARS (MDA mg1 protein) of egg yolks during different incubation time reduced from 21.14 to 12.12 ($P < 0.0001$) at 0 d of incubation and from 16.69 to 14.67 ($P < 0.0001$) at 7 d of incubation. At 14 and 18 d of incubation no statistical response were detected. The supplementation of Rovimix MaxiChick in the broiler breeders diet improved all hatchability parameters evaluated in this trial. An antioxidant effect was observed in eggs from birds fed with MaxiChick.

Key Words: antioxidant, breeder, 25-hydroxycholecalciferol

699 Sparing vitamin E effects of a synthetic antioxidant blend in broilers. J. Zhao*, M. Vazquez-Anon, R. J. Harrell, J. D. Richards, F. Yan, T. Wineman, and S. Carter, *Novus International Inc.*

A total of 720 ROSS 308 female broilers were used to determine vitamin E sparing effects of a synthetic antioxidant blend (AOX, Novus International Inc., St Louis, MO). The trial was a 4 × 2 factorial design with 4 levels of vitamin E (5, 15, 30, and 60 IU/kg) with or without antioxidant (AOX at 0.025%). Birds were randomized into 8 treatments with 9 replicates per treatment and 10 birds per pen. Oxidized soybean oil was added in all diets to provide peroxide value of 6mEq/kg in the final diet. Without AOX, quadratic vitamin E response was observed on weight gain ($P = 0.04$) and feed intake ($P = 0.07$) with the maximum response between 15 and 30 IU/kg. AOX tended to improve feed efficiency regardless of dietary vitamin E levels ($P = 0.07$). A significant 2-way interaction of dietary vitamin E and AOX was observed on body weight and weight gain ($P = 0.05$) in that AOX improved gain at the low vitamin E but not at high vitamin E diets (interaction, $P = 0.05$). Weight gain for the 21 d growth period was 699 and 791 g at 5 IU/kg, 783 and 773 g at 15 IU/kg, 788 and 777 g at 30 IU/kg, 775 and 762 g at 60 IU/kg dietary vitamin E without and with AOX, respectively. Similar to weight gain, birds fed AOX ate more feed and had better feed efficiency at 5 IU/kg dietary vitamin E compared with birds fed non-AOX diet (by contrast, $P < 0.05$) but the benefits were not observed at high vitamin E diets. Plasma and liver vitamin E were linearly increased with increased dietary vitamin E ($P < 0.05$) regardless of AOX. In addition, plasma and liver vitamin E concentration increased with AOX addition regardless of dietary vitamin E levels ($P < 0.05$). Liver vitamin E were 8.7 and 11.1 ug/g at 5 IU/kg, 18.1 and 21.4 ug/g at 15 IU/kg, 27.8 and 36.2 ug/g at 30 IU/kg, and 51.1 and 59.4 ug/g at 60 IU/kg vitamin E without or with AOX. In summary, AOX spared vitamin E based on performance and tissue vitamin E concentration, and can be used to spare dietary vitamin E as an antioxidant in broiler diets.

Key Words: antioxidant, vitamin E, broiler

700 Effect of percentage pellet fines and house-walking schedule on broiler growth performance. W. J. Pacheco*, R. D. Malheiros, C. R. Stark, P. R. Ferket, and J. Brake, *North Carolina State University*.

Feed accounts for around 65–75% of total broiler production costs. Pelleted feed has been shown to reduce feed wastage and improve growth as it encourages broilers to eat feed faster. The objective of the study was to evaluate the effect of quantity of pellet fines and house-walking schedule on broiler growth performance. The experiment was a 2 × 2 factorial of pellets fines (0% or 50% fines) and house-walking (1 or 3 times daily). A total of 1,024 male 1-d-old broiler chicks were randomly assigned to 2 different blocks and 2 treatments with 8 replicate pens per treatment in each block and 32 birds per pen. The starter diet was fed in crumbled form to 21 d while the grower and finisher diets were in pelleted form. The 0% fines diet was created by screening the pellets and the 50% fines diet was created by re-combining the screened pellets with the fines. Body weight (BW) and feed consumption were determined at 21, 42, and 49 d of age and feed/gain ratio (FCR) was calculated. The fines in the 0% and 50% treatment grower diets was found to be 20% and 62%, respectively, while the finisher diets contained 3% and 54%, respectively. No pellet fines by walking treatment interaction effects were observed. The 50% fines treatment decreased 42 d BW (2,848 g vs. 2,998 g, $P < 0.0001$) and increased 1–42 d FCR (1.74 vs. 1.70, $P < 0.05$) relative to 0% fines. The 50% fines treatment continued to adversely effect 49 d BW (3,637 g vs. 3,774 g, $P < 0.0001$) but not on 1–49 d FCR (1.84 vs. 1.82). House walking 3 times daily decreased BW at 42 d (2,891 g vs. 2,954 g, $P < 0.005$) without affecting FCR. There were no walking treatment effects observed at 49 d. This experiment demonstrated the adverse effects of fines in pelleted feed on growth performance of broilers, regardless of whether they were encouraged to get up by walking the pens more frequently. Indeed, entering the pens 3 times per day may have disturbed eating and resting behavior before 42 d.

Key Words: broilers, feed fines, growth performance

701 The effects of feeder-trough space and gap setting on growth performance of finishing pigs. A. J. Myers*, R. D. Goodband, M. D. Tokach, S. S. Dritz, J. R. Bergstrom, J. M. DeRouchey, and J. L. Nelssen, *Kansas State University*, *Manhattan*.

A total of 288 pigs (initial BW 41.3 kg) were used in a 91-d study to evaluate the effects of feeder trough space (4.45 vs. 8.9 cm/pig) and minimum feeder gap opening of 1.3 cm (narrow), vs. 2.5 cm (wide) on finisher pig performance. Our hypothesis was that at minimal feeder trough space (4.45 cm/pig), feeders should be set at a wide gap opening to not limit feed intake and ADG. The feeders were adjusted to the minimum gap setting but the agitation plate could be moved upwards to a maximum gap opening of 1.9 or 3.2 cm, respectively. The treatments were arranged in a 2 × 2 factorial with 6 replications per treatment. All pens had the same feeder with 2 35.6 wide by 11.4 cm deep feeder holes. Feeder trough space was adjusted by having pens of either 8 to 16 pigs per pen. Gating was adjusted giving each pig 0.74 m2 of floor space. Pigs had ad libitum access to feed and water. A corn-SBM based diet containing 20% DDGS was fed in 4 phases to all treatments. Pen weights and feed disappearance were measured every 2 wk. Overall (d 0 to 91) there were no trough space × feeder adjustment interactions observed ($P > 0.10$). However, there was a tendency ($P = 0.08$) for increased ADG as feeder trough space increased from 4.45 to 8.9 cm/pig. Pigs fed with the wide feeder gap setting had increased ($P < 0.01$) feed disappearance and decreased ($P < 0.01$) G:F compared with pigs with the narrow feeder gap setting. These results suggest that regardless of feeder trough space, pigs with the wide feeder adjustment appeared to waste more feed as evidenced by the poorer G:F.

Table 1. Effects of feeder gap setting and feeder space on finisher pig performance, (d 0 to 91)

	4.45 cm trough space		8.9 cm trough space		P-value	
Item	Narrow	Wide	Narrow	Wide	Space	Adjustment
ADG, kg	0.99	1.01	1.02	1.03	0.08	0.33
ADFI, kg	2.99	3.16	3.04	3.24	0.18	<0.01
G:F	0.33	0.32	0.34	0.32	0.90	<0.01

Key Words: finishing pigs, feeder gap, feeder space

702 Modeling the response of growing turkeys to nutrition: from experimental to commercial data. V. Rivera-Torres*[1,2], P. Ferket[3], and D. Sauvant[4], [1]*Techna*, *Couëron, France*, [2]*AgroParisTech*, *Paris, France*, [3]*North Carolina State University*, *Raleigh,* [4]*INRA-AgroParisTech*, *Paris, France*.

A mechanistic model was previously built to describe growth profiles of turkeys in a controlled environment. The model was further developed to be used as a predictor of turkey growth performance in commercial conditions. The model used protein and lipid turnover rates in carcass, viscera and feathers to define the expression of the growth potential in a specific environment. Feed intake depended on the limiting amino acid requirement, or on net energy utilization when no nutrient was limiting. Nutrient ingestion was assumed as glucose, amino acid and fatty acid equivalents, driven by homeostatic regulations to maintain a constant plasma concentration. Nutrient oxidation was expressed as the formation of acetyl coenzyme A. Data from calorimetry measurements and slaughter analyses were used to calibrate the model using performance of male and female turkeys fed standard diets. Protein and lipid deposition were calibrated with the turnover rates, whereas nutrient oxidation was calibrated on CO_2 production. The homeostatic response to different energy and amino acid levels was calibrated using literature data. Finally, protein and lipid deposition in carcass were adapted to the body weight (BW) and feed efficiency observed in commercial facilities, while variability between flocks was supposed to be due to feed intake differences. Based on the calibration on calorimetry measurements, females had a lower protein turnover in viscera ($P < 0.01$), and a greater lipid turnover than males ($P < 0.01$). A 3% increase in dietary nutrient density tended to result in increased feed efficiency ($P = 0.08$), mostly because of increased protein deposition in viscera ($P = 0.05$). The variability in final BW and feed efficiency of commercial turkey flocks at 18 wk of age was due to a variation from 95 to 105% of average feed intake. The calibration on experimental data enabled the model to be used as a predictor of nutritional responses of turkey populations grown in commercial conditions.

Key Words: turkey, model, growth

703 Maximum profit feed formulation: 3. Interaction between energy content and temperature. S Cerrate* and P. W. Waldroup, *University of Arkansas*, *Fayetteville*.

Nutritional models for comparison of 2 environmental conditions on responses to dietary energy using data from literature were evaluated to formulate broiler diets by maximum profit feed formulation with real or simulated prices of corn and soybean meal. These diets were formulated based on corn and soybean meal (C-SBM) diets and others with wheat and cottonseed meal (+W-CM) as alternatives sources. Average body weight gain or feed intake slopes at normal temperature were significantly higher than those at heat stress. The rate of gain per calorie was 2 times higher at normal compared with heat stress and the rate of feed intake per calorie was half time higher at normal than did at heat stress. At real or simulated prices, the economic energy content in most cases was reduced by heat stress compared with those at normal temperature. For real prices the energy reductions from normal temperature to heat stress were from 3.254 to 3.015 kcal/g for diets based on C-SBM or from 3.2 to 2.961 kcal/g for diets based on +W-CM. These economic energy reductions were around 7% from real prices, up to 10% from simulated corn prices and up to 9% from simulated SBM prices. The inclusion of +W-CM reduced the economic energy content and increased the profitability compared with those based on C-SBM diets. These data indicate that broiler diets fed during heat stress should be formulated with reduced economic energy content due to decreased rate of gain or feed intake per calorie compared with those at normal temperature.

Key Words: temperature, economic energy content, profit

Physiology and Endocrinology: Neuroendocrinology and Hormone Receptors

704 Chicken Pit-1 isoforms: Expression, nuclear localization, and involvement in growth hormone promoter activation. M. Mukherjee* and T. E. Porter, *University of Maryland*, *College Park*.

A POU-Homeodomain transcription factor, Pit-1, is expressed in lactotrophs, thyrotrophs and somatotrophs of the anterior pituitary gland. Pit-1 regulates expression of Prolactin, thyroid-stimulating hormone and growth hormone (GH). Multiple isoforms of Pit-1, differing from each other primarily in the N-terminal transactivation domain, have been reported. In chickens, 4 Pit-1 mRNA isoforms have been reported, Pit-1α, Pit-1β1, Pit-1β2 and Pit-1γ, but functional assays of these isoforms have not been completed. This study aimed at characterizing each isoform in its ability to translocate to the nucleus and regulate the chicken GH gene. We hypothesized that the isoforms will differ in their ability to translocate to the nucleus and/or regulate the GH gene, due to the presence of different transactivation domains. Expression of all isoforms from recombinant expression plasmids in HEK-293 cells was confirmed by Western blotting using antiserum against rat Pit-1. Pit-1α and Pit-1β2 were found to activate the GH promoter, while Pit-1γ had no effect. Interestingly, the level of expression of Pit-1γ was considerably lower than the other isoforms. Nuclear localization of the isoforms was tested in HEK-293 cells using immunofluorescence localization of expressed proteins. All isoforms except Pit-1γ showed efficient nuclear localization. To eliminate the possibility that lower expression of Pit-1γ was due to translational inefficiency, N-terminal HA- and c-myc-tagged proteins were expressed in HEK-293 cells. All tagged isoforms, except Pit-1γ were detected using antibodies directed against the tag, indicating that reduced expression of Pit-1γ was not due to inefficient translation. A remaining possible explanation for the reduced Pit-1γ levels observed is proteolytic degradation of an unstable Pit-1γ, a hypothesis that we will test empirically using inhibitors of protein degradation pathways. Future work will focus on elucidating potential physical interactions between the isoforms and their ability to interact with other transcriptional co-activators involved in regulation of Pit-1 regulated genes.

Key Words: transcription factor, anterior pituitary, growth hormone

705 Ras-dva is a novel Pit-1 and glucocorticoid regulated gene in the developing avian pituitary gland. L. E. Ellestad* and T. E. Porter, *Department of Animal and Avian Sciences and Molecular and Cell Biology Program, University of Maryland*, *College Park*.

Corticosterone (CORT) initiates growth hormone (GH) and prolactin (PRL) expression during embryogenesis. Microarray screens identified Ras-dva as a glucocorticoid-induced gene that may play a role in regulating GH and PRL expression. The objective of this study was to characterize tissue-specific and glucocorticoid regulation of Ras-dva expression in the developing chick embryo. Pituitary Ras-dva mRNA increased from embryonic day (e) 10 to a maximum just before hatch, then decreased post-hatch ($P < 0.05$; n = 3). Ras-dva mRNA was highly enriched in the pituitary relative to other tissues ($P < 0.05$; n = 3). CORT increased Ras-dva mRNA in mid- and late-stage embryonic pituitary cells, both in the presence and absence of a protein synthesis inhibitor ($P < 0.05$; n = 3), suggesting it may be a direct target of the glucocorticoid receptor (GR). We identified 5 putative Pit-1 binding sites (−0.35, −2.2, −2.5, −3.2, and −3.4kb) and 2 putative GR binding sites (−2.1 and −4kb) within the 5′-flanking region of the chicken Ras-dva gene that may be responsible for pituitary specificity and glucocorticoid regulation. E11 pituitary cells were transfected with reporter constructs containing 2kb (pGL3–2kb) and 4kb (pGL3–4kb) of the 5′-flanking region and cultured in the presence or absence of CORT (n = 3). Under basal conditions, pGL3–2kb was activated 40-fold over an empty reporter vector ($P < 0.05$), indicating that the most proximal Pit-1 site may be responsible for basal promoter activity in embryonic pituitary cells. Mutagenesis of this site in pGL3–2kb substantially reduced basal promoter activity ($P < 0.05$), confirming that this Pit-1 site is necessary for full activation of the promoter. CORT treatment had no effect on pGL3–2kb activity, but increased activity of pGL3–4kb 5-fold ($P < 0.05$). Surprisingly, mutagenesis of the potential GR binding sites did not affect CORT induction, indicating that neither putative GR binding site is necessary for CORT stimulation. In conclusion, Ras-dva is a novel glucocorticoid-regulated gene in the developing pituitary that is expressed in cells of the Pit-1 lineage, including GH- and PRL-producing cells.

Key Words: growth hormone, prolactin, corticosterone

706 Hypothalamic galanin-like peptide and kisspeptin may regulate the hypothalamo-pituitary-gonadal axis in the Mallard duck (*Anas platyrhyncos*). G. S. Fraley*, *Hope College*, *Holland, MI*.

The Mallard duck is a seasonal breeder and an excellent model for studying the neural mechanisms that regulate the activation of the hypothalamo-pituitary-gonadal axis (HPG). Recently, 2 neuropeptides have stood out as important modulators of the mammalian HPG, namely kisspeptin (KP) and galanin-like peptide (GALP). The goals of these studies were to determine (a) if KP and GALP regulate the avian HPG, (b) if KP and GALP are expressed in the mallard brain, and (c) if KP and/or GALP are co-localized with aromatase in the avian brain. Central administration of both KP and GALP significantly (ANOVA; $P < 0.01$) increased plasma luteinizing hormone, an effect blocked by pretreatment with the GnRH antagonist, acyline. Kisspeptin and aromatase immunoreactive (ir) cell bodies were observed in the medial preoptic nucleus (POM) and in fibers throughout the anseriforme brain. Virtually all POM kisspeptin-ir soma also expressed aromatase, suggesting that autocrine mechanisms may predominate in the interaction between steroid provision and kisspeptin expression. No colocalization was observed between kisspeptin-ir and GnRH-ir, although the respective fibers were in dense close proximity throughout the tuberoinfundibular area. GALP cell bodies were observed in the tuberoinfundibular nucleus and GALP-ir fibers were observed in close proximity to both GnRH- and KP-ir cell bodies and fibers. Taken together, these data suggest that estradiol synthesized by aromatase- and kisspeptin co-expressing POM neurons may regulate the HPG via an effect on GnRH secretion. Furthermore, as is observed in mammals GALP is anatomically positioned to regulate the HPG via interactions with both GnRH and KP. These observations suggest a conservation of HPG regulation in birds and mammals.

Key Words: luteinizing hormone, KiSS1

707 Gene expression profiling of dopamine-melatonin neurons in the avian premammillary nucleus. S. Kosonsiriluk*, S. W. Kang, L. J. Mauro, J. R. Garbe, S. C. Fahrenkrug, and M. E. El Halawani, *University of Minnesota*, *St. Paul*.

Dopamine-melatonin (DA-MEL) neurons of the hypothalamic premammillary nucleus (PMM) are proposed as a site for photoperiodic time measurement regulating reproductive seasonality in birds. Gene expression profiles of PMM DA-MEL neurons from photosensitive long day

(LD; n = 4 pools with 6 birds/pool) and short day (SD; n = 4 pools with 6 birds/pool) turkey hens were determined at circadian time 14 (CT14). The chicken 20.7k long oligo microarrays purchased from the University of Arizona were validated and used for this study. After hybridization and image acquisition, fluorescence intensities were extracted and graded using BlueFuse software (BlueGnome Ltd., Cambridge, United Kingdom). Microarray data was processed and normalized using JMP Genomics (SAS Institute Inc., Cary, NC). Expressed probes were identified as those whose median signal intensity was brighter than the 99th percentile of negative control expression values. Significance of gene expression was determined by ANOVA. P-values were adjusted for a false discovery rate controlled P-value threshold of 0.05. The results from expression arrays confirmed expression of clock genes in PMM DA-MEL neurons. The upregulation of *Per3*, *Cry2* and *Bmal1* was observed in SD birds (CT14, dark phase). In contrast, *Cry1*, *Per2*, *Bmal2* and *Clock* were upregulated in LD birds (CT14, light phase). In addition, expression of photopigment molecules was observed in PMM DA-MEL neurons including rhodopsin, panopsin and melanopsin. Upregulation of the rhodopsin gene was also observed in LD birds, as compared with SD birds, along with the genes encoding rod cGMP-specific phosphodiesterase 6B (PDE6B) and retinal pigment epithelium-specific protein (RPE65). This interesting expression shift following photostimulation implies possible light perception. The expression of photopigments, signaling molecules, and clock genes in PMM DA-MEL neurons provides additional support for this hypothalamic region as a site of photoreception and photoperiodic time measurement.
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Key Words: birds, circadian rhythm, photoreception

708 Septal and hypothalamic structures activated following sexual and agonistic encounters in male broiler breeders. W. J. Kuenzel*, J. Xie, and A. Jurkevich, *University of Arkansas*, *Fayetteville*.

Induction of Fos protein, an indicator of neuronal activation, was utilized to identify groups of neurons activated by either sexual or aggressive interactions in roosters. Experimental groups included handled controls, non-contact interaction with a female (M-FN), or contact interaction with a taxidermy female (M-FT), a live female (M-FC) or a live male (M-M). Eight brain areas were examined and 6 will be discussed. Results showed that the medial portion of the bed nucleus of stria terminalis, subnucleus 2 (BSTM2) was activated solely by appetitive sexual behavior (M-FN). Consummatory sexual behavior (M-FT and M-FC) resulted in significantly higher Fos protein counts in the medial preoptic nucleus (POM), lateral septum (SL), paraventricular nucleus (PVN),ventral lateral thalamic area (VLT) and bed nucleus of the pallial commissure (NCPa). Aggressive behavior (M-M) resulted in activation of the POM, SL, PVN, VLT and NCPa. It is seen that 5 neural structures were activated for both sexual and aggressive behavior suggesting that the same neural structures are utilized for functionally distinct behaviors. The most pronounced increase in Fos counts due to agonistic behavior was seen in the PVN and dual immunocytochemical studies showed that induced Fos protein occurred in magnocellular arginine vasotocin (AVT) neurons. Since magnocellular AVT neurons project directly to the posterior pituitary, it suggests that the stress response depends upon peripheral release of AVT independent of the established peptide release into the median eminence and portal system for activating ACTH secretion from the anterior pituitary. In summary, results demonstrate that use of Fos protein is effective for elucidating differential sets of neurons involved in specific behaviors of chickens.

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Key Words: Fos protein, bed nucleus of stria terminalis, arginine vasotocin

709 Various social behaviors induce differential activation of aromatase neurons in the brain of male broilers. J. Xie*, W. J. Kuenzel, and A. Jurkevich, *University of Arkansas*, *Fayetteville*.

Several steroid-sensitive nuclei in the brain form a network regulating various social behaviors. The medial preoptic area (POM) and the medial portion of bed nucleus of stria terminalis (BSTM) are important components of this network. Our previous study demonstrated that the POM is activated following male sexual behavior and intermale conflict. The subnucleus 2 of BSTM (BSTM2) was specifically activated by appetitive sexual behavior. The objective of this study was to investigate the activation of aromatase-immunoreactive (ARO-ir) neurons in the POM and BSTM using dual immunolabeling for ARO and immediate early gene product, Fos. Males were subjected to a 20-min non-contact interaction with a female (M-FN), or contact interaction with a female (M-FC) or another male (M-M). Handling (HC) and open-field (OF) groups were used as controls. In the POM, intermale interactions decreased the total number of ARO-ir cells, while M-FN had more ARO+Fos-ir neurons than other groups. The lateral portion of POM had more ARO+Fos-ir cells than the medial portion. In the BSTM1, M-FN had a higher percentage of ARO+Fos-ir cells than HC and M-M groups. In the BSTM2, social interactions resulted in a decrease of ARO-ir cells with lowest number of ir cells in the M-FC group. M-FN had significantly more ARO+Fos-ir cells than any other treatment group. In the lateral POM, ARO+Fos-ir cells positively correlated with the frequency of waltzing toward a female (courtship), while waltzing toward a male (agonistic display) negatively correlated with ARO-ir cell counts in the medial POM. In the BSTM1 and 2, positive correlations were found between ARO+Fos colocalization and waltzing toward a female, while chasing and waltzing frequency in intermale interactions negatively correlated with ARO-ir cell counts in the BSTM1 and 2, respectively. The findings suggest that activation of different ARO-ir cell groups may underlay the roles of POM and BSTM in distinct behaviors.
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Key Words: neuroendocrine regulation, mating, aggression

710 Fos protein induction in vasotocinergic neurons of male broilers following different social contexts. A. Jurkevich*, J. Xie, and W. J. Kuenzel, *University of Arkansas*, *Fayetteville*.

Vasotocin (VT) in avian species and its mammalian counterpart vasopressin are important peptidergic regulators of social behavior. The medial portion of the bed nucleus of stria terminalis (BSTM) of chickens contains parvocellular neurons producing VT in a sex dimorphic pattern with males having abundant VT cells and projections and females virtually devoid of VT in this location. In males, these cells also express galanin, corticotropin-releasing hormone and estradiol-producing enzyme aromatase suggesting important roles of this relatively small neural system in neuroendocrine regulation. The aim of this study was to reveal vasotocinergic neurons activated in roosters following different social encounters using Fos protein as an indicator of metabolic stimulation. Individual roosters were placed in an observation pen where they were provided with restricted or unrestricted access to a female (groups M-FN and M-FC), unrestricted access to a male (group M-M) or were exposed

to an empty pen (open field control, OF). After completion of tests, neurons immunolabeled for VT and Fos were quantified in 2 portions of the BSTM. In the dorsolateral subnucleus of the BSTM (BSTM1), male-female or male-male interactions did not change the total number of VT cells or percentage of VT cells co-expressing Fos. In the ventromedial subnucleus of the BSTM (BSTM2), there was a significant increase ($P < 0.05$) in percentage of VT cells co-expressing Fos in males that had non-contact interactions with females (group M-FN, 49.2 ± 4.8) as compared with control males exposed to an empty pen (group OF, 29.4 ± 7.1). Same-sex interactions resulted in lower percentage of VT and Fos co-expressing cells in BSTM2 than opposite-sex interactions ($P < 0.05$). The findings demonstrate that vasotocinergic neurons in BSTM2 of males are preferentially activated following opposite-sex interactions and confirm our previous observations regarding a key role of BSTM2 in control of male sexual behavior in roosters.

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Key Words: broiler breeders, mating, aggression

711 Effects of RFamide-related peptide-3 (RFRP-3) on secretion of LH in ovariectomized prepubertal gilts. N. L. Heidorn[1], C. R. Barb[2], C. J. Rogers[1], G. J. Hausman[2], and C. A. Lents*[1], [1]*University of Georgia*, *Athens,* [2]*USDA-ARS Richard B. Russell Agriculture Research Center, Athens, GA*.

Pulses of LH are suppressed before puberty in the gilt. RFRP-3 is proposed to be a hypophysiotropic hormone in mammals. A series of experiments (EXP) were conducted to test the hypothesis that RFRP-3 inhibits LH release in ovariectomized (OVX) prepubertal gilts. All gilts were OVX at least 2 weeks before being fitted with indwelling jugular catheters for the collection of serial blood samples. In EXP I, blood samples were collected every 15 min for 6 h. Commencing at 120 min after the start of sampling, all gilts (n = 3) received a loading dose of 1 mg of RFRP-3 followed by repeated injections of 40 μg of RFRP-3 every 5 min for 2 h resulting in a total infusion of 2 mg of RFRP-3. All injections were administered by hand in 2 mL of 0.9% saline. Area under the curve (AUC) was determined in each of 3 periods; 1 h before treatment (period 1), the first h of treatment (period 2), and the second h of treatment (period 3). In EXP II, blood samples were collected every 15 min for 8 h. Commencing at 240 min after the start of sampling, animals received intracerebroventricular (i.c.v.) injections of 10, 50, or 100 μg of RFRP-3 in 0.9% saline (n = 6/group). Control animals received 0.9% saline alone (n = 7). AUC was determined for each of 2 periods (4 h before and 4 h after i.c.v. treatment). Mean LH (1.33 ± 0.13 ng/mL), number of LH pulses (2.0), or pulse amplitude (1.32 ± 0.25 ng/mL) was not different during the 2-h treatment period when compared with 2 h pre- or the 2 h post-treatment. However, there was a tendency ($P = 0.09$) for total LH release, as indicated by AUC, to be reduced in period 3 compared with periods 1 or 2. In EXP II, central administration of 10 μg of RFRP-3 yielded an apparent suppression in area under the curve (59.4 ± 20.91% of the pre-i.c.v. value), but this did not reach significance ($P = 0.27$). We conclude that RFRP-3 does not act to inhibit the pulsatile release of LH in prepubertal gilts.

Key Words: GnIH, RFRP-3, LH

712 The effects of fluoxetine on lactation and lamb growth in sheep. P. L. Black*[1], R. A. Halalsheh[1], L. M. Lankford[1], M. M. Marricle[1], M. M. Christiansen[1], M. M. Scroppo[1], L. L. Hernandez[2], and T. T. Ross[1], [1]*New Mexico State University*, *Las Cruces*, [2]*University of Cincinnati*, *Cincinnati, OH*.

Fluoxetine (a selective serotonin reuptake inhibitor; FLX) has been shown to cause a delay in the onset of lactogenesis stage II when taken during pregnancy and/or lactation. A study was conducted to evaluate if ewes would be an appropriate model to determine the effects of FLX on milk production. Twenty-nine ewes (85 ± 12 kg; body condition score 2.6 ± 0.3) in late gestation were used in this study. Ewes allotted to treatments were stratified by fetal numbers and breeding date. Ewes were orally dosed daily with an empty capsule for controls or a capsule containing 40 mg of FLX. Dosing began on about d 121 of gestation and continued until lambing. Ewes were dosed every morning at 0700 h. Following parturition and before nursing, milk and blood samples were collected from each ewe and her lamb(s). The first milk yield was measured 8 h after birth and subsequent milkings were conducted at 1500 and 1800 h every other day for 9 d. Milk letdown was induced by a 1 mL intravenous injection of oxytocin, 1 min before milking. Milk yields were measured over a 3 h period when lamb(s) were removed. We observed a treatment by parity interaction, as ewes with multiple lambs treated with FLX had greater ($P = 0.01$) milk yields than treated or control ewes giving birth to single lambs and control ewes giving birth to multiple lambs. Lambs were weighed at birth (d 0) and following the milk yield study (d 9). We observed no differences ($P > 0.05$) in either birth weight or d 9 weights. Lamb gain over the 9 d milking period was similar among treated and control ewes ($P > 0.05$). No interactions were observed between parity and treatment in lamb weights or gain. Fluoxetine treatment during late pregnancy resulted in greater milk production in ewes giving birth to multiple lambs. However, FLX had no effect on lamb weights or lamb weight gain.

Key Words: fluoxetine, lactation, sheep

714 Cloning and characterization of chicken galanin and galanin receptors. J. C. W. Ho*[1], Y Wang[2], and F. C. Leung[1], [1]*The University of Hong Kong*, *Hong Kong, HKSAR, China*, [2]*Sichuan University*, *Chengdu, Sichuan, China*.

Galanin is a neuropeptide of 29 to 30 amino acids, widely distributed in the mammalian nervous systems and peripheral tissues. It exerts multiple physiological functions including modulation of cognitive functions and hormones release through the interaction with at least 3 known G protein-coupled receptors (GalR1, 2 and 3), which have only been identified in mammals. In the present study, 4 transcript variants of galanin prepropeptide precursor (cGAL), 3 galanin receptors (cGalR1, 2 and 3) and 2 additional receptors with considerable homology to cGalR1 and cGalR2, thus herein designated cGalR1-L and cGalR2-L, were cloned from chicken whole brain and intestine tissue respectively. Four variant cDNAs for chicken galanin prepropeptide, resulted from alternative splicing, encode precursor peptides of 88, 117, 141 and 150 amino acids respectively, while the 5 cloned receptors are ranged from 357 to 405 amino acids in lengths, sharing considerable amino acid sequence identities (50% to 86%) to their mammalian homologs. Using reverse transcription-polymerase chain reaction (RT-PCR), cGAL and its receptors were found to be widely distributed in the 12 adult chicken tissues and different regions of oviduct examined, with particularly high abundances in brain, small intestine, ovary and pituitary, except for cGalR3 in which its expression was restricted to ovary. Using different luciferase reporter systems, we also demonstrated that chicken galanin peptide was capable of altering luciferase activities, in dose-depending manners, in Chinese hamster ovary (CHO) cells expressing each cloned receptor, thus suggesting the differential functional couplings of each receptor to various classes of G proteins. The characterization of chicken galanin receptors would provide a better understanding to the physiological functions of galanin in avian species.

Key Words: chicken, galanin, galanin receptor

715 Influence of dairy herd longevity and productivity on lifetime N use efficiency. J. M. Moorby*, *Institute of Biological, Environmental and Rural Sciences*, *Aberystwyth, UK*.

Excretion of excess dietary N from dairy cows contributes to environmental pollution, with ammonia, nitrate, and nitrous oxide being the major pollutants. Apparent efficiency of feed N use for milk protein production is typically about 25%, depending on diet. However, there are long periods when a dairy cow is not productive (during heifer growth and when dry) which reduce lifetime apparent N use efficiency (NUE) because the animal excretes N with little useful output at these times. This situation is exacerbated as cow longevity decreases, and the ratio of non-productive to productive periods of life increases. A simple modeling exercise was carried out to investigate the effect of dairy cow productivity and longevity on lifetime NUE of a dairy herd yielding an assumed fixed quantity of milk. Opportunistic losses in milk production caused by disease and infertility were included to take into account the number of extra animals required for target herd milk yield. N losses during growth (including heifer mortality), pregnancy, and culling were included. With an assumed baseline NUE largely determined by nutrition (e.g., 25%) herd longevity of milking cows with a mean lactation yield of 7,500 kg resulted in lifetime NUEs of 11.8, 18.6, 21.0, 22.1 and 22.7% for lactations 1 to 5 respectively. The response was well described (R^2 = 0.99) by a general saturation curve model (Morgan-Mercer-Flodin). For a fixed herd milk yield, increased individual animal productivity resulted in better lifetime NUE because of fewer cows in the herd (e.g., 19.7, 21.0, 21.8% for 5,000, 7,500, and 10,000 kg cows completing 3 lactations). This equates to less N excretion per kg milk produced by higher yielding cows. However, this assumes rates of disease incidence and longevity are unaffected by productivity, which may not be achieved in practice. In conclusion, for herds with very high replacement rates, overall lifetime NUE is significantly affected by animal longevity. For animals surviving for about 3 lactations or more the major factor determining lifetime NUE efficiency is nutrition, and the unproductive periods of the cow's life have a relatively minor influence.

Key Words: dairy cows, longevity, N use efficiency

716 Optimal dry period length and management to maximize production and health. D. E. Santschi*[1], C. L. Girard[2], R. I. Cue[3], D. Pellerin[4], and D. M. Lefebvre[1], [1]*Valacta*, *Ste-Anne-de-Bellevue, Qc, Canada*, [2]*Agriculture and Agri-Food Canada*, *Sherbrooke, Qc, Canada*, [3]*McGill University*, *Ste-Anne-de-Bellevue, Qc, Canada*, [4]*Université Laval*, *Québec, Qc, Canada*.

The objective of this study was to determine optimal dry period (DP) length to maximize milk production and facilitate transition according to management (MGMT) used. Data were obtained from a previous study comparing effects of short (SDP; 35d dry; pre-calving ration only) and conventional DP (CDP; 60 d dry; dry-off ration until d-21 and 21d of pre-calving ration). The current data set included information on 964 cows managed with either 21d (CDP) or 35d (SDP) of pre-calving ration. Optimal DP length was determined within each MGMT group. Fixed effects of the model were DP, parity, block, herd and DP*Parity in Proc GLIMMIX (disorder incidences) or Proc MIXED (other variables). For both MGMT groups, previous lactation ECM yield was not different among DP length groups ($P \geq 0.18$). Within the CDP MGMT strategy, DP ≤ 42d tended to lower incidence of ketosis but to increase incidence of retained placenta (RP) compared with the other DP lengths ($P \leq 0.09$). However, DP length did not affect average ECM yield in the following lactation ($P = 0.62$). Within the SDP MGMT strategy, DP ≤ 28d decreased incidence of ketosis ($P = 0.01$), but increased incidence of RP ($P = 0.01$). DP ≤ 28d also decreased average ECM yield compared with DP ≥ 29d ($P = 0.01$). No effect was observed on dystocia, displaced abomasum, metritis and milk fever in either MGMT group. DPxParity was not significant. Results suggest a minimal DP of 29d is required to maximize milk yield and facilitate transition when a MGMT of 35d of pre-calving ration is used. Further analyses on reproduction and total lactation milk and component yields are required to formulate adequate recommendations.

Table 1. DP groups according to MGMT

	CDP MGMT								
	≤42d	43-49d	50-56d	57-63d	64-70d	≥71d	se	P(DP)	P(Parity)
N	59	63	112	107	48	163			
DP, d	41.9^{a}	50.6^{ab}	58.2^{c}	65.1^{c}	69.5^{c}	105.8^{d}	3.9	0.01	0.2
ECM, kg/d	29.5	32.5	31.9	30.9	31.5	31.2	1.0	0.6	0.01
Ketosis,%	13.5^{a}	33.0^{ab}	31.5^{ab}	34.8^{ab}	33.4^{ab}	41.0^{b}	7.9	0.07	0.04
RP,%	27.6^{b}	16.1^{ab}	13.9^{ab}	13.2^{ab}	8.3^{a}	8.5^{a}	7.2	0.09	0.3
	SDP MGMT								
	≤28d	29-35d	36-42d	≥43d	se	P(DP)	P(Parity)		
N	100	132	106	74					
DP, d	22.3^{a}	31.8^{b}	38.3^{c}	56.9^{d}	1.7	0.01	0.5		
ECM, kg/d	29.8^{a}	31.8^{b}	32.5^{b}	31.5^{ab}	0.7	0.01	0.01		
Ketosis,%	7.8^{a}	25.3^{b}	15.6^{ab}	27.3^{b}	7.6	0.01	0.02		
RP,%	34.6^{b}	17.4^{a}	11.7^{a}	8.7^{a}	6.6	0.01	0.05		

Key Words: dairy cow, dry period length, transition

717 Effect of dietary phosphorus amount on milk production of dairy cows in China. Z. Liu[1], C. Wang*[1], J. X. Liu[1], D. M. Wang[1], and Z. Wu[2], [1]*Institute of Dairy Science, Zhejiang University*, *Hangzhou, 310029, P. R. China*, [2]*University of Pennsylvania, School of Veterinary Medicine*, *Kennett Square*.

The effect of reducing dietary phosphorus (P) on milk production of dairy cows in China was determined using 45 multiparous Holsteins over a full lactation period. Animals were blocked into 15 groups according to milk production of previous lactation and parity, and allocated to treatments randomly within each group. Diets contained 0.37, 0.47, or 0.57% P (DM basis), based on NRC guidelines, the level recommended by the Chinese feeding standard, and the amount currently fed by most producers, respectively. Milk yield was recorded and milk composition analyzed monthly. Blood samples were collected on d −6, −3, 0, 3, 6 relative to calving and then monthly throughout the experiment. Feces and urine were analyzed in wk 12, 24, and 36. All data were analyzed using the MIXED procedure of SAS software system with cow as the repeated subject using the covariance type AR (1). The model included phosphorus level, time, and interaction of phosphorus level × time. Neither DMI nor milk yield was affected by dietary P content (see Table 1). Milk fat was slightly higher for 0.37% P than for the other 2 dietary P concentrations. Serum P did not reflect dietary P amount, and there was no influence of dietary P on serum Ca concentration. Fecal P excretion was reduced by 25% when 0.37% P was fed compared with 0.57% P. Urinary P reached a maximum concentration for all groups during peak lactation. Reducing dietary P from 0.57 to 0.37% did not negatively affect milk production, while P excretion was significantly decreased.

Table 1. Milk performance and serum Ca and P pre- and post-partum influenced by dietary P amount in dairy cows

	Dietary P, %				
	0.37	0.47	0.57	SEM	P
Milk yield, kg/d	21.5	20.7	22.0	1.00	0.63
Milk fat, %	3.71	3.41	3.61	0.10	0.05
Milk protein, %	3.33	3.30	3.28	0.05	0.77
Serum Ca, mM					
Prepartum	2.05	2.06	2.06	0.27	0.92
Postpartum	2.03	2.04	2.00	0.13	0.87
Serum P, mM					
Prepartum	1.21	1.22	1.28	0.04	0.33
Postpartum	1.25	1.23	1.18	0.07	0.60

Key Words: dietary phosphorus amount, milk production, phosphorus excretion

718 Voluntary use of showers: Effects on behavior and physiology of dairy cattle in summer. A. L. Legrand[1,3], K. E. Schütz[2], and C. B. Tucker*[1], [1]*Department of Animal Science, University of California, Davis,* [2]*AgResearch Ltd, Hamilton, New Zealand,* [3]*Division of Animal Health & Welfare, University of Edinburgh, Roslin, UK*.

Water is often used to cool dairy cows in summer. There is limited evidence that cattle find water cooling aversive and may avoid wetting parts of the body, such as the head. Our objective was to understand whether dairy cattle will voluntarily use water located away from other resources, such as feed and lying areas, and if usage affects behavioral and physiological indicators of heat stress. Twenty-four dairy cows were used, half of which had access to a cow shower that consisted of a pressure-sensitive platform fitted with 2 shower heads; water flowed when the cow stepped on the platform. Internal body temperature and behavior were recorded 24h/d for 5d during summer, and respiration rate and skin temperature were recorded during the day. Cattle spent 3.0 ± 2.1h/d in the shower, and there was considerable variability between animals (0 to 5.8h/d). Cows preferentially used the shower during the daytime, with 89 ± 12% of use between 10:00–19:00h. Shower use increased with warmer weather by 0.3h for every 1°C increase in air temperature. Respiration rate and skin temperature did not differ between treatments (*t*-test; 53 ± 3.7 vs. 61 ± 4.3 breaths/min and 35.0 ± 0.3 vs. 35.4 ± 0.4°C in shower and control, respectively, $P \geq 0.16$). In contrast, cows provided with a shower had lower (*t*-test; 0.2 ± 0.1°C) body temperature than control cows in the evening ($P \leq 0.05$); peak body temperature occurred at this time. Weather affected cattle time budgets and physiological responses in both treatments, as assessed with regression. Cows spent less time lying when heat load index (HLI; a composite measure of air temperature, humidity, wind speed and solar radiation) increased ($P < 0.01$), but the total time spent lying, standing, and feeding did not differ between treatments (*t*-test; $P > 0.32$). Cows also had higher respiration rate, and skin and body temperature as HLI increased ($P < 0.01$), regardless of treatment. These data suggest that most cattle will make considerable use of water cooling in summer, and, as expected, this alleviated some of the effects of heat load in summer. There is, however, considerable individual variation in use of water and further work is required to understand the implications of these differences in a production setting.

Key Words: heat stress, behavior, physiology

719 The influence of technological and biological factors on productivity in dairy farms. A. H. Herlin*[1] and K. Bäckman[2], [1]*Dept. Rural Buildings, Swedish University of Agricultural Sciences, Alnarp, Sweden,* [2]*Estate Office, Swedish University of Agricultural Sciences, Uppsala, Sweden*.

There are many strategic decisions for the milk producer. The Swedish milk producers, as well as many others, have increased herd sizes and have increased use of technologies which mainly improve precision and/or are labor saving. The aim of this investigation was to explore how different biological or technological factors influence productivity in dairy farms. Eight dairy farms in southern Sweden were selected as they participated in economic extension service. Detailed economic results from book-keeping were used in the analysis together with data from milk recording scheme and data from enquiries. Different milking systems were also considered for the selection of farms. On farms, technical level were registered as milking systems and number of milking units, milking frequency, number of free-stalls and type of feeding systems. Biological factors as production level, calving age, calving interval, replacement rate and causes for replacement and health on herd level and calf mortality. Data was compiled in Excel and regression coefficients determined in Minitab. Herd sizes were 97 to 550 cows with an average of 266. Average milk production was 9775 kg (SD. 1640). Increasing herd size was associated, but not significantly, with lower production. Herds with herring bone or parallel milking systems had production of about 10 500 kg milk while the herds with robotic and carousel milking had a production of about 8500 kg. Milking frequency influenced only slightly production (R^2 24%; $P = 0.218$). Occupancy rate (cows per free-stalls) showed a positive relationship in milk per cow (R^2 40%; $P = 0.091$). Increasing herd size reduced working hours per cow ($P = 0.049$), but reduction was most evident below 260 cows per herd. Higher milk revenue minus feed costs was correlated with higher production levels. The complexity of milk production on the farm level makes it also difficult to fully acquire reliable empirical data for analysis in how different factors influence profitability. However, our data show that within the herd sizes investigated, work hours per cow and year is less likely to go below 26 h in herds larger than 260 cows but further studies have to confirm that.

Key Words: profitability, milk production

720 Management-driven heterogeneity in the relationship between milk production and reproductive performance of dairy cows. N. M. Bello*, J. P. Steibel, R. J. Erskine, and R. J. Tempelman, *Michigan State University, East Lansing*.

Although research on the relationship between milk production and reproduction of dairy cows has been extensive, many studies are conflicting. Much work is characterized by a common under-appreciation of the relative importance of the within-herd (cow-level) component versus the between-herd (herd-level) component of this relationship, and how these may depend upon herd management. We recently developed and validated a bivariate hierarchical Bayesian approach to model multifactorial sources of heterogeneity for these 2 components of variances and covariances. The objective of this study was to apply this methodology to evaluate various herd management factors as sources of potential heterogeneity on variances of and covariance between milk production and reproductive performance of Michigan dairy cows. Data consisted of 124,079 lactation records from 541 Michigan dairy farms. The means, variances, and covariances between cumulative milk yield at 305 DIM (305MILK) and calving interval (CI) were modeled as a function of management practices; significant herd management factors influencing the relationship between the 2 traits were selected using the Deviance Information Criterion. The production-reproduction relationship at the herd level was generally favorable with average herd CI estimated to

decrease 0.13 ± 0.06 d for every 100 kg increase in herd 305MILK. However, for within-herd relationships, higher producing cows had poorer reproductive performance (0.50 ± 0.03 d longer CI per 100 kg increase in 305MILK) than lower producing herdmates. This unfavorable relationship was, nevertheless, alleviated by ~12% in herds with a high level (>50% cows) of bST supplementation. Significant random herd-specific sources of heterogeneity in the magnitude of the cow-level production-reproduction relationship suggest further investigation of additional management practices. Understanding the conditions under which milk yield and fertility express different associations is critical to help guide management decisions to optimize dairy cow and herd performance at its dual production-reproduction core.

Key Words: dairy cow, production-reproduction relationship, management

721 Milking frequency and milk production in pasture-based lactating dairy cows. A. G. Rius*, J. K. Kay, C. V. C. Phyn, S. R. Morgan, and J. R. Roche, *DairyNZ*, *Hamilton, New Zealand*.

The objective of this study was to test the effect of modified milking frequency (MF) during early lactation on milk production in grazing dairy cattle. Multiparous Holstein-Friesian cows (n = 150) were randomly assigned to one of 5 treatments at parturition: milked once daily (1X) for 21 d (1X21), milked 1X for 42 d (1X42), milked twice daily (2X), milked thrice daily (3X) for 21 d (3X21), and milked 3X for 42 d (3X42). All cows were milked 2X post treatment until wk 24 in lactation. Animals were offered a generous allowance of fresh pasture and supplemented with 4 kg DM/d of concentrate during the first 16 wk in milk and 2 kg DM/d for 8 wk thereafter. Effects of MF, duration of MF, and interactions during treatment and post treatment periods were tested using mixed models (GenStat 12.1). During the treatment period, a MF x duration interaction was detected for milk, protein, and fat yields. Relative to 3X21, 3X42 failed to increase milk production further. However, 1X42 had lower ($P < 0.05$) milk (2.4 kg/d), protein (0.10 kg/d), and fat (0.12 kg/d) yields compared with 1X21 during the treatment period. Relative to 2X, 3X cows produced more milk (1.5 kg/d; $P < 0.05$), however, protein and fat yields were not different during or after the treatment period. There was no MF x duration interaction post treatment. An adverse effect in production occurred for 1X in the post treatment period; however, 3X cows failed to sustain increased production compared with 2X. Relative to 2X, 1X cows had lower yields of fat (0.1 kg/d; $P < 0.01$) and protein (0.05 kg/d; $P < 0.05$) post treatment. Body weights were reduced in 2X cows compared with 1X during the treatment (476 vs. 484 kg; $P < 0.05$) and post treatment periods (500 vs. 512 kg/d; $P < 0.01$). In summary, 1X for the first 21 or 42 DIM impaired milk production and the losses continued for the remainder of the lactation. Relative to 2X, 3X in early lactation did not improve milk production beyond the period of increased milking frequency.

Key Words: milking frequency, duration, milk production

722 Water use and effectiveness of a low pressure mister system for cooling lactating dairy cows during chronic heat stress. J. K. Bernard*[1], D. R. Bray[2], N. A. Mullis[1], and C. P. Rowe[1], [1]*University of Georgia*, *Tifton,* [2]*University of Florida*, *Gainesville*.

A replicated switchback design trial was conducted during June and July, 2009 to determine the effectiveness of a low pressure mister system for providing supplemental evaporative cooling compared with a high pressure mister system. Both mister systems were mounted to the face of 91.4 cm high speed fans spaced every 18.3 m over the feed alley and free stalls in a 4-row free stall barn. The low pressure mister system (Arato Dairy Cooling System, Aratowerk GmbH & Co. KG, Germany) operated at an average line pressure of 3.4 bar (50 psi) whereas the high pressure system operated at an average line pressure of 12.4 bar (180 psi). The fans were set to operate when the ambient temperature inside the barn exceeded 22.2 C (72 F) and the mister systems operated anytime the fans were on and the relative humidity was less than 85%. Conditions within the free stall barn were continuously monitored using a Hobo ProRH/Temp data logger. Each replicate of the trial consisted of 3 wk and there were 2 replicates. For each replicate, the body temperature of 10 lactating Holstein cows each in 2 groups was continuously recorded every 5 min for 3 d using a water probe placed in the vagina each wk. Water usage for each system was measured during the second replicate using inline water meters. Environmental conditions inside the free stall barn were characteristic of chronic heat stress in that the temperature-humidity index was greater than 72 throughout the trial. The body temperature of the cows cooled with the low pressure and high pressure systems were similar ($P = 0.69$) and averaged 38.794 and 38.789 C (101.83 and 101.82 F), respectively. No differences ($P = 0.58$) were observed in respiration rates of cows which averaged 61.0 and 62.5 breaths per min for low pressure and high pressure systems, respectively. The low pressure mister system used 43% less water per day than the high pressure system. Results of this trial indicate that a low pressure mister system that uses less water can be used to provide supplemental cooling of lactating dairy cows housed in a free stall barn during chronic heat stress conditions.

Key Words: heat stress, evaporative cooling, dairy cows

723 A point-in-time comparison of the environmental impact of Jersey vs. Holstein milk production. J. L. Capper*[1] and R. A. Cady[2], [1]*Department of Animal Sciences, Washington State University*, *Pullman,* [2]*Elanco Animal Health*, *Greenfield, IN*.

This study investigated the environmental impact of producing 500,000 MT of cheddar cheese using either Jersey or Holstein cow populations. The model used current DRMS DairyMetrics population data for milk yield and composition (Jersey: 20.9 kg/d, 4.8% fat, 3.7% protein; Holstein: 29.1 kg/d, 3.8% fat, 3.1% protein), age at first calving, calving interval, and culling rate. Each population contained lactating and dry cows, bulls and herd replacements for which rations were formulated according to NRC at breed-appropriate bodyweights. Resource inputs included feedstuffs, water, land, fertilizers and fossil fuels. Waste outputs included manure and greenhouse gas emissions. Cheese yield (kg) was calculated according to Van Slyke (1949). Increased daily milk yield in Holstein cows reduced the population size required to produce 500,000 MT of cheese by 8.5%. The potential magnitude of the difference in population size was mitigated by the earlier age at first calving and shorter calving interval of Jersey cows, which reduced replacement heifer and dry cow numbers respectively. Despite the increase in total animal numbers, decreased bodyweight of individual Jersey animals reduced the total body mass of the Jersey population. In consequence, maintenance energy was reduced by 21%, water use by 27% and cropland use by 23% per unit of cheese. Fossil fuel use was reduced by 21% per unit of cheese made using milk from the Jersey population. Methane and nitrous oxide emissions associated with cheese produced by the Jersey population were reduced by 18% and 7.1% respectively. The carbon footprint (total CO_2-equivalents) was reduced by 18% per unit of cheese in Jerseys compared with Holsteins. Results demonstrate that reductions in environmental impact conferred by the 'dilution of maintenance' effect are not simply mandated by changes in milk pro-

duction, but are also markedly affected by the interplay between animal bodyweight and nutrient density of milk.

Key Words: environmental impact, carbon footprint, dilution of maintenance

724 Bio-economic value of extended lactations in Italian Holstein farms. A. S. Atzori*, R. Steri, C Dimauro, A. Cannas, and G. Pulina, *Dipartimento di Scienze Zootecniche, University of Sassari*, *Sassari, Sardinia, Italy*.

The extension of lactations over the standard 305 DIM might be suitable due to the low feeding cost in late lactation and the negative effect of pregnancy on milk yield. About 50% of the > 1,000,000 heads of Italian Holstein cows (about 9000 kg of milk/y per cow) became pregnant after 143 DIM and had a mean calving interval (CI) > 450 d. Farmers usually try to inseminate the cows as early as possible to achieve a short CI to maximize daily milk yield. Unfortunately, higher milk yields tend to reduce cow fertility in early lactation due to genetic and management constraints, reducing the economic benefit of the farm plan. A bio-economic model was developed in Excel to assess possible advantages of extended lactations. The model accounted for feeding, reproductive, milking, culling and replacement costs, based on data from farm surveys or Italian literature if needed. Total feeding costs, expressed as cost of total energy requirements at each lactation stage, were calculated per energy unit (€/Mcal) and decreased from early lactation to dry (<120, 120–250, > 250 DIM and dry). Income came from the selling of milk and live animals. The model assumed a fixed number of lactations per productive life, which increases proportionally to CI. The annual gain per cow when first insemination was delayed, voluntarily or not, from 85 to 285 DIM was calculated. To quantify the effect of pregnancy on milk yield, the estimates of Genizi et al. (1992) were used. The model showed that: 1) the annual gain per cow increased by 6.7% as lactation length increased voluntarily from 305 to 385 DIM and then decreased due to higher culling and cost of Mcal in short lactations; 2) the annual cow gain was reduced, due to infertility costs, by 2.9% and 5.6% for lactation of 385 and 505 DIM, respectively, in relation to voluntarily delayed insemination. The application of this model indicated the need for testing it in a wide range of dairy farms taking into account the milk yield level, to ascertain the effect of peak of lactation on economic results.

Key Words: extended lactation, economic value, model

725 Physiological and nutritional changes of dairy goats for maintaining milk yield during extreme heat stress conditions at late lactation. S. Hamzaoui, A. A. K. Salama*, G. Caja, E. Albanell, C. Flores, and X. Such, *Universitat Autònoma de Barcelona*, *Bellaterra, Barcelona, Spain*.

Eight Murciano-Granadina dairy goats (43.5 ± 2.6 kg BW; 194 ± 3 DIM) kept in metabolic cages were allocated in 2 balanced groups and randomly assigned to 2 climatic treatments according to a crossover design (35 d periods). Treatments were (temperature, °C; humidity, %; THI, Thorn heat index):1) thermal neutral (TN, 15 to 20°C and 35 to 45%; THI = 59 to 64), and 2) heat stress (HS, 12 h/d at 37°C and 40%, and 12 h/d at 30.5°C and 40%, THI = 85 and 77, respectively). Goats were fed daily 0.8 kg concentrate, 0.65 kg alfalfa pellets, and dehydrated fescue ad libitum. Concentrate was adjusted daily to maintain constant the forage:concentrate ratio. Feed and water intake, milk yield, and rectal temperature and respiration rate at 8, 12 and 17 h were recorded daily. Milk and blood samples were collected weekly. Blood samples for acid-base balance indicators (d 25), as well as feces and urine for digestibility and N balance (d 31 to 35) were also collected in each period. Rectal temperature (38.7 vs. 39.2°C), respiration rate (34 vs. 82 per min), water intake (5.5 vs 11.1 L/d) and evaporation (1.1 vs. 3.3 L/d), were greater in HS ($P < 0.001$) than in TN, while feed intake (2.0 vs. 1.6 kg/d) was lower ($P < 0.001$). Blood NEFA (37 vs.12 mmol/L) and haptoglobin (0.134 vs. 0.105 ng/mL) were greater ($P < 0.05$) in HS than TN only at d 7. Despite the lower feed intake of HS goats, milk yield (1.23 L/d) did not vary, but milk of HS goats contained less ($P < 0.05$) protein (3.36 vs. 3.84%) and casein (2.84 vs. 3.21%) than TN goats. Panting decreased blood CO_2 (21.9 vs. 25.7 mmol/L; $P < 0.01$) in HS goats, but they maintained blood pH at a similar value to TN goats by lowering HCO_3^- (20.9 vs. 24.6 mmol/L; $P < 0.01$) and increasing Cl^- (109 vs. 107; $P < 0.05$) in blood. Digestibility of DM, OM, and ADF tended ($P < 0.15$) to be greater in HS goats, which partially compensated for the reduction in feed intake. In conclusion, late lactating dairy goats were able to adapt to severe heat stress conditions maintaining milk yield but with reduced milk protein content.

Key Words: heat stress, dairy goat, nutrition

726 Impact of evaporative pads and cross ventilation on core body temperature and resting time of lactating cows. J. F. Smith[1], B. J. Bradford*[1], J. P. Harner[1], K. Ito[2], M. vonKeyserlingk[2], C. R. Mullins[1], J. C. Potts[1], and M. W. Overton[3], [1]*Kansas State University*, *Manhattan*, [2]*University of British Columbia*, *Vancouver, Canada*, [3]*University of Georgia*, *Athens*.

A trial was conducted to determine the impact of evaporative pads (EP) on core body temperature (CBT), time spent lying and number of lying bouts of Holstein cows housed in cross ventilated freestall facilities. Two facilities were used; 1 with EP and 1 without evaporative pads (NP). Each facility had 4 pens, 1 baffle/pen and a nominal width of 122 m. Cows (n = 143) were fit with data loggers (HOBO Pendent G) to determine resting activity and 87 cows were fit with data loggers (HOBO U12) attached to blank CIDRs to determine CBT every 5 min. Ambient conditions were collected every 15 min on both sites. Individual cow CBT and activity data (9 d/cow) were analyzed to determine the amount of time CBT was above 38.9 and 39.2°C, time spent lying, and lying bouts/d. These variables were analyzed using pen as the experimental unit, with cow and day as random effects. Parity, reproductive status, and days in milk were tested as covariates in each model but removed if they did not contribute significantly to the prediction equation. Average maximum temperatures were 25°C. Lying times and lying bouts were similar for both treatments; means for lying time and bouts were 666 min/d and 12.0/d for EP and 654 min/d and 12.9/d for NP. CBT was above 38.9°C for 566.3 and 704.5 min/d for EP and NP, respectively ($P = 0.06$), and above 39.2°C per day for 321 and 378 min/d for EP and NP ($P = 0.06$). Despite the cool ambient conditions, cows in NP tended to have CBT above 38.9°C for 2.3 more h/d and CBT above 39.2°C for 1.0 more h/d. These trends were evident even though the stocking density of the freestalls in EP was higher than NP (123.4% vs. 113.1%). These results indicate that CBT tends to be reduced even under relatively mild ambient conditions when EP are used in cross ventilated facilities.

Key Words: heat stress, lying behavior, evaporative cooling

Ruminant Nutrition: Beef: Proteins and Carbohydrates

727 Evaluation of triticale dried distillers grain as a barley silage substitute in feedlot finishing diets. K. T. Wierenga*[1], T. A. McAllister[2], D. J. Gibb[2], A. V. Chaves[2], E. K. Okine[1], K. A. Beauchemin[2], and M. Oba[1], [1]*University of Alberta*, *Edmonton, AB, Canada*, [2]*Agriculture and Agri-Food Canada*, *Lethbridge, AB, Canada*.

The objective of this study was to assess the value of triticale dried distillers grains with solubles (DDGS) as a substitute for barley silage in a dry-rolled barley (DRB) grain-based feedlot finishing diet. The trial used 144 intact (478 ± 84 kg) and 16 rumen cannulated (494 ± 50 kg) crossbred yearling steers arranged in a complete randomized design and a replicated 4 × 4 Latin square design, respectively. Steers were housed in 16 pens; 8 pens with 10 intact steers / pen, and 8 pens equipped with the GrowSafe system housing 8 intact and 2 rumen cannulated steers / pen. Steers were fed one of 4 diets (DM basis): 1) 85% DRB and 10% barley silage (CON); 2) 65% DRB, 20% triticale DDGS, and 10% barley silage (D-10S), 3) 65% DRB, 25% triticale DDGS, and 5% barley silage (D-5S), and 4) 65% DRB, 30% triticale DDGS (D-0S). Ruminal pH was measured with indwelling electrodes over 4 7-d periods. Steers fed D-10S had less variation in mean ruminal pH ($P = 0.008$) and DMI ($P = 0.009$), and tended to have higher DMI ($P = 0.08$), but similar ADG and gain:feed ratio (G:F) as compared with those fed CON. In addition, steers fed D-10S tended to have increased back fat ($P = 0.10$), and lower dressing percentage ($P = 0.06$), rib eye area ($P = 0.10$) and meat yield ($P = 0.06$) compared with those fed CON. Severity and number of abscessed livers was higher ($P = 0.006$) in steers fed D-10S as compared with CON. Replacing barley silage with triticale DDGS linearly decreased mean ruminal pH ($P = 0.006$), while duration ($P = 0.006$ and $P = 0.01$) and area ($P = 0.02$ and $P = 0.05$) below pH 5.5 and 5.2 linearly increased, and tended to linearly decrease DMI ($P = 0.10$) and increase ($P = 0.06$) G:F. Although mean ruminal pH decreased as triticale DDGS replaced barley silage, the trend for improved growth performance suggests that lower ruminal pH did not affect animal performance; however a dietary additive for liver abscess control is advised.

Key Words: triticale DDGS, finishing diet, cattle

728 Examination of rumen bacterial community changes in feedlot cattle. R. M. Beliveau*[1,2], W. Z. Yang[2], R. J. Forster[2], J. J. McKinnon[1], and T. A McAllister[2], [1]*Department of Animal and Poultry Science, University of Saskatchewan*, *Saskatoon, Saskatchewan, Canada*, [2]*Agriculture and Agri-Food Canada Research Center*, *Lethbridge, Alberta, Canada*.

A feeding trial was conducted to determine the effects of 2 finishing rations on rumen fermentation conditions and the diversity of rumen bacterial populations. Eight animals used in a concurrent replicated 4 × 4 Latin square feeding trial were sub-sampled over 4–21 d periods. The 2 diets representing extremes in forage to concentrate ratio were a typical finishing ration (85% barley, 10% silage, 0% DDGS) and an atypical ration containing no forage (60% barley, 0% silage, 35% DDGS). Rumen digesta was collected one hour before- and 3 h post-feeding on d 14 of each period. Samples were divided into liquid and solid fractions and bacterial DNA was extracted. Continuous in-dwelling pH measurements were averaged over 5 d (d11 – d16). PCR-DGGE profiles were created using universal bacterial 16S rDNA primers and analyzed using Dice coefficients to obtain percent similarity between branch clusters using UPGMA in BioNumerics software. Cluster analysis showed high levels of similarity (90.6%) between pre and post-feeding samples, however there was low similarity (≤40%) in banding profiles within each of the dietary treatments. Dendrogram representation of the cluster analysis showed no divergence between the 2 treatments based on the banding patterns of each sample. Diversity profiles of the liquid and solid fractions of digesta also showed a low level of similarity (37.0%), however clustering within liquid and within solid samples was visible. Daily range in ruminal pH, pH at time of sampling or nadir did not appear to alter bacterial diversity as determined by cluster analysis. These results indicate that the detectable bacterial community structure in the rumen is highly diverse and influenced by a variety of environmental and host factors. Animals fed high concentrate feedlot rations maintain similar bacterial profiles despite a wide divergence in forage to concentrate ratio.

Key Words: DGGE, rumen microbial diversity, pH

729 Longitudinal gene network and pathway analysis in skeletal muscle from early-weaned Angus steers fed high-starch or low-starch diets during the growing phase. S. J. Moisa*, D. E. Graugnard, L. L. Berger, D. B. Faulkner, S. L. Rodriguez-Zas, R. E. Everts, H. A. Lewin, and J. J. Loor, *Department of Animal Sciences, University of Illinois*, *Urbana*.

Metabolic regulation in complex organisms relies partly on transcriptional control of gene networks as a long-term mechanism affecting the level of expression of several key enzymes. Objectives were to evaluate temporal gene expression profiles in longissimus lumborum (LL) of early-weaned (155 ± 10 d age at weaning) Angus steers (n = 7/diet) fed a high-starch (HiS, NEG = 5.98 MJ/kg diet dry matter) or low-starch (LoS, NE_G = 4.97 MJ/kg) diet for 120 d, at which point all steers were switched to a common feedlot diet until slaughter. LL biopsies for transcript profiling and blood for metabolite analyses were collected at 0, 56, 112, and 224 d of feeding. A 13,257 bovine oligonucleotide (70-mers) array was used for transcript profiling. Functional analysis was performed by means of Ingenuity Pathways Analysis and DAVID. Analysis of variance using a false discovery rate <0.01 revealed ca. 5,000 differentially expressed genes (DEG) due to time alone. During the growing phase, the most striking differences occurred at 60 vs. 0 d when a total of 1,471 DEG were observed. The number of DEG due to time, however, was 3,702 at 224 vs. 0 d. Within the 1,471 DEG, the functional analysis revealed >45 enriched canonical pathways (e.g., acute phase response signaling, fatty acid metabolism, ERK/MAPK signaling). However, initial analysis based on expression pattern (i.e., up- or downregulation) of the genes within pathways indicated that the putative function of most of those was inhibited. Fewer canonical pathways were enriched within DEG at 224 vs. 0 d. These included oxidative phosphorylation, mitochondrial dysfunction, and LPS/IL-1 Mediated Inhibition of RXR Function. Expression patterns of genes within these pathways revealed an overall activation. Results revealed marked adaptations in networks and pathways during rapid growth of skeletal muscle.

Key Words: systems biology, transcriptomics, energy

730 Carbohydrate-responsive element binding protein (MLXIPL) and PPARγ gene network expression in longissimus lumborum of early-weaned and normal-weaned Angus steers fed a high-starch diet during the growing phase. S. J. Moisa*, D. W. Shike, D. B. Faulkner, and J. J. Loor, *University of Illinois*, *Urbana*.

Our previous work indicated precocious upregulation of adipogenic gene networks in longissimus lumborum (LL) of early-weaned Angus steers

fed a high- vs. low-starch diet during the growing phase (Graugnard et al., 2009; Br. J. Nutr. Dec. 21 [E-pub ahead of print]). Further, data provided evidence of metabolic imprinting effects of high-starch on the transcription factors sterol regulatory element-binding transcription factor 1 (SREBF1) and carbohydrate responsive element binding protein (MLX interacting protein-like, MLXIPL), both of which had greater expression in the early-weaned/high-starch-fed group after 120 d of feeding a common finishing diet. To examine the effect of weaning age on transcriptional networks associated with adipogenesis due to high-starch, 7 early-weaned (EW, 163 ± 17 d old) and 7 normal-weaned (NW, 213 ± 17 d old) calves were used and managed to receive a corn-based creep supplement (NW) or a high-starch diet (EW). For the ~100 d treatment period, EW calves remained in the feedlot and NW calves nursed their dams while on pasture. NW calves were weaned ca. 230 d postpartum and joined the early-weaned calves at the feedlot at which point both groups were fed a common finishing diet until slaughter. LL biopsies were collected at 0 (early weaning), 25, 50, 100 (normal weaning), mid-way through finishing, and 1 wk before slaughter for transcript profiling using quantitative PCR. Preliminary results from the treatment period showed that expression of both PPARG and MLXIPL was greater (ca. 2.5- and 3-fold, $P < 0.05$) in NW vs. EW steers at the start of the study. However, EW steers had gradual increases (diet × time $P < 0.05$) in both PPARG and MLXIPL such that at the end of the treatment period their expression averaged 3.4- and 5-fold relative to start of treatments. During that time-frame, expression of both genes averaged 1.3-fold of the expression at the start of treatments in NW steers. Results indicated a marked pro-adipogenic response of high-starch feeding at an early age.

Key Words: adipogenesis, nutrition, transcriptomics

731 Effects of fructose-based block supplement on ruminal concentration of lactate and growth of lactate-utilizing bacteria in forage-fed cattle. K. A. Miller*, G. L. Parsons, M. J. Quinn, and J. S. Drouillard, *Kansas State University*, *Manhattan*.

Acidosis is common among cattle as they are transitioned from forages to concentrates due to accumulation of lactate and other organic acids. This study was conducted to determine if supplementation with a fructose-based supplement could stimulate ruminal production of lactic acid and subsequent growth of lactate-utilizing bacteria in forage-fed cattle. A mixture of fructose corn syrup and vegetable oil (4%, DM basis) was dehydrated in a steam-jacketed kettle (121°C), subjected to a vacuum, discharged into containers, and cooled to form a hardened, amorphous mass. Ruminally fistulated heifers (n = 12) were blocked by BW (535 ± 54 kg), placed into individual pens, and randomized to CONTROL (no block) or BLOCK (fructose block fed at 0.9 kg/d) treatments. Heifers had ad libitum access to prairie hay and salt for 10 d, after which supplement was offered to cattle in the BLOCK treatment for 3 d by dosing directly into the rumen via the fistula at 0700 h. Ruminal digesta was sampled after 1 and 3 d of supplementation every 30 min for 8 h post-feeding to determine effects on ruminal pH, lactate, and VFA. Anaerobic cultures containing lactic acid as substrate were inoculated with strained ruminal fluid, and turbidity changes were monitored for 24 h as an indicator of capacity for lactate utilization. Ruminal pH was lower ($P < 0.01$) for the first 3 h after administration of the block. Ruminal concentrations of lactate (3.38 m*M* versus 0.66 m*M*) and butyrate (6.6 versus 4.0 m*M*) were greater for BLOCK heifers compared with CONTROLS ($P < 0.01$). Incubation of ruminal contents in lactate media revealed greater ($P < 0.05$) capacity for lactate utilization in BLOCK heifers. Feeding fructose-based blocks increased ruminal lactate production and subsequent growth of lactate-utilizing bacteria. These data provide a foundation for further investigations into possible application of fructose-based supplements to prevent acidosis when cattle are transitioned from forages to concentrate-based diets.

Key Words: fructose, lactic acid, acidosis

732 Effects of corn steep liquor in low-moisture blocks processed under vacuum or at atmospheric pressure on performance of growing heifers fed forage-based diets. K. A. Miller*, G. L. Parsons, L. K. Thompson, and J. S. Drouillard, *Kansas State University*, *Manhattan*.

A study was conducted to evaluate a novel process for manufacturing low moisture supplement blocks containing corn steep liquor (CSL) and effects on growing heifer performance. Crossbred heifers (n = 359; BW 236 ± 8.9 kg) were utilized in a randomized complete block design. Heifers were fed a basal diet containing (DM basis) 44% corn silage, 29% corn stalks, and 27% alfalfa hay, along with no supplement (CON), blocks containing 15% CSL processed at atmospheric pressure and high temperatures (HT-15), blocks processed under vacuum at low temperatures (LT-15), or blocks containing 40% CSL and processed under vacuum at low temperatures (LT-40). Heifers were fed their respective treatments 84 d, then fed a common diet 14 d to minimize differences in gut fill. Supplementing LT-15 or LT-40 blocks increased ADG over non-supplemented CON and HT-15 supplemented heifers ($P < 0.05$), but ADG were similar between the CON and HT-15 groups ($P > 0.8$), as well as for LT-15 and LT-40 treatments ($P > 0.6$). Forage DMI was similar among treatments ($P > 0.1$). Daily consumption of block supplements was greater for heifers fed LT-15 and LT-40 compared with those fed HT-15 ($P < 0.01$), but daily intakes of LT-15 and LT-40 blocks were not different ($P > 0.2$). Total intake (block intake + forage intake) was greater for heifers fed LT-15 and LT-40 blocks than non-supplemented heifers ($P < 0.05$). Total intakes of heifers fed HT-15 were intermediate and not different from CON or other block treatments ($P > 0.2$). Feed efficiency was not different among treatments ($P > 0.2$). Supplementing blocks containing CSL processed at low temperatures improves performance over non-supplemented heifers. However, when processed at high temperatures and at atmospheric pressure, adding CSL to low-moisture blocks yields no discernable benefit to cattle fed forage-based diets. This study reveals limitations in using heat sensitive ingredients in block supplements.

Key Words: low-moisture blocks, vacuum processing, condensed corn fermented extractives

733 Relationship between eating pattern and performance of Holstein bulls and steers fed high-concentrate rations using a computerized concentrate feeder. M. Devant*[1], S. Marti[1], and A. Bach[2,1], [1]*Department of Ruminant Production, IRTA*, *Barcelona, Spain*, [2]*ICREA*, *Barcelona, Spain*.

A total of 132 animals (initial BW = 220 ± ± 22 kg and age = 172 ± 0.4 d) were used to study the relationship between feeding pattern and performance. Animals were randomly allocated in 6 pens with 2 pens for each treatment: 44 intact bulls, 44 steers castrated at 3 mo of age (CAS3), and 44 bulls castrated at 8 mo of age during the study (CAS8). The study finished at 285 d of life. Each pen had one computerized concentrate feeder (GEA WestfaliaSurge, Germany), one straw feeder, and one drinker. Concentrate and straw were offered ad libitum. Animals were weighed every 14 d and concentrate eating pattern (daily mean, CV, minimum and maximum) was averaged for each 14-d period. The relationships between each eating pattern parameter and ADG or concentrate efficiency were evaluated by regression analyses using a fit model procedure of JMP with animal as random effect. Overall, average

BW was 305 ± 58.3 kg, ADG 1.4 ± 0.53 g/d, feed efficiency 22 ± 9.1%, daily intake 6.3 ± 1.01 kg/d (21 ± 0.5% CV), daily feeder visits 6.3 ± 1.29 /d (28 ± 1.0% CV), meal size 1.1 ± 0.25 kg (63 ± 1.3% CV), meal duration 10.2 ± 2.20 min (59 ± 1.2% CV), inter-meal time 244.8 ± 55.38 min (59 ± 0.7% CV), and eating rate 112 ± 16.9 g/ min (32 ± 2.1% CV). In bulls, as CV of daily intake increased ($P < 0.001$, r = −0.40) ADG decreased. In addition, in bulls as maximum daily intake increased ($P < 0.001$, r = −0.34) efficiency decreased. In steers CAS8 as CV of daily intake increased ($P < 0.001$, r = −0.36) ADG decreased. In steers CAS3 as mean daily intake and maximum daily intake increased ($P < 0.001$, −0.53 and −0.55, respectively) efficiency decreased. In addition, in CAS3 steers as mean and minimum eating rate increased ($P < 0.001$; r = −0.47 and r = −0.37, respectively) concentrate efficiency decreased. Also in steers CAS3 as mean and maximum meal size increased ($P < 0.001$; r = −0.33 and −0.33, respectively) efficiency decreased. Bulls and steers have different relationships between feeding pattern parameters and performance.

Key Words: beef, monitoring, eating pattern

734 Effect of supplemental protein source during the winter on pre- and postpartum glucose metabolism. F. W. Harrelson*[1], S. L. Ivey[1], S. H. Cox[1], R. L. Dunlap II[1], J. T. Mulliniks[1], B. H. Carter[1], C. A. Löest[1], and M. K. Petersen[2], [1]*New Mexico State University*, *Las Cruces,* [2]*USDA-ARS Fort Keogh Livestock and Range Research Laboratory*, *Miles City, MT*.

Circulating serum glucose concentrations as well as glucose utilization have been shown to be affected by forage quality. Supplemental protein provided to grazing range cows while consuming low quality forage may improve glucose metabolism. The objective of our study was to determine the effects of winter protein supplement strategy on serum glucose half-life, insulin response, as well as identify the effects of previous gestational protein supplementation on mid lactation milk yield. The study was conducted 2 consecutive calving seasons utilizing 5-yr old Angus and Angus crossbred cows (n = 8/trt each yr, 530 kg average BW). Cows were supplemented until calving with 1) a control 36% CP (35% UIP of CP) cottonseed meal based cube (CON), hand-fed at 454 g/d delivered 3d/wk ($16/45.4 kg), or 2) a self-fed 50:50 loose mineral and fishmeal 33% CP (60% UIP of CP) small supplement (SSP), formulated for a targeted consumption of 113g/d ($52/45.4 kg). After calving, cows were supplemented similarly (CON at 908 g/d offered 3 d/wk). Supplemental protein source affected ($P = 0.03$) glucose half-life, whereby the SSP cows had a lower half-life compared with CON (62 and 85 min respectively). Supplement also influenced insulin area under the curve (AUC; $P < 0.01$) with CON having a larger area compared with the SSP treatment (95.18 ± 4.9 and 75.02 ± 4.8 respectively). Prepartum glucose AUC ($P = 0.10$) and insulin half-life ($P = 0.75$) were unaffected by supplement treatment. Milk yield or components was not affected ($P > 0.05$) by supplement; however year showed a significant ($P < 0.05$) effect on these parameters. Milk yield was decreased from 7531 g ± 299 in yr 1 to 4328 g ± 293 in yr 2, possibly due to lower forage quality (~3% CP vs. ~8% CP in yr 1). These results suggest that supplemental undegradable intake protein, during times of low quality forage, may improve glucose clearance.

Key Words: beef cattle, glucose, supplementation

735 Ruminal and rectal temperatures during acidosis challenge in beef cattle. J. L. Wahrmund*, J. R. Ronchesel, C. R. Krehbiel, and C. J. Richards, *Oklahoma State University, Department of Animal Science*, *Stillwater*.

An experiment was conducted to determine the effects of ruminal acidosis challenge on ruminal temperature of beef steers. Twelve ruminally cannulated steers with ruminal temperature monitoring devices which recorded current temperature every 2 min were fed a 63% concentrate diet at 1.6% BW and randomly assigned to one of 3 challenge treatments: no dietary change (CON), half of diet replaced with cracked corn (HALF), or all of diet replaced with cracked corn (CORN). Acidosis challenge was initiated by ruminally dosing steers with their daily allotment of challenge treatment diets. Ruminal pH and rectal temperatures were recorded every 3 h for 72 h. All steers were offered CON diets at 24 and 48 h after challenge. Effects of treatment, day, hours since challenge/feeding, and all interactions were determined using the MIXED procedure of SAS. Relationships between ruminal and rectal temperatures and pH were measured using the CORR procedure of SAS. Ruminal pH showed a treatment × d effect, as pH of CORN steers was lower ($P < 0.05$) than CON and HALF steers by 0.44 units on d 1, 0.67 units on d 2, and 0.34 units on d 3. Treatment did not affect ($P > 0.05$) rectal temperatures. There was a treatment × hours since feeding effect for temperature change since initial ruminal temperature ($P < 0.05$). At time of feeding 24 and 48 h post-challenge, ruminal temperatures of CON and CORN steers were 0.04°C less than initial temperature, while those of HALF steers were 0.21°C greater ($P < 0.05$) than initial temperature. CORN and HALF steers exhibited a 0.21°C greater ($P < 0.05$) increase in ruminal temperature than CON steers 9 h after feeding. Rectal temperatures were correlated ($P < 0.05$) with ruminal temperatures for all treatments. Ruminal and rectal temperatures were negatively correlated ($P < 0.05$) with pH in HALF and CORN steers, but not in CON steers ($P > 0.05$). A 1.44 unit decrease since initial pH in CORN steers was correlated ($P < 0.05$) with a 0.14°C increase since initial ruminal temperature, but changes in these measurements were not correlated ($P > 0.05$) in HALF or CON steers. Decreasing pH associated with acidosis results in a rise in ruminal temperature.

Key Words: beef cattle, acidosis, body temperature

736 The influence of dietary protein regimens on crude protein and dry matter apparent digestibility in steers fed a steam-flaked corn based diet. E. C. Westover*[1], J. J. Wagner[1], T. E. Engle[1], T. C. Bryant[2], S. L. Archibeque[1], and J. Ham[1], [1]*Colorado State University*, *Fort Collins,* [2]*JBS Five Rivers Cattle Feeding*, *Greeley, CO*.

Four hundred crossbreed steers (330 kg ± 0.8 initial BW) were used to investigate the effects of dietary protein regimens on dry matter (DM) and crude protein (CP) digestibility, using acid insoluble ash (AIA) as an indigestible indicator substance. Cattle were randomly assigned to the following treatments that were applied to a 91% concentrate (steam-flaked corn based) diet: 1) High CP (HCP; 13.5% CP), 2) Oscillating CP (OCP; 11.62% CP diet fed Wednesday, Thursday, and Sunday and the HCP diet fed Monday, Tuesday, Friday, and Saturday), 3) Intermediate CP (ICP; 12.56% CP), and 4) Low CP (LCP; 11.62% CP). Urea was used to modify dietary CP concentrations. At the initiation of the experiment, steers were implanted with controlled release implant containing 200 mg trenbolone acetate and 40 mg estradiol. Steers were weighed every 28 d throughout the experiment and fecal grab samples were obtained over 2 d (d73 or d74; from 12 of pens per treatment) and frozen immediately. Weekly feed samples were collected, frozen, and then composited monthly. Feed and fecal samples were analyzed for DM, N (conversion factor = 6.25), and acid insoluble ash. Treatment tended ($P < 0.06$) to be a significant source of variation for CP digestibility. Steers receiving HCP diet had similar CP digestibility relative to steers receiving OCP and ICP diets. However, steers receiving the LCP diet had higher ($P < 0.04$) CP digestibility when compared with steers fed

HCP. Treatment was a significant ($P < 0.001$) source of variation for DM digestibility. Dry matter digestibility tended ($P < 0.06$) to be higher in OCP fed steers and was higher ($P < 0.001$) in LCP steers compared with HCP fed steers. Acid insoluble ash has been documented to be an accurate prediction of digestibility of DM and CP; however digestibility can be overestimated due to low AIA content in feed and feces samples. These data indicated that DM and CP digestibility can be influenced by dietary CP concentration.

Key Words: protein, digestibility, acid insoluble ash

737 Effects of rumen-protected methionine on performance and health of growing feedlot heifers. M. R. McDaniel*, D. A. Walker, K. M. Taylor, and C. A. Loest, *New Mexico State University*, *Las Cruces*.

Methionine is a limiting AA in growing cattle fed diets low in rumen undegradable protein. An experiment at the Clayton Livestock Research Center (Clayton, NM) evaluated the effects of supplementing rumen-protected Met (RPMET; METHIOPLUS, Kemin AgriFoods, Des Moines, IA) on performance and health of 718 Angus-cross heifers (average BW = 265 ± 27.8 kg). Heifers were randomly assigned to 4 treatments in 36 pens (9 pens/treatment), and were fed once daily diets that consisted of 77% Sweet Bran (Cargill Inc., Minneapolis, MN), 19.8% wheat silage, 0.24% urea, 2.95% supplement, and treatments (DM basis). Treatments were daily supplementation with 0, 7.5, 15.0, and 22.5 g of RPMET per head (estimated to supply 0, 4, 8, and 12 g/d of metabolizable DL-Met, respectively) that was mixed with the diet for a treatment group of cattle before feeding. Feed bunks were managed to maintain ad libitum intake. Performance and health were monitored for 56 d. Increasing RPMET from 0 to 12 g/d in the diets of heifers increased DMI (quadratic; $P = 0.02$), ADG (linear; $P = 0.02$), and G:F (linear; $P = 0.04$; Table 1). Supplying RPMET did not affect mortality ($P = 0.38$) and morbidity ($P = 0.19$). Supplementing a wet corn-gluten feed-based diet with RPMET improves performance of heifers during the growing phase.

We acknowledge R. Musser of Kemin AgriFoods for supplying METHIOPLUS and Cargill for supplying Sweet Bran.

Table 1. Effects of METHIOPLUS supplementation for 56 days on performance of growing feedlot heifers

	METHIOPLUS, g/d					P-value		
Item	0	7.5	15.0	22.5	SEM	Linear	Quadratic	0 vs suppl
DMI, kg/d	7.7	7.8	7.9	7.7	0.11	0.59	0.02	0.09
ADG, kg/d	1.48	1.55	1.57	1.55	0.045	0.02	0.06	<0.01
G:F	0.192	0.198	0.199	0.200	0.0027	0.04	0.47	0.04

Key Words: methionine, supplement, cattle

738 Influence of feeding increasing levels of dry or modified wet corn distillers grains plus solubles in whole corn grain-based finishing diets on pancreatic mass, and α–amylase and trypsin activity in feedlot cattle. H. Salim*[1], K. M. Wood[1], P. L. McEwen[2], I. B. Mandell[1], S. P. Miller[1], and K. C. Swanson[1], [1]*University of Guelph*, *Guelph, Ontario, Canada*, [2]*Ridgetown Campus*, *Guelph, Ontario, Canada*.

One hundred and fourteen cross-bred steer calves and 17 heifers (BW = 357.2 ± 5.8 kg) were used in a completely randomized block design (2 × 3 factorial arrangement of treatments plus a control) to determine the effect of inclusion level and form of distillers grains plus solubles (DGS) on pancreatic mass, and α-amylase and trypsin activity using whole corn grain-based finishing diets. The DGS were fed at 0 (control), 16.7, 33.3, and 50% of ration DM using dry (DDGS) or modified wet (50% DM; MWDGS) product. Data were analyzed using GLM of SAS; treatment means were compared using contrast statements (control vs. other treatments, DDGS vs. MWDGS, inclusion levels of DGS (linear, quadratic), and interactions between form and linear and quadratic inclusion levels). There were no effects ($P > 0.10$) of dietary treatment on pancreatic weight (g and g/kg BW), however pancreatic protein concentration (mg/g) was greater ($P = 0.10$) in cattle receiving DGS vs. control. Pancreatic concentration of α–amylase activity (U/g) increased ($P = 0.09$) in cattle receiving DGS vs. control. Pancreatic concentration of trypsin activity (U/g) increased linearly ($P = 0.02$) with increasing inclusion of DGS. A form by quadratic effect of inclusion level interaction ($P = 0.02$) was observed for pancreatic trypsin activity (U/g) because pancreatic trypsin activity (U/g) decreased as DDGS increased from 16.7 to 33.3% of diet DM and then increased as DDGS increased from 33.3 to 50%, while pancreatic trypsin activity (U/g) increased linearly with increasing inclusion of MWDGS. These data indicate that pancreatic concentration of α–amylase and trypsin activity may be influenced by the form and inclusion level of DGS in whole corn grain-based finishing diets.

Key Words: beef cattle, pancreas, distillers grains

739 Effects of lauric and myristic acids on ruminal fermentation, production, and milk fatty acid composition in lactating dairy cows. A. N. Hristov*[1], C. Lee[1], T. Cassidy[1], M. Long[1], K. Heyler[1], and B. Corl[2], [1]*Pennsylvania State University*, *University Park,* [2]*Virginia Tech*, *Blacksburg*.

The objective of this experiment was to investigate the effects of lauric and myristic acids on ruminal fermentation, production, and milk fatty acid (FA) profile in lactating dairy cows. The experiment was conducted as a replicated 3 × 3 Latin square. Six ruminally-cannulated cows (95 ± 26.4 DIM), were subjected to the following treatments: 240 g/cow/d of each, stearic (SA, control), lauric (LA), or myristic (MA) acids. The basal diet contained (DM basis) 15.2% CP and 33.9% NDF. Experimental periods were 28 d and cows were refaunated between periods. LA reduced ($P < 0.001$) protozoal counts in the rumen by 96% (no effect of MA), acetate, total VFA, and ammonia concentrations, and microbial N outflow from the rumen (by 32%; $P = 0.002$), compared with SA. Ruminal methane production was not affected by treatment. DMI was severely depressed ($P < 0.001$) by LA (18.6) compared with SA (26.7) and MA (24.7 kg/d), which decreased ($P = 0.017$) milk yield (35.8 and 43.6 kg/d, LA and SA, respectively). Feed efficiency, however, was the highest ($P = 0.008$) for LA (1.91), followed by MA (1.81), and SA (1.63 kg/kg). Milk fat content was also severely depressed ($P = 0.021$) by LA (2.59) compared with SA (3.42%). Treatment had no effect on milk protein content. Milk N efficiency was greater ($P = 0.022$) for LA (34.9) than SA (30.6%). Concentration of milk FA < C16 was 20% lower ($P = 0.011$) for LA than MA. Concentration of C12:0 was more than doubled ($P < 0.001$) by LA and C14:0 was increased by MA (by 45%; $P < 0.001$), compared with SA. LA resulted in lower ($P = 0.027$) C16, but greater ($P = 0.014$) long-chain FA, compared with SA and MA. Concentrations of trans C18:1 and *cis*-9, *trans*-11 CLA were doubled ($P < 0.01$) by LA compared with SA and MA. In conclusion, LA had profound effects on ruminal fermentation, mediated through inhibited microbial populations, and decreased DMI, milk yield, and milk fat content. Both LA and MA modified significantly milk FA profile.

Key Words: lauric acid, myristic acid, dairy cow

740 Time course of recovery from diet induced milk fat depression in dairy cows. D. E. Rico* and K. J. Harvatine, *The Pennsylvania State University*, *University Park*.

Nine ruminally cannulated cows were randomly assigned to treatment sequence in a Latin Square designed for analysis of recovery from diet-induced milk fat depression (dMFD). A control diet with 32% NDF was fed during the Control and Recovery periods. A low fiber and high oil diet containing 27% NDF and 3.0% soybean oil was fed during the diet-induced MFD period (dMFD). Treatment periods were 21 d in length. Milk yield and DMI were measured daily. Milk samples were taken every other day and milk was analyzed for fat and true protein. Data was analyzed using the repeated measures statement of Proc Mixed (SAS Institute); the model included period, sequence, and cow nested in sequence as random effects, and treatment, day on diet and the interaction of treatment and day on diet as fixed effects. Day was the repeated variable and the heterogeneous autoregressive covariance structure was used. Denominator degrees of freedom were adjusted by the Kenward Rogers method. DMI progressively decreased when cows were switched to dMFD and was significantly different from control after d 6 ($P < 0.05$). Intake recovered after d 15 of the recovery period. Milk yield was not affected by treatment and averaged 32.5 ± 2.1 kg. Milk fat percent and yield decreased progressively from d 1 when fed the MFD diet and were significant by d 3 ($P < 0.05$) and 7, respectively ($P < 0.05$). After switched to the recovery diet, milk fat concentration and yield progressively increased from d 1 and were the same as control on d 19 and 11, respectively. Milk protein percent increased progressively when cows were on the MFD diet and was significantly different from control after d 11 ($P < 0.001$ from d 11 to 21), reaching a plateau on d 13. Milk protein percent was 6% higher on average for dMFD vs. control cows between d 11 and 21. Milk protein yield was not affected by treatment. Our data shows that recovery from diet induced milk fat depression occurs progressively with a very short lag when dietary NDF and polyunsaturated fatty acid concentration are corrected.

Key Words: milk fat depression, dairy cows

741 Meta-analysis to calculate volatile fatty acid production in the rumen of cattle. D. Sauvant*[1] and P. Noziere[2], [1]*AGROPARISTECH-INRA MoSAR*, *Paris, France,* [2]*INRA-URH*, *63122 St Genes Champanelle, France.*

The estimation of the production of volatile fatty acids (VFA) in the rumen remains a limit for diet evaluation and formulation. To progress on this topic, a meta-analysis of published data where apparently digestible organic matter in the rumen (ADOMr) and VFA profiles were documented was performed. A database was compiled from 237(nexp) experiments (599 treatments, tr), 59% being conducted on lactating cows. Most were focused on the effects of dietary protein (32%), starch (23%), NDF (18%), or particle size (11%). There were large variations of dry matter intake (2.7 ± 0.8%LW), dietary NDF (37.4 ± 12.0%DM) or concentrate (CO, 46.8 ± 22.8%DM). The OM digestibility in the whole tract (OMDt), and intake of ADOMr were 70.3 ± 6.7% and 10.6 ± 3.7 g/kgLW, respectively. The ADOMr represented 61.6 ± 15.4% of OM digested in the whole tract. The molar percentages were 62.9 ± 5.7 for acetate, 21.4 ± 5.0 for propionate, 11.7 ± 2.0 for butyrate, and 3.8 ± 1.6 for minor VFA. ADOMr being considered as the OM recovered as VFA and gas, it was interpreted as C flows, assuming 37 and 45 mmol of C per g of carbohydrate and protein, respectively. Production of VFA was calculated from C flows and VFA profiles assuming 0.33, 0.0, 0.33, 0.15 mol of C as gas per mol of C as acetate, propionate, butyrate and minor VFA, respectively. The calculated production of VFA was 121.2 ± 42.7 mmol/kgLW, i.e. 7.1 ± 1.8 mmol/g OM digested in the whole tract. The % of C as VFA in C from ADOMr was 74.2 ± 1.5. This ratio increased with the % CO (73.0 + 0.02%CO, R2 = 0.82, RMSE = 0.8, nexp=43). For 513 of the tr, the true DOMr (TDOMr) was also measured, and the ratio VFA/TDOMr was 8.3 ± 1.2 mmol/g TDOMr. This is close to the value obtained by other approaches. Thus, Noziere et al. (2010, Animal, in press) obtained a ratio of 8.0 ± 0.6 with a database of VFA production measured in vivo with labeled VFA. In conclusion, it is possible to interpret experimental data on ADOMr and VFA profile to calculate realistic values of production of VFA from ADOMr.

Key Words: volatile fatty acid, rumen, meta-analysis

742 Forage physically effective fiber source alters ruminal pH and site of digestion. M. B. Hall*, *U.S. Dairy Forage Research Center, USDA-ARS*, *Madison, WI.*

The study objective was to evaluate the effects of physically effective fiber source (peNDF) and starch sources with different rates of fermentation (ST). Thirty-two lactating Holstein cows (8 cannulated) were

used in an incomplete Latin square design with 3 21-d periods. Dietary treatments were inclusion of chopped wheat straw (WS) or ensiled corn stover (ES) to provide 10% of diet DM as NDF, and inclusion of dry ground corn (DC) or high moisture shelled corn (HC) as the starch sources. Diets were formulated to contained similar concentrations of starch, N, and NDF. DMI was not affected by treatment. Time per day spent ruminating did not differ by diet, but time spent eating tended to be greater for cows with DC than for HC. At 2 h post-feeding, ruminal digesta DM% was greater with WS than ES. Rumen digesta DM kg did not differ by treatment. Ruminal digesta liquid kg tended to be greater with DC than HC on ES diets, but HC was greater than DC on WS diets. Ruminal pH was lower with WS than ES. In contrast, fecal pH was lower with ES than with WS. Neither pH was affected by ST. Lower ruminal pH and higher fecal pH with WS suggests that WS retained more feed to be digested in the rumen, whereas the reverse response with ES suggests that this peNDF source allowed more fermentable carbohydrate to pass from the rumen to ferment in the hindgut. Forage peNDF source may affect passage of carbohydrate.

Table 1. Effects of physically effective fiber (peNDF) and starch (ST) sources

	Diets					P-values		
	ESHC	ESDC	WSHC	WSDC	SED	peNDF	ST	Int.
DMI, kg	22.3	22.8	22.7	23.4	0.69	0.38	0.18	0.86
Rumination, min/d	485	474	494	486	15	0.34	0.36	0.89
Eating, min/d	232	240	225	239	11	0.58	0.13	0.73
Digesta, DM%	15.9	15.7	16.3	16.8	0.46	0.04	0.66	0.31
Digesta DM, kg	15.5	16.2	15.9	16.2	1.03	0.77	0.47	0.76
Digesta liquid, kg	81.7	86.4	83.7	80.0	3.5	0.42	0.83	0.12
Rumen pH	6.01	5.97	5.90	5.84	0.10	0.02	0.31	0.71
Fecal pH	6.05	5.95	6.30	6.26	0.07	0.01	0.47	0.55

Key Words: forage, fiber, dairy cattle

743 Evaluation of 2-hydroxy-4-(methylthio) butanoic acid isopropyl ester (HMBi) and methionine (Met) supplementation on digestibility and efficiency of bacterial growth in continuous culture. C. M. Fowler[1], S. K. R. Karnati[1], B. J. Bequette[2], Z. Yu[1], and J. L. Firkins*[1], [1]*The Ohio State University*, *Columbus*, [2]*University of Maryland*, *College Park*.

Assuming that HMBi metabolism is slower than dl-Met in the rumen, we hypothesized that HMBi would provide a more continual supply of Met for direct incorporation into protein or for methyl donating reactions or else spare common intermediates for bacterial synthesis of other AA. Four 50% concentrate:50% crushed alfalfa pellet diets were fed to 4 dual flow fermenters every 8 h (100 g/d). Diets were moderately limited in RDP (7.8% of DM) and CP (14.2%) to ensure that preformed AA would limit bacterial growth. The 4 treatments were 1) control (no infusion), 2) dl-Met (0.097% of DM) or isomolar 3) HMBi or 4) a 50:50 mix of HMBi and dl-Met, which were pulse-dosed 3 times daily with the feedings. On d 9, C-13 labeled HMBi or dl-Met replaced a portion of the unlabeled doses for 6 continuous infusions (over 2 d) to analyze isotopic plateau and elimination kinetics. N-15 was dosed 3 d before and during sampling, and enrichment measured in effluent, bacterial, and ammonia N. Neither NDF nor ADF digestibility were affected, but hemicellulose (NDF-ADF) digestibility and total VFA production were linearly decreased ($P < 0.05$) as HMBi replaced Met. Although flow and efficiency of bacterial N production were not affected, ammonia N concentration and flow linearly decreased ($P < 0.08$) and, conversely, peptide concentration linearly increased ($P < 0.05$) as HMBi replaced Met. Correspondingly, the bacterial N derived from ammonia increased ($P < 0.05$) with increasing HMBi. Preformed Met was transferred extensively into bacterial Met (25% for Met and 48% for the dl-Met/HMBi mix). The HMBi washout from the fermenters [kp/(kd+kp)] averaged 62%, although there likely would be significant absorption from the rumen. HMBi that did not pass out of the fermenters was readily converted to Met, which accumulated in the free Met pool, with only 5% transfer into bacterial Met. Future research is evaluating if HMBi is converted to d-Met, which would accumulate if mixed bacterial cultures lack sufficient racemase activity.

Key Words: HMBi, methionine, bacterial protein synthesis

744 Ruminal degradability of forages and diets in lactating dairy cows fed a hemicellulose extract. K. J. Herrick*[1], M. Abdullah[2], A. R. Hippen[1], D. S. Schingoethe[1], K. F. Kalscheur[1], and R. S. Patton[3], [1]*South Dakota State University*, *Brookings*, [2]*University of Veterinary and Animal Sciences*, *Lahore, Pakistan*, [3]*Temple Inland, Inc.*

Inclusion of hemicellulose extract in cattle diets has shown potential for improving fiber digestibility and production efficiency. The objective of this research was to evaluate production and in situ digestibility effects of a hemicellulose extract (Temple Inland Inc.) on mid-lactation cows. Twelve multiparous Holstein cows (142 ± 44 DIM, 685 ± 19 kg BW) including 4 with ruminal fistula were used in a 2 × 2 Latin square with 21-d periods. Cows were fed a control diet containing 55% forage (DM basis, 2/3 corn silage and 1/3 alfalfa hay) or a similar diet where 1.0% of the diet DM forage was replaced with the extract. Dry matter intake averaged 27.1 and 26.9 kg/d for the control and treatment, respectively, and was not affected by treatment. The percentage of protein (3.40 vs. 3.29) in milk was less ($P = 0.03$) and the percentage of fat (3.91 vs. 3.80) tended ($P = 0.06$) to be less for cows fed the treatment diet. Because of numerically greater milk production (38.8 vs. 39.2 kg) for cows fed the treatment diet, there were no differences in component yields other than lactose (1.86 vs. 1.94 kg/d) which tended to be greater ($P = 0.08$) for cows fed the treatment. For in situ determinations, Dacron bags containing corn silage, alfalfa hay, and either the control or treatment TMR were incubated in triplicate in the rumens of the cannulated cows at 0, 3, 6, 9, 12, 24, and 48 h on d 18 of each period. Each TMR was incubated only in cows assigned to the corresponding diet. For corn silage, the rate of disappearance (K_d) of NDF (1.7 vs. 4.3) and ADF (1.8 vs. 4.7%/h) increased ($P < 0.05$) for cows fed the treatment diet. For alfalfa hay, the disappearance of fraction A of DM, NDF, and ADF decreased and fraction B of DM and NDF increased with treatment ($P < 0.05$). The K_d for DM (8.0 vs. 11.0), NDF (6.3 vs. 10.3), and ADF (5.5 vs. 9.2) increased greatly for the alfalfa hay in rumens of treated cows ($P < 0.05$). Results demonstrated that supplementing diets of lactating dairy cows with a hemicellulose extract had a beneficial effect on fiber degradation characteristics and provide opportunities for improving animal performance.

Key Words: hemicellulose extract

745 Effect of replacing canola meal with wheat-based dried distillers grains with solubles on ruminal fermentation, microbial nitrogen supply and milk production in dairy cows. G. E. Chibisa*, D. A. Christensen, and T. Mutsvangwa, *University of Saskatchewan*, *Saskatoon, Canada*.

The objective was to determine the effect of replacing canola meal (CM) with wheat–based dried distillers grains with solubles (WDDGS) on ruminal fermentation characteristics, microbial N supply, and animal

performance. Eight lactating dairy cows were used in a replicated 4 × 4 Latin square design with 28-d periods (20 d of dietary adaptation and 8 d of measurements). Four cows in one Latin square were ruminally cannulated for measurement of ruminal fermentation characteristics and total tract nutrient digestion. Cows were fed either a standard barley silage–based TMR containing CM as the major protein supplement (control) or rations formulated to contain 10, 15 and 20% WDDGS (DM basis). Wheat-based DDGS replaced CM. Inclusion of WDDGS linearly increased DMI ($P < 0.01$; 29.5, 31.2, 30.2 and 31.9 kg/d for 0, 10, 15 and 20% WDDGS diets, respectively; n = 8). Ruminal VFA concentrations were unaffected, except that the inclusion of 20% WDDGS resulted in a decrease ($P < 0.01$) and a tendency ($P = 0.09$) for a decrease in molar concentrations of isobutyrate and total VFA, respectively. There were no differences ($P > 0.05$) among treatments for ruminal pH and ammonia concentrations, and apparent total tract nutrient digestibilities. Urinary excretion of purine derivatives (PD) was not different ($P = 0.20$) among diets; consequently, microbial N supply, estimated using urinary PD excretion, was not affected ($P = 0.19$). The addition of WDDGS in place of CM resulted in a quadratic change ($P < 0.01$) in milk yield (42.8, 42.2, 43.6 and 40.5 kg/d for 0, 10, 15 and 20% WDDGS diets, respectively; n = 8). There were no differences ($P > 0.05$) among treatments for concentrations and yields of milk fat, protein, and lactose. These data indicate that WDDGS can substitute for CM in dairy cow diets without a negative impact on ruminal fermentation characteristics, microbial N supply and animal performance.

Key Words: wheat-based DDGS, nutrient supply, milk production

746 Shifts in fermentation and intermediates of biohydrogenation induced by potassium supplementation into continuous cultures of mixed ruminal microorganisms. T. C. Jenkins*[1], E. Block[2], and J. H. Harrison[3], [1]*Clemson University*, *Clemson, SC,* [2]*Arm and Hammer Animal Nutrition*, *Princeton, NJ,* [3]*Washington State University*, *Puyallup*.

Recent studies have reported increased fat percentages in milk of lactating dairy cattle when diets were supplemented with potassium carbonate. Because milk fat yield has been associated with ruminal production of certain conjugated linoleic acid (CLA) isomers, this study was conducted to determine if increasing K exposure to ruminal microorganisms alters biohydrogenation and CLA production. Five dual-flow continuous fermenters were fed 60 g/d of a 1:1 forage (10% alfalfa hay and 90% corn silage) to concentrate mix in 2 equal portions at 0800 and 1600 h for 10-d periods (n = 4). Three of the 5 fermenters were injected just before each feeding with a 10% (w/w) stock potassium carbonate solution to provide the equivalent of 0.6 (K1), 1.2 (K2), and 1.8 (K3) g K/d. One of the remaining fermenters received no injection (K0) and the last fermenter (pHCON) was injected with adequate NaOH stock solution (10%, w/w) to match the pH observed for the K3 treatment. pH and acetate/propionate in fermenters increased ($P \leq 0.05$) linearly for K0 to K3. pH was the same but acetate/propionate was lower ($P \leq 0.05$) for pHCON compared with K3. Losses of oleic, linoleic, and linolenic acids averaged 216, 872, and 125 mg/d, respectively and were not affected by treatment. Stearic acid production changed ($P = 0.14$) from K0 to K3 (397, 449, 562, and 316 mg/d), but K3 and pHCON (206 mg/d) did not differ. Production of *trans*-10 C18:1 declined ($P \leq 0.05$) and *trans*-11 C18:1 increased ($P \leq 0.05$) linearly from K0 to K3, but pHCON and K3 were the same for both C18:1 isomers. The *cis*-9, *trans*-11 and *trans*-9, *trans*-11 isomers increased ($P \leq 0.05$) linearly from K0 to K3, but K3 and pHCON did not differ. There was a numerical decrease in production of *trans*-10, *cis*-12 from K0 to K3 (11.4, 11.5, 7.9, and 8.5 mg/d), but its production remained high (13.2 mg/d) for pHCON. The results show that increasing K in the diet has effects on shifting fermentation and biohydrogenation pathways, which can only partially be explained by elevation of pH.

Key Words: potassium, biohydrogenation, rumen

747 Methane production, fermentation patterns and protozoa numbers In Vitro as related to source of rumen fluid and feed as substrate from different cattle feeding systems. M. A. Froetschel*, C. L. Ross, S. Buaphan, S. Chinnasamy, and K. C. Das, *The University of Georgia*, *Athens*.

Rumen fluid, collected by stomach tube, and samples of diet of beef cattle grazing pasture, lactating dairy cattle fed a total mixed ration, and beef cattle fed a feedlot ration were used to determine the influence of substrate and rumen microbial population on In Vitro methane production and fermentation in a 3x3 factorial designed experiment. A modified Tilley and Terry, procedure was used and fermentation gas was collected in sampling bags with septum valves. Dry matter and gross energy digestion and volatile fatty acids and ammonia production and protozoa counts were measured using standard techniques after 24 h incubations. All parameters were corrected with measurements from rumen fluid blank incubations without substrate. Rumen fluid from feedlot and dairy cattle produced 32.8% more methane volume ($P < 0.01$). Dairy and feedlot substrate produced 60% to 116% more methane volume than grazing substrate ($P < 0.01$). Although rumen fluid source from dairy and feedlot cattle increased moles of methane per digestible energy fermented by 70.5% as compare with that from grazing cattle ($P < 0.05$), methane production per energy fermented was not influenced by substrate. Methane production efficiency was positively related to VFA production ($r = 0.98$, $P < 0.01$) and the molar percentages of propionate and butyrate but negatively related to the molar percentage of acetate ($r = 0.92$, $P < 0.02$). Protozoa counts in rumen fluid from feedlot and dairy cattle were several-fold higher than that from grazing cattle but numbers decreased dramatically in vitro after 24 h. These results imply that the methane production is more related to the level of energy fed than the pattern of rumen fermentation.

Key Words: rumen fermentation, methane, digestible energy

748 Time course of changes in ruminal chemistry and bacterial community composition following exchange of ruminal contents between lactating Holstein cows. P. J. Weimer*[1,2], D. M. Stevenson[1], H. C. Mantovani[3], and S. Man[2], [1]*USDA-ARS*, *Madison, WI,* [2]*University of Wisconsin*, *Madison,* [3]*Universidade Federale de Viçosa*, *Viçosa, MG, Brazil*.

The purpose of this study was to examine the stability and host specificity of a cow's ruminal bacterial community following massive challenge with the ruminal microflora from another cow. In each of 2 experiments, one pair of cows was selected on the basis of differences in ruminal bacterial community composition (BCC), determined by automated ribosomal intergenic spacer analysis, a culture-independent "community fingerprinting" technique. Each pair of cows was then subjected to a one-time exchange of > 95% of ruminal contents without changing the composition of a corn silage/alfalfa haylage-based TMR. In experiment 1, the 2 cows differed ($P < 0.01$) in pre-feed ruminal pH (mean = 6.88 vs. 6.14) and pre-feed total VFA concentration (mean = 57 vs. 77 m*M*), averaged over 3 d. Following exchange of ruminal contents, ruminal pH and total VFA concentration in both cows returned to their pre-exchange values within 24 h. Ruminal BCC also returned to its original profile, but this change required 14 d for one cow and 61 d for the other cow. In experiment 2, the 2 other cows differed ($P < 0.01$) in pre-feed

ruminal pH (mean = 6.69 vs. 6.20) and total VFA concentration (mean = 101 vs. 136 m*M*). Following exchange of ruminal contents, the first cow returned to its pre-exchange pH and VFA values within 24 h; the second cow's rumen rapidly stabilized to a higher pre-feed pH (mean = 6.47) and lower pre-feed VFA concentration (mean = 120 m*M*) that was retained over the 62 d test period. Both cows reached somewhat different BCCs than before the exchange. However, the BCC of both cows remained distinct and were ultimately more similar to that of the pre-exchange BCC than of the donor animal BCC. The data indicate that the host animal can quickly re-establish its characteristic ruminal pH and VFA concentration despite dramatic perturbation of its ruminal microbial community, and that ruminal BCC displays substantial host specificity that can re-establish itself when challenged with a microbial community optimally adapted to ruminal conditions of a different host animal.

Key Words: rumen, ruminal bacterial community

749 Acute phase protein response during acute bovine ruminal acidosis. A. M. Danscher*[1], M. B. Thoefner[1], P. M. H. Heegaard[2], C. T. Ekstroem[1], P. H. Andersen[1], and S. Jacobsen[1], [1]*University of Copenhagen*, *Denmark*, [2]*Technical University of Denmark*, *Copenhagen, Denmark*.

The aim was to describe the acute phase protein response during acute oligofructose-induced ruminal acidosis. Two experiments involved oral oligofructose (OF) overload (17g/kg BW) to non pregnant Danish Holstein heifers. Trial 1 included 12 heifers (8 fed grass hay and 4 barley silage) sampling was done in a 3 d control period before overload (baseline) and 9 d after overload. Trial 2 included OF overload in 10 heifers and 6 control heifers receiving tap water. Blood samples (6–48 h intervals) were analyzed for serum amyloid A (SAA), haptoglobin and fibrinogen. Heifers receiving OF generally developed a profound ruminal and systemic acidosis. In Trial 1, SAA concentrations exceeded baseline on all time points from 6 to 216 h ($P < 0.001$). Heifers fed hay had higher SAA levels (max. 290 ± 151 mg/L) than heifers fed silage (max. 225 ± 137 mg/L, $P < 0.001$). In Trial 2, SAA concentrations in OF heifers were higher than controls on all time points from 6 to 72 h (max. 325 ± 149 mg/L, $P < 0.05$). In Trial 1, haptoglobin concentrations in hay fed heifers exceeded baseline on all time points from 36 to 168 h (max. 3449 ± 1702 mg/L, $P < 0.05$). Heifers fed silage had lower haptoglobin concentrations than heifers fed hay at 60, 72 and 120 h (max. 1802 ± 950 mg/L, $P < 0.05$). In Trial 2, haptoglobin concentrations in OF heifers were higher than controls on all time points from 18 to 72 h (max. 4226 ± 924 mg/L, $P < 0.001$). In Trial 2, fibrinogen concentrations in OF heifers were higher than control heifers at all time points from 36 to 72 h (max. 12.2 ± 3.3 g/L, $P < 0.01$).
Acute ruminal acidosis caused by OF overload resulted in a distinct acute phase protein response in dairy heifers. The magnitude of the response was dependent on the feeding of the animals before overload. This difference might be due to specific adaptation of the ruminal flora and mucosa to the carbohydrate substrate supplied in the feed. Although the acute phase response is nonspecific, measurement of acute phase proteins may be used to monitor the inflammatory reaction occurring in bovine ruminal and systemic acidosis.

Key Words: ruminal acidosis, acute phase proteins, oligofructose overload

750 Redox potential measurement: A new way to explore ruminal metabolism. C. Julien*[1], J. P. Marden[2], R. Moncoulon[1], and C. Bayourthe[1], [1]*Université de Toulouse, INRA, UMR 1289 INRA/INPT/ENVT TANDEM*, *31326 Toulouse, France*, [2]*Lesaffre Feed Additives*, *59520 Marquette-Lez-Lille, France*.

Microbial metabolism is thermodynamically driven by numerous biochemical reactions that can be assessed either by free energy (ΔG) calculation or redox potential (E_h) measurement. Recent studies reported that positive E_h values recorded in a buffered sterile rumen fluid, i.e., deprived of any living organism, revealed oxidative conditions (+270 mV). On the contrary, in vivo E_h values ranged generally between –220 and –110 mV which confirmed that ruminal reducing conditions directly originated from microbial activity. Furthermore, considering that the evolution of pH with time around meal reveals ruminal metabolism, the simultaneous E_h evolution seemed to reflect the varying energetic transfers involved. Therefore, ruminal metabolism could be associated to a redox equilibrium also expressed by means of Clark's exponent (rH) which combines both E_h and pH measurements. Several experiments revealed that E_h and rH equilibrium varied with diet composition in lactating dairy cows. For example, ruminal E_h and rH were significantly different in cows receiving a corn silage-based diet complemented with different degradable protein sources: –166 mV and 6.36 for soybean meal and –147 mV and 7.48 for tanned soybean meal, respectively. To go a step further, live yeast used as ruminant feed additive proved to be a potent modulator of E_h and rH equilibrium in rumen. Recent studies showed that live yeast significantly improved ruminal reducing power in dairy cows fed a high concentrate diet: –115 mV and 8.05 for the control diet and –149 mV and 7.31 for the yeast diet. Even if ruminal E_h is not easy to assess in field conditions, it proved to be an endogenous parameter as meaningful as ruminal pH or fermentative profiles, allowing a different focus on rumen metabolism. It should be considered as a precious and interesting tool for future investigations in ruminant feeding.

Key Words: ruminal redox potential, metabolism, microflora

Small Ruminant: Sheep and Goat Production 2

751 Live and carcass leg characteristics in terminally sired lambs. M. R. Mousel*[1], T. D. Leeds[2], D. R. Notter[3], H. N. Zerby[4], S. J. Moeller[4], and G. S. Lewis[1], [1]*USDA, ARS, U.S. Sheep Experiment Station*, *Dubois, ID,* [2]*USDA, ARS, National Center for Cool and Cold Water Aquaculture*, *Leetown, WV,* [3]*Virginia Polytechnic Institute and State University*, *Blacksburg,* [4]*The Ohio State University*, *Columbus*.

Live and carcass leg characteristics of F_1 wether lambs were investigated to determine whether there were terminal-sire breed differences. Over a 3-yr period, Columbia, MARCIII, Suffolk, and Texel rams were mated with mature Rambouillet ewes to produce the lambs (n = 521). Lambs were finished in a feedlot to a mean BW of 61.9 kg (SD = 9.5 kg) and harvested at comparable ages. Before transport to slaughter, width of hind legs was measured at the widest point of the hind legs above the twist and BW was recorded for all lambs. For each carcass, weight and leg width were measured and a subjective leg score was assigned. Carcasses were fabricated into subprimal cuts, which were weighted. Live leg width (LLW), carcass leg width (CLW), leg score (LS), bone-in leg weight (BIL), and boneless leg weight (BLL) were described using mixed models that included fixed effects of breed of sire (breed), year of birth (YR), age of dam (ADAM), and type of rearing (TR) to weaning (i.e., single or as twins) and random effects of sire and maternal grandsire. The ADAM was not significant in any model, but YR and TR affected ($P < 0.01$) LLW, CLW, BIL, and BLL. The TR, but not YR, affected ($P < 0.01$) LS. Leg widths, scores, and weights were greater for single-reared than for twin-reared lambs. Breed affected ($P < 0.01$) LLW, CLW, and LS. Texel-sired lambs had the greatest leg widths, and MARCIII-sired lambs had the least. Texel-sired lambs had the greatest LS, and Columbia-sired lambs had the least. The BIL and BLL differed with breed ($P < 0.01$). Suffolk-sired lambs had the heaviest weights and MARCIII-sired lambs had the lightest. Even though breed of terminal sire affected F_1 lamb live and carcass leg traits, breeds that excelled for progeny leg shape differed from those that excelled for progeny leg weights. With this information, producers could select a terminal sire breed that would fit their production system to improve market lamb leg shape or weights.

Key Words: lamb, leg traits, terminal sire

752 The relationship of real-time ultrasound body composition measurements, body weight and hip height with body condition score in mature Suffolk x Hampshire ewes. J. A. Carter*, C. A. Hughes, K. N. Gates, and F. R. B. Ribeiro, *Texas A&M University-Commerce*, *Commerce*.

The objective of this study was to determine the relationship between real-time ultrasound (RTU) measurements of body composition, BW, and hip height (HH), with body condition score (BCS) in mature Suffolk × Hampshire ewes (n = 48). BCS was assessed visually using a 1 to 5 scale. The body composition traits measured by RTU were 12–13th rib *longissimus lumborum* muscle area (uLMA, mean = 11.75 cm^2), 12–13th rib fat thickness (uBF, mean = 0.28 cm), and ultrasound rump fat thickness (uRUMP, mean = 0.24 cm). Ultrasound measurements were taken using an Aloka 500 with a 12 cm 3.5 MHz transducer, each animal′s wool was clipped to no longer than 0.64 cm, and vegetable oil was used as a coupling agent to enhance image quality. Data were analyzed using the Proc CORR and Proc REG procedures of SAS. BW was correlated ($P < 0.05$) with BCS and HH (−0.33 and 0.60, respectively). BCS was correlated ($P < 0.05$) with HH, uLMA and uRUMP (−0.33, 0.32, and 0.46, respectively) and HH was not correlated with any of the RTU traits measured. Linear regression to predict BCS was developed using a stepwise selection. The first variable added in the model was uRUMP accounting for 21% of the variation. HH entered next in the model, accounting for an additional 6% of the variation. The full model included BW, uLMA and uRUMP and accounted for 35% of the variation in BCS. When evaluating sheep for BCS, evaluators should palpate the rump area to get a better assessment of total body fat of sheep. These results show that RTU and BW can be used to predict BCS in ewes. However, more research needs to be done to ensure the accuracy of the model.

Key Words: ultrasound, body composition, sheep

753 Redberry juniper as a roughage source in lamb finishing rations: wool and carcass characteristics, meat fatty acid profiles, and sensory panel traits. T. R. Whitney* and C. J. Lupton, *Texas AgriLife Research*, *San Angelo*.

This study was used to determine if dry redberry juiper leaves can replace cottonseed hulls in lamb finishing rations without negatively affecting wool and carcass characteristics and meat fatty acid profiles of Rambouillet ram lambs (n = 24, initial BW = 28.6 ± 4.9 kg). In a study with 2 feeding periods (Period 1 = 65% concentrate ration, 28 d; 5-d transition; Period 2 = 85% concentrate ration, 49 d), lambs were individually fed ad libitum diets containing cottonseed hulls (control; CSH), half of the cottonseed hulls replaced by dry juniper leaves (CSHJ), or all the cottonseed hulls replaced by dry juniper leaves (JUN). Lambs were completely shorn on d −1 and 83 and wool characteristics were evaluated. Lambs fed CSH, CSHJ, and JUN grew the same amount of wool when measured as greasy fleece ($P > 0.18$), clean fleece ($P > 0.45$; 0.85, 0.88, 0.81 kg ± 0.06), and clean wool production per unit of BW ($P > 0.54$;15.2, 15.8, 16.0 g/kg of BW ± 1.0). Average fiber diameter measured on mid-side samples quadratically decreased ($P = 0.04$; 20.6, 20.8, and, 19.7 μm ± 0.28) as percentage of juniper increased in the diet. On d 86, 6 lambs per treatment were randomly selected, humanely slaughtered and evaluated for carcass characteristics and meat fatty acid profiles and sensory panel traits of the LM. Carcass characteristics were not affected ($P > 0.16$) by diet, but myristic, palmitic, palmitoleic, CLA (18:2 cis-9,trans-11; 0.59, 0.64, and 0.81% ± 0.08), and arachidic fatty acids increased ($P < 0.09$) as percentage of juniper increased in the diet. Sensory panel traits were similar ($P > 0.36$) among lambs, except for off-flavor linearly increasing ($P = 0.02$) as percentage of juniper increased in the diet. Results suggest that replacing cottonseed hulls with dry juniper leaves can reduce fiber diameter and negatively affect meat flavor, but can increase CLA.

Key Words: carcass characteristics, juniper, wool

754 Evaluating roughage level in lamb finishing diets containing 40% distillers dried grains: Carcass characteristics, meat fatty acid profiles, and sensory panel traits. T. R. Whitney*, M. G. Williamson, and J. K. Mceachern, *Texas AgriLife Research Center*, *San Angelo*.

Cottonseed hulls are a common roughage source used in lamb finishing diets, especially in Texas, because of their high concentrations of NDF and ADF. Cottonseed hulls also contain condensed tannins, which can reduce rumen solubility and degradability of protein. Effects of increasing concentrations of cottonseed hulls in diets containing high concentrations of DDG on carcass characteristics, meat fatty acid profiles, and sensory panel traits are unknown. Rambouillet wether

lambs (n = 33 ± 2.3 kg) were individually fed ad libitum pelleted diets for 100 d containing 40% distillers dried grains and other ingredients, with 10% (CSH10), 20% (CSH20), or 30% (CSH30) cottonseed hulls replacing an increasing amount of ground milo. On d 100, 8 randomly selected wethers per treatment were humanely slaughtered and evaluated. Quadratic trends ($P < 0.07$) were observed for hot carcass weight (27.7, 29.3, and 27.4 kg ± 1.56) and body wall thickness (1.5, 1.8, and 1.4 cm ± 0.04) as percentage of cottonseed hulls increased in the diet. The LM area was similar ($P > 0.59$) among lambs. Quadratic trends ($P < 0.05$) were also observed for oleic acid, CLA *cis*-9,trans-11 isomer (0.19, 0.26, and 0.27% ± 0.01), CLA isomers other than *cis*-9,trans-11 (0.13, 0.13, 0.12% ± 0.01), myristic acid, palmitoleic acid, arachidic acid, and arachidonic acid as percentage of cottonseed hulls increased in the diet. The *cis*-vaccenic acid linearly decreased ($P = 0.04$) as percentage of cottonseed hulls increased in the diet. Sensory panel traits were similar ($P > 0.13$) among lambs except for initial juiciness and sustained tenderness linearly decreasing ($P < 0.05$) as percentage of cottonseed hulls increased in the diet. Results suggest that increasing percentage of cottonseed hulls in lamb finishing diets affects some carcass characteristics, meat fatty acids, and sensory traits and can increase meat CLA concentrations.

Key Words: roughage level, distillers dried grains, carcass characteristics

755 Accuracy of the FAMACHA system for estimating degree of *Haemonchus contortus* induced anemia in Hampshire, Polypay and percentage White Dorper ewes. D. K. Aaron*, M. M. Simpson, D. G. Ely, E. Fink, B. T. Burden, M. E. Hoar, and J. Farris, *University of Kentucky*, *Lexington*.

The FAMACHA system is designed to provide sheep producers with tools for on-farm detection and treatment of *Haemonchus contortus* infection. The objective of this study was to evaluate accuracy of the FAMACHA system for categorizing ewes on the basis of severity of anemia as measured by packed cell volume (PCV). A total of 1,507 records was collected on Hampshire (H; n = 414), Polypay (PP; n = 385) and percentage White Dorper (WD; n = 708) ewes from 2005 through 2009. Eyelid scores based on color of the ocular conjunctiva (1 = red, healthy to 5 = white, anemic) were assigned by the same trained technician using the FAMACHA card. Blood samples were collected and PCV were determined using a digital microhematocrit reader. Percentages of eyelid score values in each category (from 1 to 5) were 19, 38, 31, 10 and 2%, respectively. PCV decreased linearly as eyelid scores increased; however, the magnitude of change (percentage of red cells per unit change in eyelid score) was dependent upon breed (H: −2.26 ± 0.28, PP: −4.06 ± 0.22, WD: −3.69 ± 0.18; $P < 0.01$). Similarly, strength of the linear association between PCV and eyelid score varied among breeds (H: −0.388, PP: −0.671, WD: −0.610; $P < 0.01$ as per Chi-squared test of homogeneity). Across breeds, measured PCV were higher than expected within each eyelid score. Percentages of PCV exceeding the expected upper limit of the eyelid score category (from 1 to 5) were 93, 80, 92, 91 and 78% ($P < 0.01$). Few PCV were below the expected lower limits in any eyelid score category. These data confirm the FAMACHA system will allow detection of anemic animals. However, if ewes with eyelid scores of 3, 4 and 5 are considered anemic, many non-anemic ewes will be treated for parasite infection. Also, the association between eyelid score and PCV may be influenced by face color.

Key Words: anemia, *Haemonchus contortus*, sheep

756 Using FAMACHA and alternative dewormers to manage gastrointestinal nematodes in a dairy goat herd. S. P. Hart*[1] and L. J. Dawson[2,1], [1]*E (Kika) de la Garza American Institute for Goat Research, Langston University*, *Langston, OK,* [2]*Oklahoma State University CVM*, *Stillwater*.

Gastrointestinal nematodes (GIN) are the greatest health problem in goat production. FAMACHA eye color scores have been developed for selective treatment of animals to reduce the rate of development of anthelmintic resistance. Alternative anthelmintics generally are only moderately effective (40–60% fecal egg count reduction; FECR) which may not be adequate for use with FAMACHA. The purpose of this study was to test the use of alternative anthelmintics in a FAMACHA program. Lactating Alpine dairy goats (n = 91) were FAMACHA scored at 2 wk intervals from June 10 to October 15. Does with FAMACHA scores of 4 were administered one of 3 alternative anthelmintics and those with FAMACHA score of 5 were treated with levamisole HCl at 12 mg/kg BW (L). Fecal samples were taken for fecal egg counts (FEC) and blood samples were taken for packed cell volume (PCV) and serum total protein (TP). The 3 alternative anthelmintics were: 1) 2.0 g of copper oxide wires in a gelatin capsule (W), 2) 2.0 mL of a 4% solution of copper sulfate per 4.5 kg of BW as an oral drench (S), and 3) 4.0 g of cayenne pepper in a gelatin capsule (P). At least 3 animals in each period that had FAMACHA score of 3 were used as controls. FECR was low and not significantly different ($P > 0.10$)among anthelmintics (35, 52, 3, 1, and −11% for L, W, P, S, and C, respectively). FAMACHA score was improved ($P < 0.05$; except for treatment P) by administering an anthelmintic (−0.48, −0.41, −0.16, −0.37, and +0.67, for L, W, P, S, and C, respectively). TP was improved ($P < 0.01$) by administering an anthelmintic (0.45, 0.10, 0.08, 1.20, and −0.96 for L, W, P, S and C respectively). PCV was improved ($P < 0.05$) by administering an anthelmintic (−1.2, 1.0, 0.3, 1.6, and −2.4% for L, W, P, S and C, respectively. Most anthelmintics improved physiological values above the control, but W appeared superior to other alternative anthelmintics and comparable to L and would be the alternative anthelmintic of choice to use with a FAMACHA program.

Key Words: anthelmintic, alternative dewormer, gastrointestinal nematodes

757 Effects of garlic supplementation on nematode parasite infection in grazing goats. Z. Wang*, A. L. Goetsch, G. D. Detweiler, S. P. Hart, and T. Sahlu, *American Institute for Goat Research, Langston University*, *Langston, OK*.

Effects of garlic supplementation on internal parasitism and performance of lactating meat goat does grazing grass/forb pastures in the summer were determined. Forty multiparous Boer does (2 to 5 yr of age) naturally infected with nematode parasites, mainly *Haemonchus contortus*, were used in the 84-d experiment. Litter size was 1 or 2, with kids 1 to 4 mo of age when the experiment began. Five does with their kids grazed each of the 8 0.4-ha pastures. Treatments were control and garlic, with 4 pastures per treatment. Control does received 80 g/d of a mixture of 25% molasses and 75% ground corn. Does on the garlic treatment received the same supplement plus 20 g/d of garlic powder. A loose mineral-vitamin supplement was available free-choice. Means were separated by LSD. Initial mean fecal egg count (FEC; number per gram) of does was 448 (range of 0 to 1,450) and 500 (range of 0 to 2,450) for control and garlic, respectively (SEM = 119; $P > 0.05$). On d 42, doe FEC was less ($P < 0.06$) for garlic vs. control (2,837 and 6,105, respectively; SEM = 927). Does with high FEC and appreciable BW loss were treated with Levasole on d 42. Thereafter, FEC of the garlic treatment remained steady and tended to be lower compared

with the control (1,739, 1,689, and 1,303 for garlic and 1,532, 2,340, and 1,967 for control at d 56, 70, and 84, respectively; SEM = 280, 517, and 340, respectively). Doe BW was similar between treatments ($P > 0.05$). These data suggest that garlic supplementation of lactating meat goats grazing grass/forb pastures in the summer can lessen level of nematode parasitism.

Key Words: garlic, goats, internal parasitism

758 Efficacy of ginger and pumpkin seeds in controlling internal parasites in meat goat kids. D. J. O'Brien[1], M. C. Gooden[2], J. C. Warren*[1], E. K. Crook[1], J. E. Miller[3], N. C. Whitley[4], and J. M. Burke[5], [1]*Delaware State University*, *Dover,* [2]*University of Maryland Eastern Shore*, *Princess Anne,* [3]*Louisiana State University*, *Baton Rouge,* [4]*North Carolina A&T State University*, *Greensboro,* [5]*USDA, ARS, Dale Bumpers Small Farms Research Center*, *Booneville, AR*.

Twenty-two naturally infected Boer crossbred kids (mixed sex), averaging 144.4 ± 1.1 d of age and 17.6 ± 0.6 kg were used to determine the effect of 2 possible natural dewormers on BW, packed cell volume (PCV) and fecal egg counts (FEC). Goats were randomly assigned to treatments of water (CON; n = 7), 170 g pumpkin seed drench/34.0 kg BW (PUM; n = 10) or 3 g ginger/kg BW (GIN; n = 5). Treatments were administered orally to individually penned animals every other day starting at d 0 and ending on d 40. All treatment groups received a 15% CP meat goat feed daily fed at approximately 3% of their BW daily and BW and blood and fecal samples were collected weekly throughout the study period. Blood PCV were measured using microhematocrit tube centrifugation and FEC were determined using the Modified McMaster's technique (reported as eggs per gram; epg) with a sensitivity of 50 epg. Data for FEC were log-transformed for analysis but actual means ± SEM are reported. Goat BW were influenced by day, increasing over time such that d 42 BW (20.1 ± 0.6 kg) were greater ($P < 0.01$) than d 0 BW (17.6 ± 0.6 kg). Goats in the CON group had greater ($P < 0.05$) FEC than both the PUM and GIN groups (4,683 ± 483 epg, 3,409 ± 404 epg, and 2096 ± 572 epg, respectively). Goat FEC were also influenced by day with d 0 (6194 ± 750 egg) and d 7 (3749 ± 750 epg) FEC greater ($P < 0.01$) than d 35 (661 ± 750 epg) and d 42 (1308 ± 750 epg). Treatment influenced PCV with PCV for GIN (31.4 ± 1.2%) treated animals being greater than that of both CON (25.2 ± 1.0%) and PUM (27.4 ± 0.9%) treated animals. In conclusion, under the conditions of this study, additional research using ginger and pumpkin seeds are needed to further evaluate the efficacy of these natural dewormers in controlling internal parasites in goats.

Key Words: parasite, pumpkin, ginger

759 Casein glycomacropeptide (CGMP) in the diet of early weaned piglets reduces the *Escherichia coli* attachment to the intestinal mucosa and increases lactobacillar numbers in digesta. R. G. Hermes*, F. Molist, J. F. Pérez, A. G. de Segura, M. Ywazaki, and S. M. Martín-Orúe, *Universitat Autonoma de Barcelona*, *Barcelona, Spain*.

Adherence of bacteria to the intestinal mucosa is considered a prerequisite step for the colonization of pathogens. In this study we evaluated if CGMP in the diet can reduce the attachment of *E. coli* to the intestinal mucosa of oral challenged animals by enterotoxigenic *E. coli* (ETEC) K88. The experiment included 72 piglets (24 ± 3 d old) with an average BW of 6.9 ± 0.46 kg, divided into 4 treatments according to a 2 × 2 factorial design (2 diets including or not 1.5% of CGMP; ETEC challenged or not). Four days after a single 2-mL oral dose (10 CFU/ml) of the ETEC, 24 animals were killed and ileal (digesta and tissue) and colonic samples (digesta) were collected. Enterobacteria and lactobacilli were quantified in digesta by real time PCR (using SYBR green dye). Attachment of *E. coli* to ileal mucosa was monitored by FISH (fluorescent in situ hybridization) staining technique using EC1531 oligonucleotide probe, specific for *E. coli* and labeled with cyanine 3). The data were analyzed using the GLM procedure of SAS (1999), with factorial ANOVA design ($P = 0.05$). The ETEC challenge produced a mild diarrhea with increases in enterobacteria in ileal (9.2 vs. 8.4 log of 16S rDNA copies/g, $P = 0.033$) and colonic digesta (11.2 vs. 10.2 log of 16S rDNA copies/g, $P = 0.004$), and *E. coli* attachment to the ileum mucosa (34.6 vs. 8.6% of villi with bacteria adhered, $P = 0.031$). The inclusion of CGMP did not produced significant changes in the animal performance. However, it increased the lactobacilli in the colonic digesta (11.7 vs. 10.9 log of 16S rDNA copies/g, $P = 0.007$) and reduced the ileal enterobacteria, especially in the challenged animals (8.3 vs. 10.1 log of 16S rDNA copies/g, P interaction = 0.006). The CGMP most relevant result was observed on the reduction of *E. coli* adhered to the ileal mucosa (10.9 vs. 32.4% of villi with bacteria adhered, $P = 0.034$), although it was not observed significant interaction. Our results suggest that the inclusion of 1.5% of CGMP in piglet diets modify the intestinal microbial populations and impair the *E. coli* attachment to the intestinal mucosa after an ETEC oral challenge.

Key Words: casein glycomacropeptide, *Escherichia coli*, piglet

760 Early- vs. late-gestation dietary lysine requirement of young sows. R. S. Samuel*[1], S. Moehn[1], P. B. Pencharz[1,2], and R. O. Ball[1,2], [1]*Department of AFNS, University of Alberta*, *Edmonton, Alberta, Canada*, [2]*Research Institute, Hospital for Sick Children*, *Toronto, Ontario, Canada*.

Pregnant sows are traditionally fed a single dietary formulation during the entirety of gestation. The optimal feeding strategy should account for changing dietary requirements due to the linearly increasing growth rate of fetuses during the last third of gestation and the development of the mammary gland close to parturition. Young, rapidly growing sows might be expected to have greater requirements than older, slower growing sows. The objective of this study was to determine the lysine requirement of a population of 2nd and 3rd parity sows in early- (d 24 – 45) and late- (d 86 – 110) gestation. Pregnant Hypor Hybrid (Hypor Inc.) sows (n = 7; 185.7 ± 9.6 kg BW) were adapted to individual intakes of a semi-synthetic diet containing 14.0 MJ ME/kg. Each sow received 6 different test diets, in random order. These ranged from 60 – 150% and from 60 – 185% of the requirement suggested by NRC (1998) in early- and late-gestation, respectively. These were equivalent to dietary lysine intakes of 7.5 – 19.3 g/d in early- and 8.1 – 23.7 g/d in late-gestation. Oxidation of the indicator amino acid L-[1-^{13}C]-phenylalanine (Phe) during a primed-constant oral infusion was measured. The average number of piglets born alive was 13.7 ± 1.9, but ranged from 4 to 20. The average piglet birth weight was 1.5 ± 0.1 kg. Sows gained 600 g/d from breeding and weighed 258.8 ± 8.3 kg before farrowing. Breakpoint analysis of Phe oxidation indicated that the lysine requirement of 2nd parity sows was 13.1 g/d and 18.7 g/d in early- and late-gestation, respectively. For 3rd parity sows, the dietary lysine requirement was 8.2 g/d and 13.0 g/d for early- and late-gestation, respectively. The dietary requirements for lysine in early- and late-gestation were greater than previously reported by NRC (1998). Growing evidence indicates that phase feeding of sows would be economically advantageous by reducing feed costs and maximizing lifetime productivity.

Key Words: sow, gestation, lysine

761 A wheat bran extract shows a high attachment to K88 *Escherichia coli in vitro*. F. Molist, R. G. Hermes*, J. F. Pérez, and S. M. Martín-Orúe, *Universitat Autonoma de Barcelona*, *Barcelona, Spain*.

The aim of this study was to elucidate in vitro the ability of wheat bran (WB) and other fiber sources to bind K88 *E. coli* as a likely blocking mechanism of its attachment to the intestinal mucosa. The in vitro adhesion test was done in polystyrene 96-well plates using WB, rice hulls, soybean hulls, cereal straw, sugar beet pulp, pea hulls and oat hulls as possible blocking agents and 2 *E. coli* strains (K88 and non-fimbriated), isolated from the feces of post-weaning piglets. The fiber sources were diluted in phosphate buffer (PBS, 4%, w/v), sonicated 3 times and centrifuged. The supernatant was introduced in the plate and incubated at 4°C overnight. After that, the plate was washed with sterile PBS and the non-specific adhesion sites blocked with 1% BSA. The test of adhesion started when *E. coli* strains were inoculated at a concentration of 10^8 CFU/mL and allowed to adhere during 30-min at room temperature. Finally the plate was washed with sterile PBS to remove the non-attached bacteria and Luria Broth media was added to promote the growth of the attached bacteria. Plates were incubated at 37°C/10 h in a spectrophotometer where the optical density (OD, 650 nm) was recorded every 10 min. All OD data were processed using the PROC NLIN of SAS. The parameters thus obtained were used to calculate $t_{OD = 0.05}$ (delay time (h) for the cultures to reach an OD of 0.05 at 650nm). Analysis of variance of the $_{OD = 0.05}$ values was done using the PROC GLM of SAS. Results showed that the non-fimbriated *E. coli* adhered less to the fiber substrates compared with the K88 (3.14 vs. 2.72h, $P = 0.001$) which indicates that the presence of fimbria (F4) play an important role in the interaction bacteria-fiber substrate. Regarding the fiber sources, more bacteria bind to the WB (0.94 and 2.73 h for K88 and non-fimbriated, respectively, $P = 0.001$) compared with the other fiber sources (average 2.97 and 3.20 h). Our results suggest that WB could act as an anti-adhesive ingredient against pathogenic *E. coli* and improve the animal health in the post-weaning period.

Key Words: wheat bran, *E. coli*, adhesion

762 Effect of a softer surface in the farrowing crate on feed intake of lactating sows. A. Da Silva*, S. S. Anil, J. Deen, and S. K. Baidoo, *University of Minnesota*, *Saint Paul*.

Lameness in swine herds is both an economic and welfare concern. The pain associated with lameness may decrease lactation feed intake. An

important cause for lameness has been suggested to be claw lesions. Claw lesions in pigs are the result of the interaction between claw and the floor surface. However, the effect of floor type on lameness and its effects on feed intake of sows are poorly understood. The present study aimed to explore the effect of providing rubber mats in farrowing crates as a measure to minimize the adverse effects of lameness on feed intake of lactating sows. This study involved 70 lame and 70 non-lame gestating sows (gestation stall n = 63 and group pens with ESF n = 77) identified based on their ability to bear weight on all limbs without favoring any particular limb, on d 109 of gestation when they were moved from the gestation housing systems to farrowing rooms. Equal numbers of sows were randomly allocated to farrowing crates with cast iron total slatted floor or to crates with rubber mats on the cast iron total slatted floor in the posterior half. Sows in farrowing crates were hand-fed twice daily weighed amount of feed which was recorded. Feed consumed was assumed to be equal to that fed if the feeder was empty. Orts were weighed on weaning day to estimate feed intake during the lactation period. The frequency of the number of lactation days was calculated for all sows using daily feed intake (d 2 to 14 of lactation) category of 0 to 5 lbs (2.27 kg). The feed intake of lame and non-lame sows with and without rubber mats were compared using separate models for each category, controlling for the effect of housing system (Proc Genmod, SAS v 9.2). The number of days sows consumed less than 5 lbs (2.27 kg) was 42% higher in lame sows and 30% lower in stall housed sows ($P < 0.05$ for both). Rubber mat was not found to be associated with feed intake in this study.

Key Words: lameness, sow, feed intake

763 Effect of P.G. 600 on estrous cycles in gilts. M. J. Estienne* and R. J. Crawford, *Virginia Polytechnic Institute and State University*, *Blacksburg*.

A combination of eCG (400 IU) and hCG (200 IU) (P.G. 600, Intervet/Schering-Plough Animal Health, De Soto, KS) is labeled for stimulating first estrus in prepubertal gilts. Variation exists among farms, however, in the estrual response. Perhaps at least some of the variation is due to inadvertent treatment of gilts that are already cycling. The objective was to determine the effect of i.m. P.G. 600 on estrous cycle length. Prepubertal gilts (110 kg BW and 175 d of age) were checked for estrus in the presence of a boar daily throughout the experiment. Gilts in Treatment (TRT) 1 (n = 16) received P.G. 600 at the onset of boar exposure. Gilts in TRT 2 – 5 (n = 16/TRT) were allowed to express a natural first estrus and were then treated with P.G. 600 as follows: TRT 2, at d 6 ; TRT 3, at d 12 ; and TRT 4, at d 18 of the cycle. Gilts in TRT 5 received no P.G. 600. More ($P < 0.05$) gilts in TRT 1 (43.8%) were in estrus by d 7 of the experiment compared with gilts in TRT 2 – 5 (20.3%), and for gilts in estrus by d 7, the interval from the start of the study was lesser ($P < 0.01$) for TRT 1 compared with TRT 2 – 5 (4.7 ± 0.3 vs. 6.1 ± 0.3 d). Gilts displaying estrus during the entire experiment (97.5%) was not affected by treatment ($P = 0.28$). Gilts that displayed a normal estrous cycle (17 – 24 d) was greater ($P < 0.05$) for TRT 4 (100%) and 5 (100%) compared with TRT 1 (73.3%) and 3 (60%), with TRT 2 having a value (87.5%) that was not different from the other groups. Abnormal cycle lengths were 37.0 ± 9.4 d for TRT 1, 23.7 ± 13.2 d for TRT 2, and 32.5 ± 7.6 for TRT 3 ($P < 0.75$). The percentages of gilts that expressed a first estrus but then were anestrus for the remainder of the experiment was 6.7 for each of TRT 1 and 3, and 0 for TRT 2, 4 and 5 ($P < 0.23$). Although mechanisms responsible for these effects must be further scrutinized, the results demonstrate to swine producers the need to correctly classify replacement gilts as prepubertal or cycling before administering P.G. 600.

Key Words: P.G. 600, estrous cycle, gilts

764 Analysis of the association between lameness and claw lesions in stall-housed gestating sows. A. Da Silva*, S. S. Anil, J. Deen, and S. K. Baidoo, *University of Minnesota*, *Saint Paul*.

Lameness in sows has both economic and welfare implications. Severe claw lesions can cause lameness in pigs. Not all claw lesions may lead to lameness in pigs. Housing conditions and management practices may be associated with the development of claw lesions. An evaluation of the association between claw lesions and lameness would provide strategies to minimize the incidence of such lesions and reduce removal of sows for lameness. The objective of this study was to analyze the association of lameness with different types of claw lesions in sows. Claws of 63 stall-housed sows (parities 1 to 8) in a breeding herd at the University of Minnesota, Southern Research and Outreach Center, Waseca, MN were individually examined for lesions on d 110 of gestation when sows were in the farrowing crates, before farrowing. Lesions included erosions, cracks, and overgrowths. Areas in the claw were categorized as side wall, heel including overgrown heel, sole, heel-sole junction, white line and overgrown dew claw and toe. Lesions were scored on a scale of 0 (no lesion) to 3 (severe lesion). The total score for each claw area was obtained by adding the scores for that area in the lateral and medial claws of front and hind limbs. The level of lameness in these sows was assessed when they were moved to the farrowing crates, based on their ability to bear weight on all 4 limbs without favoring any particular limb. A multivariate logistic regression analysis was performed (Proc Logistic, SAS v 9.2) to assess the association of lesion scores of different claw areas with lameness (lame vs. non-lame). Lesions on the heel and the white line were associated with lameness. Total heel lesion score was negatively associated with lameness (odds ratio 0.65, $P < 0.05$). For every unit increase in total white line lesion score, the likelihood of lameness increased by 31% ($P < 0.05$). The likelihood of lameness increased with an increase in the severity of lesions in other claw areas as well, though the associations were not statistically significant.

Key Words: claw lesions, lameness, gestation stall

765 Design of porcine lactoferricin-based antimicrobial peptides with improved activity. F. F. Han*, Y. F. Liu, Y. G. Xie, Y. H. Gao, and Y. Z. Wang, *Feed Science Institute of Zhejiang University*, *Hangzhou, Zhejiang, China*.

Structure-function relationships in antimicrobial peptides have been extensively investigated to obtain improved analogs. In the present study, a series of synthetic derivatives of porcine lactoferricins were prepared with an aim to understand the structural basis of activity as well as improve its activity. We found that the 20-residue porcine lactoferricin (LP20) and its derivatives LF2A, LF-1, LF-3 displayed antimicrobial activity against *Escherichia coli*, *Staphylococcus epidermidis*, *Salmonella choleraesuis*, and *Salmonella typhimurium*. The minimal inhibitory concentrations of LP20 ranged from 64 to 128Î1/4g/mL; LF2A, LF-1 and LF-3 were 2–8 times more effective than LP20. The studies demonstrate that replacing the Cys with Ala not only increased the activities against gram-negative bacteria but also decreased hemolytic activity. Replacing the Ile with Trp both increased the antimicrobial and hemolytic activity at 4, 32, 64, 128, and 256 Î1/4g/mL ($P < 0.05$). The cytotoxic potential of LP20 analogs were quantified by colorimetric WST-1 and LDH assays in PBMC. LF2A, LF-1 and LF-3 increased cell proliferation and viability in a dose dependent Fashion. Compared with LP20, 25–200 Î1/4g/mL LF-1 improved the cell proliferation significantly ($P < 0.05$), while 400 Î1/4g/mL LF-1 decreased the cell proliferation ($P < 0.05$). Both 200Î1/4g/mL and 400Î1/4g/mL LF-1 induced an increase ($P < 0.05$) in LDH release from PBMC whereas 25–50Î1/4g/mL decreased the LDH release ($P < 0.05$). Moreover, LF-1, LF-3 able to disrupt the

cytoplasmic membranes at relatively low concentrations. In contrast, LP20 and LF2A had more-modest antibacterial activities, a lesser ability to depolarize the cytoplasmic membrane.

Key Words: porcine lactoferricin, antimicrobial peptide, cytotoxic activity

ADSA Production Division Symposium: Dairy Products and Human Health: The Facts

766 Dairy products and human health: The facts. D. I. Givens*, *University of Reading, Reading, Berkshire, United Kingdom*.

Increasing obesity and an aging population increase substantially the risk of chronic disease and its associated cost. Diet is a modifier of risk and since milk and its products are staple components of most Western diets providing key nutrients, it is very important to understand whether these foods also increase or decrease the risk of chronic disease. This paper will assess the current evidence available. A recent meta-analysis (Elwood et al., 2008) showed the relative risk of stroke and/or heart disease in subjects with high milk or dairy consumption was 0.84 (95% CI 0.76, 0.93) and 0.79 (0.75, 0.82) respectively, relative to the risk in those with low consumption. Four studies reported incident diabetes as an outcome, and the relative risk in the subjects with the highest intake of milk or diary foods was 0.92 (0.86, 0.97). The World Cancer Research Fund (2007) report confirmed that increased milk consumption will probably decrease the risk of colorectal cancer. Some studies have shown a positive association between increased milk consumption and prostate cancer but the increased risk is small and not consistent across studies. It should however not be ignored. Set against the proportion of total deaths attributable to the life-threatening diseases in the EU i.e. vascular disease, diabetes and cancer, the available data provide evidence of an overall survival advantage from the consumption of milk although the situation with other dairy foods is much less clear and needs urgent clarification. For milk in particular there appears to be an enormous mismatch between both the advice given on milk/dairy foods items by various authorities and public perceptions of harm from the consumption of milk and dairy products, and the evidence from long-term prospective cohort studies. These foods do however supply a sizeable proportion of dietary saturated fatty acids in many countries but simply reducing milk consumption to reduce saturated fatty acid intake is not likely to produce benefits overall though the production of dairy products with reduced saturated fatty acid contents is likely to be helpful.

Key Words: milk, health, epidemiology

Wednesday, July 14, 2010

POSTER PRESENTATIONS

Animal Health: Probiotics and Diet

W1 Improved health status of newborn calves from dairy cows treated intravaginally with probiotic bacteria. Q. Zebeli*, S. Iqbal, S. M. Dunn, and B. N. Ametaj, *University of Alberta*, *Edmonton, AB, Canada*.

Improving cow's reproductive health during the transition period might be beneficial for the health status of newborn calves. We recently developed an intravaginal probiotic treatment to prevent uterine infections in dairy cows. This study sought to evaluate the effects of probiotic treatment of dairy cows on selected plasma variables and the incidence of diarrhea in newborn calves. Nineteen dairy calves coming from control (CTR; n = 10) or cows administered intravaginally with a probiotic culture (PRO; n = 9) at −2 and −1 wk prepartum as well as at +1, +2, +3, and +4 wk postpartum were used in this study. A total of 10^{10} to 10^{12} cfu of a probiotic culture consisting of *Lactobacillus sakei* FUA 3089, *Pediococcus acidilactici* FUA 3140, and *P. acidilactici* FUA 3138 was dissolved in 1 mL reconstituted skimm milk. Calves were supplied with 4 kg colostrum/d up to 3 d after birth, and blood samples were collected from the jugular vein on d 3 and 10. The incidence of diarrhea was monitored daily in all calves up to 2 wk. Blood data were submitted to repeated measures ANOVA, whereas the incidence of diarrhea was analyzed by chi-squared test with SAS. Significance and tendency levels were considered at $P < 0.10$ and $P < 0.15$, respectively. Data indicated that PRO calves showed greater concentration of glucose (89.4 vs. 101.5, ± 4.6 mg/dL), but lower lactate (5.7 vs. 4.3, ± 0.5 mmol/L) in the plasma ($P < 0.10$). Also, concentrations of haptoglobin (444 vs. 347, ± 60.1 μg/mL) and β-hydroxy-butyrate (125 vs. 107, ± 6.9 μmol/L) in the plasma tended to be lower in the PRO calves ($P = 0.11$). There was no effect of treatment on calf's body weight at birth, plasma non-esterified fatty acids, and cholesterol ($P > 0.15$). Frequency tables revealed that 6 out of 10 calves (60%) pertaining to the CTR group were affected by diarrhea, whereas the PRO calves showed lower ($P = 0.09$) incidence of diarrhea (2 from 9; 22.2%). In summary, results suggested that intravaginal treatment of the pregnant cows with probiotics during the transition period enhanced the metabolic health status of newborn dairy calves.

Key Words: probiotics, dairy calf, plasma metabolites

W2 Infusion of commensal bacteria intravaginally improved overall health status of transition dairy cows. Q. Zebeli*, S. Iqbal, S. M. Dunn, and B. N. Ametaj, *University of Alberta*, *Edmonton, AB, Canada*.

Transition period is associated with high incidence of metabolic and infectious diseases in dairy cows. Because commensal lactobacilli exert immune-stimulating properties, we hypothesized that intravaginal administration might promote health status of the transition dairy cows. This study sought to evaluate the effects of intravaginal administration of commensal lactobacilli on the incidence of metabolic diseases in transition dairy cows. Eighty Holstein cows were blocked by parity and incidence of disease in the previous lactation, and randomly allocated to 1 of the 2 different treatment groups. Forty cows (incl. 12 primiparous cows) were administered intravaginally with 10^{10} to 10^{12} cfu bacterial culture (*Lactobacillus sakei* FUA 3089, *Pediococcus acidilactici* FUA 3140, and *P. acidilactici* FUA 3138) dissolved in 1 mL reconstituted skim milk (TRT). The control cows (CON) received 1 mL of reconstituted skim milk only. Infusion was carried out by an insemination pipette at −2 and −1 wk prepartum and at +1, +2, +3, and +4 wk postpartum. Urine and vaginal pH were measured before the culture administration. Cows were monitored daily for incidence of disease, starting from −2 wk up to +8 wk postpartum. Data were analyzed statistically by chi-squared test with SAS. Results showed that TRT cows had lower incidence of lameness (56.1 vs. 34.2%; $P = 0.04$) and susceptibility from more than one disease such as metritis, pyometra, and mastitis (27.5 vs. 15.9%; $P < 0.01$). Treatment tended to lower the number of medications (7.3 vs. 4.5 medications/cow; $P = 0.09$) throughout the experiment in multiparous cows. Also, multiparous TRT cows showed greater urine pH (7.9 vs. 8.2; $P = 0.03$). Vaginal pH was affected only by day of sampling being the lowest at −3 d before parturition ($P = 0.02$). Data showed that 51.9% of multiparous CON cows had a strong (>25%) day-to-day variation of feed intake, whereas this variable was 21.4% in the TRT cows ($P = 0.02$). In conclusion, results indicated that intravaginal treatment of the pregnant cows with commensal lactobacilli improved health status of transition dairy cows.

Key Words: dairy cow, metabolic disorder, intravaginal lactobacilli

W3 Intravaginal administration of commensal lactobacilli modulated plasma metabolites and innate immunity in periparturient dairy cows. S. Iqbal, Q. Zebeli, S. M. Dunn, and B. N. Ametaj*, *University of Alberta*, *Edmonton, AB, Canada*.

Dairy cows experience a high incidence of uterine infections after parturition which initiates major changes in metabolism and activation of an acute phase response. The objective of this study was to test the effects of an intravaginal infusion of a mixture of lactobacilli around parturition on selected plasma metabolites and innate immunity in transition dairy cows. Eighty pregnant Holstein heifers and dairy cows were randomly assigned to one of the following treatments: 1) intravaginal administration of 1 mL of carrier alone (reconstituted skim milk) for the control cows, or 2) intravaginal administration of 10^{10}-10^{12} cfu of probiotic bacteria dissolved in 1 mL of reconstituted skim milk. The probiotic preparation contained a mixture of *Lactobacillus sakei* FUA 3089, *Pediococcus acidilactici* FUA 3140, and *P. acidilactici* FUA 3138 isolated from the vaginal tracts of healthy cows. Probiotics were applied intravaginally with a sterile syringe and insemination pipette once during wk −2, −1, +1, +2, +3, and +4 relative to parturition. Blood samples were collected from 15 cows per group (5 heifers and 10 cows) to be analyzed for β-hydroxybutyrate (BHBA), non-esterified fatty acids (NEFA), glucose, lactate, and haptoglobin (Hp). Results showed lower concentrations of BHBA (647 vs. 846 μmol/L; $P < 0.05$) and greater plasma NEFA (266 vs. 136 μEq/L; $P < 0.01$) in primiparous cows of treatment group. These cows also showed an interaction between treatment and wk of sampling for NEFA which were higher on wk +1, +2, and +4 ($P < 0.05$), and tended to be greater on wk +6 ($P = 0.11$). Also, an

interaction between treatment and time of measurement for cholesterol in multiparous cows ($P = 0.13$) was obtained. Interestingly, the overall analysis showed an interaction between treatment and wk of measurement for plasma Hp which was lower in the treatment group on wk −1 ($P = 0.05$) and tended to be lower on wk +2 ($P = 0.07$). In summary, intravaginal administration of lactobacilli modulated plasma metabolites and improved innate immunity in periparturient dairy cows.

Key Words: dairy cow, intravaginal probiotics, plasma metabolites

W4 Intravaginal treatment with probiotics decreased the incidence of subclinical mastitis in dairy cows. S. Iqbal, Q. Zebeli, S. M. Dunn, and B. N. Ametaj*, *University of Alberta*, *Edmonton, AB, Canada*.

The decrease in milk production and high culling rate associated with mastitis are major concerns of the dairy industry. The aim of this study was to evaluate the effect of an intravaginal administration of a probiotic preparation around parturition to prevent development of subclinical mastitis in dairy cows. Eighty pregnant Holstein cows were randomly assigned to one of the 2 treatment groups: 1) intravaginal administration of 1 mL of carrier alone (reconstituted skim milk) for control cows, or 2) intravaginal administration of 1 mL of reconstituted skim milk containing 10^{10} to 10^{12} cfu of probiotic bacteria. The probiotic preparation contained a mixture of *Lactobacillus sakei* FUA 3089, *P. acidilactici* FUA 3140, and *Pediococcus acidilactici* FUA 3138 isolated from the vaginal tracts of healthy cows. Probiotic bacteria were applied intravaginally with a syringe and a sterile insemination pipette once during wk −2, −1 and +1, +2, +3, and +4 around calving. Milk samples were collected from 15 cows (5 heifers and 10 cows) per group to be analyzed for different milk variables. Results of the overall ANOVA showed that treatment lowered SCC (85,000 vs. 236,000 cells/mL; $P = 0.02$); whereas, there was a tendency for higher protein yield (1.06 vs. 0.91 kg; $P < 0.10$), as well as lactose content (4.37 vs. 4.30%; $P = 0.12$), and yield (1.59 vs. 1.35 kg; $P < 0.10$). Data also indicated higher milk lactose yield (1.74 vs. 1.39 kg; $P = 0.04$) in multiparous cows treated with probiotics. The latter cows showed tendencies for lower SCC (73,000 vs. 235,000 cells/mL; $P < 0.10$), fat content (4.24 vs. 4.82%; $P < 0.10$), fat to protein ratio (1.48 vs. 1.69; $P < 0.10$) and solid non fats (1.48 vs. 1.69 kg; $P < 0.10$), but higher for protein yield (1.14 vs. 0.93 kg; $P < 0.10$) and lactose content (4.37 vs. 4.26%; $P = 0.10$). Data also demonstrated that the total solids tended to be higher (13.4 vs. 12.6%; $P = 0.15$) in primiparous cows. In conclusion, intravaginal probiotic administration lowered the risk of sub-clinical mastitis and modulated several milk components in postpartal dairy cows.

Key Words: dairy cow, probiotics, somatic cell counts

W5 Improved feed intake and milk production in transition dairy cows treated intravaginally with probiotic bacteria. S. Iqbal, Q. Zebeli, S. M. Dunn, and B. N. Ametaj*, *University of Alberta*, *Edmonton, AB, Canada*.

The transition period is critical for the health and productivity of dairy cows due to major changes in the dietary composition and physiological state. The aim of this study was to investigate the effects of an intravaginal administration of a mixture of lactobacilli around parturition on health status and milk production of dairy cows. Eighty pregnant Holstein primiparous and multiparous dairy cows were assigned, 2 wk before the expected day of calving, to one of the following groups receiving either 1) intravaginal administration of 1 mL of carrier alone (controls), or 2) intravaginal administration of 1 mL of reconstituted skim milk containing 10^{10} to 10^{12} cfu of probiotic bacteria. The probiotic preparation was a mixture of *Lactobacillus sakei* FUA 3089, *Pediococcus acidilactici* FUA 3140, and *P. acidilactici* FUA 3138 prepared with commensal bacteria isolated from the vaginal tracts of healthy cows. Probiotic bacteria were applied intravaginally with a sterile syringe and insemination pipette once during wk −2, −1,+1, +2, +3, and +4 around calving. Rectal temperatures were taken during +2 wk before and +3 wk after calving, whereas milk production and feed intake were collected starting from +2 wk before until +8 wk after calving. Multiparous cows tended to have greater feed intake (32 vs. 28 kg/d; $P = 0.08$) associated with higher milk production (37 vs. 34 kg/d; $P < 0.01$). The cumulative analysis of milk data demonstrated a trend for higher milk production in the treatment group ($P = 0.14$). The overall analysis also showed a trend for feed intake to be greater (32 vs. 28 kg/d; $P = 0.10$) in treated cows. Interestingly, treatment did not influence feed intake or milk production in primiparous cows ($P > 0.05$). Treatment also had no effect on body condition score ($P > 0.05$). Results showed an interaction between treatment and day of measurement for rectal temperature in multiparous cows during wk +2 ($P = 0.02$). In summary, intravaginal administration of commensal Lactobacilli improved feed intake and milk production in postpartal multiparous dairy cows.

Key Words: dairy cow, intravaginal probiotics, milk production

W6 Effect of medicinal plants on immune system of broilers. A. Naghizadeh, S. Rahimi*, S. Askari Rankouhi, K. Gharib Naseri, M. Lotfi, and M. Rezaei, *Tarbiat Modares University*, *Tehran, Tehran, Iran*.

This study was carried out to investigate the effects of dietary administration of some medicinal plants to improve immune responses efficiency in broilers. Total of 180 d-old broilers (Arbor Acres Plus) were randomly distributed in 6 dietary treatments as follow: control; 4 groups of medicinal plants (dried powder of peppermint; thyme; basil and garlic at 1.5%); and one group fed diets containing antibiotic (15 ppm). Each treatment was replicated 3 times. Blood samples were collected from 3 birds at random from each group on d 25 and 46 of the experiment for evaluation of immune responses, including humoral immune response to sheep red blood cells (SRBC) and Newcastle disease vaccine (ND) and cellular immune response to phytohemagglutinin (PHA). Results showed that supplementation of broilers diets with garlic and peppermint increased humoral immune response significantly (4.33 ± 0.07 and 3.99 ± 0.03 for garlic and peppermint groups vs. 2.33 ± 0.11, 2.66 ± 0.08, 3.00 ± 0.13 and 3.33 ± 0.06 for control, antibiotic, basil and thyme treatments respectively) ($P < 0.05$). There were no significant differences among the treatments on cellular immune response. Also there were no significant differences in Newcastle disease antibody titer (HI) except garlic treatment ($P > 0.05$). Results indicated that use of medicinal plants as dry powder, had no significant effects on humoral immune responses, except for garlic and peppermint. However, garlic supplementation to broiler diets caused significantly higher HI titers against Newcastle disease at 46d compared with 25d.

Key Words: medicinal plants, immune system, broilers

W7 In vitro effects of plant and mushroom extracts on immunological function of chicken lymphocytes and macrophages. S.-H. Lee*[1], H. Lillehoj[1], Y.-H. Hong[1], S.-I. Jang[1], E. Lillehoj[2], and D. Bravo[3], [1]*Animal and Natural Resources Institute, Agricultural Research Service, USDA*, *Beltsville, MD,* [2]*Department of Pediatrics, School of Medicine, University of Maryland*, *Baltimore,* [3]*Pancosma S.A.*, *Grand Saconnex, Geneva, Switzerland*.

The present study was conducted to examine the effects of 4 different plant extracts from milk thistle (*Silybum marianum*), turmeric (*Curcuma*

longa), reishi (*Ganoderma lucidum*) and shiitake mushroom (*Lentinus edodes*) on innate immunity and tumor cells. The innate immunity was measured by splenocyte proliferation, NO production by an established avian macrophage cell line, HD11, and the inhibitory effect on a chicken B-cell tumor cell line, RP9. Cytokine transcript levels (IFN-α, IL-1β, IL-6, IL-12, IL-15, IL-18, TNFSF15) in the HD11 treated with turmeric or shiitake mushroom were also measured by real time RT-PCR. In vitro culture of splenocytes treated with milk thistle, turmeric, or combined extract of shiitake plus reishi induced significantly higher cell proliferation compared with the control ($P < 0.01$). Stimulation of macrophages with milk thistle or combined extract of shiitake plus reishi ($P < 0.001$), but not turmeric, resulted in robust NO production. All extracts inhibited the growth of RP9 cells at the dose ranges of 6 to 100 μg/mL ($P < 0.001$). Finally, the levels of IL-1β, IL-6, IL-12, IL-18, and TNFSF15 mRNAs were enhanced in HD11 that were treated with turmeric or shiitake mushroom compared with the untreated control ($P < 0.01$). These results show that plant extracts used in this study activate innate immune system and are cytotoxic against an avian tumor.

Key Words: innate immunity, phytonutrients

W8 Yeast autolysate combined with probiotic strains: Investigation of health effects in vitro and ex vivo. A. Ganner*[1], S. Masching[2], N. Reisinger[1], G. Schatzmayr[1], and T. Applegate[3], [1]*BIOMIN Research Center*, *Tulln, Austria*, [2]*BIOMIN Holding GmbH*, *Herzogenburg, Austria*, [3]*Purdue University*, *West Lafayette, IN*.

Yeast derivates have been proposed to improve animal health by preventing infectious diseases, by modulating the immune system and by controlling pathogenic bacteria. Probiotics have been described as being capable of protecting the intestinal mucosa by being antagonistic to undesirable microorganisms. The study was conducted to evaluate a product, consisting of yeast autolysate, lactobacilli, *Enterococcus* sp., *Pediococcus* sp. and bidifobacteria, on jejunal structure, apoptotic enterocytes, blood profile and health status of broilers. To exclude weakening effect of live probiotic components, the yeast autolysate was examined in vitro for its capacity to bind *Lactobacillus* sp., *Enterococcus* sp. and *Bifidobacterium* sp. with a microplate assay by measuring the OD as growth parameter of adhering bacteria. In a 35 d study, 300 broilers were distributed into 2 groups: control and trial group (0.1% autolysate + probiotic mix of 10^8 CFU/kg feed). On d 35, parts of distal jejunum were collected from 8 birds per group. Villi length and goblet cells were examined by Schiff and hematoxylin staining. Apoptotic enterocytes were examined with DeadEnd TUNEL. Blood samples were analyzed by flow cytometry. No binding was detected between autolysate and selected probiotics. A clear positive influence could be observed by the test product on weight d 14 and daily weight gain (DWG) 1–14 ($P = 0.0001$); slight improvement weight d 35 and DWG 1- 35 ($P = 0.08$). The goblet cell number was also increased by test diet with 126/villus (control 98/villus, $P = 0.1$). Villus height, crypt and apoptotic cells were not affected. Heterophils ($P = 0.08$) and lymphocytes ($P = 0.004$) were enhanced in the trial group. Our results indicate that the product consisting of yeast autolysate and probiotics is able to improve gut health, to modulate immune cells and to enhance bird performance.

Key Words: autolysate, probiotic, jejunum, performance

W9 Effects of a feed additive on neutrophil expression of immunomodulatory genes and production performance in periparturient dairy cows. R. D. Schramm, S. L. Shields*, D. L. Sevier, M. A. McGuire, and P. Rezamand, *University of Idaho*, *Moscow*.

The objectives of this study were to determine the effects of a feed additive, OmniGen-AF, on 1) neutrophil expression of immunomodulatory genes including interleukin-8 receptor (IL-8r), L-selectin (L-SEL), and interleukin converting enzyme (ICE), and 2) production performance and milk composition during the early postpartum period in dairy cows. Holstein cows were blocked by parity and randomly assigned to one of 2 treatments: OmniGen-fed (n = 11) and control-fed (n = 11). All cows received a standard dry ration before calving and were switched to a lactation ration after parturition either supplemented with OmniGen-AF (220 g/d of an inert additive containing 56 g OmniGen-AF) or received the same ration with inert additive but without OmniGen-AF. Cows were individually fed using Calan gates, and feed intake and milk yield were determined daily. Blood samples were obtained on d 28 and 7 before expected calving date and on d 9, 19, and 28 postpartum. Blood neutrophils were isolated and analyzed for mRNA expression of IL-8r, L-SEL, and ICE by rt-PCR. Populations of white blood cells were determined by flow cytometry in a subset of samples (n = 3/treatment), and milk composition was determined by a certified DHI laboratory. Data were analyzed by SAS in the mixed model procedure. No significant treatment effect was detected on feed intake, milk yield, or milk composition. Populations of leukocytes, granulocytes, T-cells and B-cells were also not different ($P > 0.05$) between treatments. Neither SCC nor neutrophil expression of immunoregulatory genes tested differed significantly between treatments. However, mRNA expression of IL-8r decreased as parturition approached, and increased beyond the initial level during the postpartum period ($P = 0.008$). Downregulation of IL-8r in the present study may explain, in part, the immunosuppression evidenced in periparturient dairy cows. Further studies are needed to clarify the specific roles of OmniGen-AF on mammary gland health in dairy cows.

Key Words: dairy cow, neutrophil, OmniGen-AF

W10 Potential of *Metharrizium anisopliae* as biological mean to control *Boophilus microplus* in tropical dairy farms. E. Maldonado-Siman*[1], P. Martinez-Hernandez[1], E. Galindo-Velasco[2], M. Alonso-Diaz[3], and R. Rodriguez-DeLara[1], [1]*Animal Science Department, University of Chapingo*, *Texcoco, Mexico, Mexico*, [2]*University of Colima*, *Tecoman, Colima, Mexico*, [3]*Autonomous National University of Mexico*, *Martinez de la Torre, Veracruz, Mexico*.

Biological control of tick (*Boophilus microplus*) infestations in tropical dairy farms can be a feasible alternative to chemical control. The aim of the study was to determine the tick load on dairy cows sprayed with *Metharrizium anisopliae* (entomopathogenic fungus) in the summer. Field work was carried out in a certified organic dairy farm in Veracruz, Mexico. Two treatments were evaluated: spraying cows with *M. anisopliae* strain Ma34 at a concentration of 1×10^8 conidia/ml every other week and no-spraying (control). Control cows were sprayed with water every time treated cows were sprayed. A completely random experimental design with 21 replicates was used. The experimental unit was a cow. Experiment lasted 16 weeks (May to August). All cows had the same management except at the spraying time. Ticks were counted every week; the first count was just before the first spraying. Treatments were compared every week. All cows showed a same initial tick load (50 ticks/cow). Afterward, in 10 out of the 15 weeks, cows sprayed with the fungus showed from 34 to 78% lower ($P < 0.05$) tick load than control cows, the largest difference in tick load was found in the last 2 weeks of the experiment. It was concluded that *M. anisopliae* represents a potential biological control of ticks.

Key Words: biological control, ticks, tropical dairy

W11 Effects of Globigen egg protein on calf health and performance. D. Wood*, R. Blome, and J. Sowinski, *Animix*, *Juneau, WI*.

Study objective was to evaluate effect on calf health and performance of supplementation of Globigen egg antibody preparation (AB). Auction sourced Holstein bull calves (n = 150; ~1 wk of age) were shipped to the facility and randomly placed in individual raised, slatted stalls. Calves were assigned to receive 1) calf milk replacer (CMR, 22% C.P. 20% fat) n = 75, or 2) same formula +AB at 1 g/calf/fdg wk 1, 2 g/calf/fdg wk 2 and 1 g/fdg wk 3, total AB 56 g/calf, n = 75. No differences were noted in individual serum total protein ($P \leq 0.22$). Total 21 kg CMR was fed over 42 d starting at 362 g/calf/day stepping up to 682 g/calf d 16. Calves in every-other-stall in the barn received AB. Manufacturer detected anticipated presence rotavirus and coronavirus titer in AB fed. Both formulas contained plasma (5%), mannanoligosaccharides and chlortetracycline. Neomycin was administered in both formulas d 1–14. Starter grain (18% CP) was introduced d 14 at 113 g/calf, increased to 227 g/d d 21 and to 454 g/day d 34. Orts were not measured. There was no effect on gain during any period of the study. Data was analyzed using F-test for variances and student *t*-test comparing 2 means. Five fecal samples from scouring calves in both groups were analyzed for presence of rotavirus and coronavirus using real-time PCR assays. Strong positive was detected in 5/5 and 4/5 fecal samples for coronavirus and rotavirus respectively in both groups. Number of calves treated during peak scours (wk 2) was 33% and 37% for control and AB respectively. Total number of calves treated was 56% and 59% for control and AB respectively ($P \leq 0.74$). Total number of treatments week one were reduced 33% in AB ($P \leq 0.62$). Avg med $/calf was $2.53 control and $2.01 AB and AB cost $9+/calf. Both mortalities were not disease related. In conclusion, under conditions of this study AB had no effect on gain or morbidity despite presence of target pathogens and incidence of FPT exceeding 50%. Calves receiving AB may have been continually re-infected from neighboring calf not receiving AB, due to every-other-calf study design.

Table 1. Calf Performance

	Control	AB	P-value
Initial Wt, kg	46.4	46.5	≤0.87
21 d ADG, g	244	231	≤0.43
21–42 d ADG, g	685	675	≤0.69
42 d ADG, g	465	453	≤0.50
Mortality	2	0	

Key Words: calf, egg, antibody

W12 The effect of three commercial herbal extracts on broilers performance. Z. Teymourizadeh, S. Rahimi*, and M. A. Karimi Torshizi, *Tarbiat Modares University*, *Tehran, Tehran, Iran*.

An experiment was conducted to evaluate the effects of 3 herbal extracts and virginiamycin on performance, immune system, blood factors and intestinal selected bacterial populations in broiler chickens. A total of 4 hundred and 80 1-d old male broiler chicks were assigned to the basal diet (control); or basal diet supplemented with 15 ppm virginiamycin; 0.1% extracts of thyme (*Thymus vulgaris*), coneflower (*Echinacea purpurea*), garlic (*Allium sativum*); or a blend of extracts with the same dose(s). Broilers in the virginiamycin and coneflower treatment groups had the highest and lowest BW (2595g ± 56.20 vs. 2269g ± 48.2) and WG (2550.60g ± 45.7 vs. 2225g ± 36.4), respectively ($P < 0.05$). Lowest and highest FCR related to virginiamycin (1.71 ± 0.08, $P < 0.05$) and coneflower (1.86 ± 0.09, $P < 0.05$) respectively. There were no differences in carcass characteristics and fat pad, but small intestinal weight differed among treatments. Animals supplemented with virginiamycin had the lowest average small intestinal weight (2.29 ± 1.2), and control animals had the highest (2.84 ± 1.4) ($P < 0.05$). Relative weight of bursa Fabricius to body weight in the garlic group showed a significant increase compared with other groups, but relative weight of spleen to body weight was unaffected by treatments. Cutaneous basophil hypersensitivity response (to phytohemagglutinin injection) and antibody response to sheep red blood cells (SRBC) was higher in coneflower group ($P < 0.05$). Garlic (*Allium sativum*) significantly reduced the serum levels of cholesterol, LDL, and triglyceride and significantly increased the level of HDL. *E. coli* in ileo-cecal digesta of birds in the blend group was significantly lower compared with control group. However, there was no difference in *E. coli* counts between blend group and other treatment groups (this excludes the basal diet). Lactic acid bacterial counts were higher in the thyme group compared with the other groups except coneflower ($P < 0.05$).

Key Words: thyme, coneflower, garlic

W13 Omega-3 fatty acid enrichment of chicken meat by using fish oil. H. Saleh[1], S. Rahimi*[1], M. A. Karimi Torshizi[1], and A. Rahimi[2], [1]*Tarbiat Modares University*, *Tehran, Tehran, Iran*, [2]*Islamic Azad University*, *Tehran, Tehran, Iran*.

A 42-d study was conducted to evaluate the influence of fish oil inclusion on performance parameters, serum lipid content, antibody responses to sheep red blood cells (SRBC) antigen and meat fatty acid composition in broilers. Two hundred and sixteen 1-d-old broiler chicks from a commercial hybrid (Cobb 500) were randomly allocated to 4 groups comprising of 0.0, 1.5, 3.0 and 6% fish oil, according to a completely randomized design (CRD). The differences among the groups were significant regarding the performance, so that low level of fish oil (1.5%) were led to the higher feed intake and improvement of feed efficiency in comparison to control group ($P < 0.01$). The result of omega-3 fatty acid evaluation indicated significant differences among groups ($P < 0.01$) and the birds in 6% fish oil fed group had the highest level of n-3 fatty acid in meat. N-6/n-3 ratio of polyunsaturated fatty acids was lower in fish oil fed groups compared with the control group ($P < 0.01$). Broilers fed diets rich in omega-3 fatty acid had higher levels of anti-SRBC titer and lower levels of serum cholesterol and triglyceride than those fed control diet ($P < 0.05$). In conclusion, administration of 3% fish oil in broilers diet can improve the performance and immune response in these birds.

Key Words: performance, immune response, broiler meat

W14 Comparison the effect of commercial probiotics on performance and morphology of small intestine in broiler chicks. M. Soleimani[1], S. Rahimi*[1], M. A. Karimi Torshizi[1], and F. Niknafs[2], [1]*Tarbiat Modares University*, *Tehran, Tehran, Iran*, [2]*Zarbal Breeding Company*, *Amol, Mazandaran, Iran*.

Objective of this study was to compare the effects of different probiotics on performance and intestinal mucosa of broiler chickens. In this trial 480 d-old male broilers (Ross 308) were assigned as a completely randomized design to 6 experimental groups with 4 replicates with 20 birds per replicate as follows: control group (no feed additive in feed or water); 4 commercial probiotics and a lab-made probiotic. Body weight gain was significantly affected by monostrain, multispecies and yeast in finisher periods ($P < 0.05$). Multustrain, and lab-made probiotics significantly reduced FCR in starter period ($P < 0.05$). In all probiotic fed groups zigzag pattern of villi in ileum was more than control in d

21 of age ($P < 0.05$). In yeast, lab- made and monostrain groups ileum, villus length ($P < 0.01$) and apparent villus surface area were more than control and other probiotic groups ($P < 0.01$).The highest number of rows were observed in control group and the lowest number was in lab-made, and yeast group in duodenum in 35 d of age ($P < 0.05$). Crypt depth in jejunum was more in monostrain group in duodenum in 35 d of age. Tongue shaped villi in multispecies, lab-made, multistrain, yeast and monostrain groups were more than control group in 49 d of age. Leaf shaped villi in multispecies, multistrain, lab-made; yeast and monostrain groups were less than control group in d 49 ($P < 0.05$). Regardless of sampling age and site, lab-made group had the highest percent of tongue shaped villi and the lowest percent of leaf shaped villi ($P < 0.05$). Mortality rate, fecal moisture, blood hemoglobin concentration, serum cholesterol, relative weight of digestive organs, relative length of duodenum, jejunum, ileum, percent of convolute, bridge and finger shaped villi, villi length to crypt depth ratio, villi number per view field were not influenced by probiotics ($P > 0.05$).

Key Words: broiler, probiotic, performance

W15 Subjective assessment versus objective measurement of FAMACHA and hematocrits in sheep and goats fed herbs and ivermectin as dewormers under natural grazing conditions. H. A. Swartz*[1], C. Clifford-Rathert[1], A. N. Stewart[1], D. K. Sommerer[1], F. P. Wulff[1], K. Schmidt[1], and M. R. Ellersieck[2], [1]*Lincoln University*, *Jefferson City, MO*, [2]*University of Missouri*, *Columbia*.

Paramount in sheep and goats in hot summer months are internal parasite losses. The objective of this study was to determine the validity of applying a color chart, FAMACHA, (FAM) a subjective measurement (S) to hematocrits (HEM), an objective measurement (O) looking at the effects of *Haemonchus contortus*, that kills many sheep and goats from anemia. This trial compared ivermectin, a commercial dewormer, commercial herbs, herbal plants fed and a control groups receiving no treatment. Fecal egg counts (FEC) were measured in each collection period. The study was conducted in May, June, July, August, September and October 2009 with collection every 4 weeks. There were 4 treatment groups: 1) control, 2) ivermectin, 3) greenhouse *Artemisia absinthium* and (4) a commercial herbal dewormer. The control groups received no treatment, the ivermectin groups were treated monthly and the herbal groups were fed the herbs weekly. The McMaster FEC was used over the 6 mo period. The FAM subjective assessment ranged from 1 to 5 examining the ocular conjunctiva eyelid. The score of 1) bright red, 2) less red, 3) pink, 4) pale pink and 5) white indicating high to low HEM. Measurement of FAM, HEM and FEC were collected in Dorset (D) (n = 39), Katahdin (K) (n = 40) and Boer (B), (n = 41) divided into the 4 groups. Correlations coefficients over the 6 mo period used the Pearson correlation in statistics for S and O: 1) FAM-1 vs. HEM-1, r = −0.33 ($P \leq 0.01$), FAM-2 vs. HEM-2, r = −0.224 ($P \leq 0.01$), FAM-3 vs. HEM-3, R = .-.33 ($P \leq 0.0003$), FAM-4 vs. HEM-4, r = −0.36 ($P \leq 0.0001$), FAM −5 vs. HEM-5 r = . < 0.37 ($P \leq 0.0001$), FAM-6 vs. HEM-6, r = −0.53 ($P \leq 0.0001$). These results were analyzed using the Pearson correlation coefficient. The McMaster FEC showed differences within breeds and months using the SAS Proc MIXED statistical procedure on the FEM, HEM and FEC. All treatments differed within breeds and months from May to October and were highly significant at the $P \leq 0.000$l. In this study, herbs and ivermectin were effective in controlling internal parasites in K, D and B.

Key Words: FAMACHA, hematocrits, sheep and goats

W16 Effects of short-term tocopherol (T) feeding on nitric oxide production and protein nitration following endotoxin (LPS) challenge in beef calves. S. Kahl*[1], T. Elsasser[1], J. Shaffer[1], C. Li[1], K. Lebold[2], M. Traber[2], and S. Block[3], [1]*USDA, Agricultural Research Service*, *Beltsville, MD*, [2]*Oregon State University*, *Corvallis,* [3]*Archer Daniels Midland (ADM), Inc.*, *Decatur, IL*.

Posttranslational protein tyrosine nitration (pTN) contributes to functional tissue damage during pro-inflammatory stress. With regard to chemical reactivity, α-T has a greater antioxidant potential while γ-T has greater ability to inactivate reactive oxynitrogen species potentially involved in pTN formation. Our objective was to determine the effects of 5-d feeding of supplemental α-T (*A*, Novatol 1490, ADM; T content (%): α = 98.2, γ < 1) or γ-T (*G*, Decanox MTS-90 G, ADM; T content (%): α = 10, γ = 69) on the generation of key biomarkers of pTN during pro-inflammatory episodes initiated with LPS (0.25 μg/kg BW, i.v., *E. coli* 055:B5). Beef calves (n = 21; 211 ± 6 kg) were group penned in equal numbers across 3 test diet assignments: control (*C*, no supplement), *A*, or *G*. A growth diet was fed daily in all pens at 90% mean group ad libitum intake and top-dressed with a premix containing the treatments (daily intake/calf: Novatol = 1.25 g; Decanox = 3.85 g). Blood samples were obtained at 0, 7, and 24 h, and liver biopsy samples at −24 and 24 h relative to LPS injection. At LPS challenge, liver [γ-T] was: $G > C$ or A ($P < 0.01$) while [α-T] was: $A > G > C$ ($P < 0.01$). In all calves mean plasma concentrations of xanthine oxidase (XO, a superoxide anion producer, $P < 0.05$) and nitrate+nitrite (NO_x, an estimate of NO production, $P < 0.01$) increased after LPS. For XO no differences were observed between treatments but the increase in NO_x was attenuated in both *A* (45.7%) and *G* (46.3%) as compared with *C* ($P < 0.05$). The generation of pTN (measured by quantitative immunohistochemical localization of nitrotyrosine pixel density) 24 h after LPS was lower in *A* (24.4%) and *G* (27.4%) than in *C* ($P < 0.01$). Results indicate that a 5-d feeding of vitamin E isoforms differentially affects the generation of mediators of pTN but both significantly decrease overall pTN.

Key Words: cattle, endotoxin, vitamin E

W17 Interactive effects of active *Saccharomyces cerevisiae* and its cell wall material on intestinal microbial ecology during the receiving period of stressed beef cattle. C. T. Collier[1], J. A. Carroll*[1], J. R. Corley[2], A. G. Estefan[2], D. N. Finck[3], and B. J. Johnson[3], [1]*ARS-USDA*, *Lubbock, TX,* [2]*Lesaffre Feed Additives*, *Milwaukee, WI,* [3]*Texas Tech University*, *Lubbock*.

The effects of active *Saccharomyces cerevisiae* (SC) addition and/or its cell wall (CW) on hindgut microbial ecology were evaluated in receiving beef cattle (203+1.45 kg). Cattle were assigned to 1 of 4 treatment groups; with SC (n = 5); with CW (n = 4); with SC and CW (n = 6) and without (control; n = 5). The cattle were fitted with indwelling jugular catheters after 38d on feed. At 39d, *E. coli*-derived lipopolysaccharide (0.25 μg/kg BW) was administered via jugular catheter. After 24h, fecal samples were collected from the rectal probes inserted ~27 cm. Nucleic acids were isolated from the fecal samples then PCR amplified using 16S-V3-specific primers. Denaturant gradient gel electrophoresis was used to separate the resultant unique bacterial amplicons. Band numbers (bacterial species) were counted and banding patterns analyzed via Sorenson's pairwise similarity coefficients (C(S)); an index measuring common bacterial species between samples. Band numbers (23.5+1.3 vs. 29.6+0.8, respectively) and band intensity were greatest ($P < 0.05$) in SC-treated cattle when compared with CW-treated cattle suggesting a more species- and numerically-dense microbial profile. Intra-treatment band number variations were greatest ($P < 0.05$) in control (+3.6 bands) and SC/CW-treated (+5.5 bands) cattle when compared with

SC- (+1.6 bands) and CW-treated (+2.5 bands) cattle. Intra-treatment C(S) values were high, ranging between SC/CW (68.3+1.2) and SC (75.6+0.8). Inter-treatment C(S) comparison values were lower ($P < 0.05$) than intra-group values. Cumulatively, the C(S) values indicate homogenous microbial profiles within treatments that were unique from each other treatment. These results suggest that potential performance and immunological modulation of SC- and CW-treated cattle may partially be the result of modifying the intestinal microbial ecology. As the dynamic nature of the hindgut microbiota is typically resistant to protracted treatment-induced alterations, the sustained altered microbial profile observed here indicates that supplementation may select for a beneficial persistent microbiota.

Key Words: cattle, 16S-V3, ecology

W18 Effects of ochratoxin A on performance of broilers and the efficacy of a mycotoxin detoxifying product. U. Hofstetter*[1], R. Borutova[1], V. Starkl[1], I. Rodrigues[1], and C. W. Kang[2], [1]*Biomin Holding GmbH*, *Herzogenburg, Austria*, [2]*Animal Resources Research Center, College of Animal Bioscience and Technology, Konkuk University*, *Seoul, Korea*.

Aim of the study was to investigate the effects of various levels of ochratoxin A (OTA) on broilers and to evaluate the effect of a mycotoxin deactivator. 200 d-old male broiler chicken were divided into 20 groups and fed 5 different diets for 5 weeks. Group 1: control (OTA free); group 2: 1mg/kg OTA; group 3: 1mg/kg OTA with 0.2% mycotoxin deactivator ; group 4: 2mg/kg OTA; group 5: 2mg/kg OTA with 0.2% mycotoxin deactivator. The statistic method used was General Linear Model (SAS, 2002) for dispersion analysis and when there were statistically significant differences Duncan's multiple range test was used. As dietary OTA increased, feed intake and weight gain significantly ($P < 0.05$) decreased. The relative weights of liver and kidneys and the activities of glutamic-oxaloacetic transaminase and glutamic-pyruvic transaminase in the groups fed diets containing OTA alone were significantly higher ($P < 0.05$) compared with the control group. The level of total serum cholesterol was significantly reduced ($P < 0.05$) by feeding OTA contaminated diets. As dietary OTA increased, the levels of OTA in liver and kidney tissue were significantly increased ($P < 0.05$). The presence of a mycotoxin deactivating product in contaminated diets significantly decreased ($P < 0.05$) the OTA accumulation in organs. Moreover the fecal excretion of OTA and the metabolite OTα were significantly increased ($P < 0.05$) by feeding the mycotoxin deactivator. This increase of fecal excretion of OTA was attributed to the bentonite which is one component of the feed additive whereas the increase of fecal excretion of OTα was attributed to the yeast strain *T. mycotoxinivorans*, which is able to biotransform OTA into this non-toxic metabolite. In conclusion, these results indicated the harmful effects of dietary OTA on broiler performance. Adversary changes of physiological responses were observed in broilers. Feeding a mycotoxin deactivating feed additive ameliorated the OTA organ accumulation and OTA-induced performance reduction. Moreover levels of OTA in liver and kidney were found to be a better biomarker of intoxication than OTA in blood.

Key Words: ochratoxin A, broilers

W19 Effects of short-term tocopherol (T) feeding on structure-localized protein tyrosine nitration (pTN) patterns of mitochondrial ATPase following endotoxin (LPS) challenge in beef calves. T. Elsasser*[1], S. Kahl[1], J. Shaffer[1], R. Castellano-Perez[1], C. Li[1], and S. Block[2], [1]*USDA, Agricultural Research Service*, *Beltsville, MD*, [2]*Archer Daniels Midland (ADM), Inc.*, *Decatur, IL*.

Mitochondrial ATPase/Complex-V (MCV) is an electron transport chain (ETC) component needed for ATP synthesis. The ETC, exquisitely sensitive to proinflammatory mediators (PIM), generates oxynitrogen reactants leading to pTN formation as mitochondrial membrane leakage occurs. Immunohistochemical localization (IHC-L) of pTN (a biomarker of pTN damage to proteins) in liver following LPS suggests that pTN responses to PIM are not uniform across liver structures. Furthermore, because of their respective oxynitrogen reactivities, α-T and γ-T may differentially affect pTN formation in cells. Our objective was to determine the effects of 5-d feeding of supplemental α-T (*A*, Novatol 1490, ADM; T content (%): α = 98.2, γ < 1) or γ-T (*G*, Decanox MTS-90 G, ADM; T content (%): α = 10, γ = 69) on the nitration of MCV in central venous (CV), portal triad (PT), and hepatocyte/paranchymal (HP) areas of the liver after LPS challenge (0.25 μg/kg BW, i.v.). Beef calves (n = 21; 211 ± 6 kg) were penned and fed in equal numbers one of 3 test diets: control (*C*, no supplement), *A* (Novatol = 1.25 g/calf/d), or *G* (Decanox = 3.85 g/calf/d). Liver biopsy samples were obtained at −24 and +24 h relative to LPS injection. The MCV was measured by quantitative IHC-L and MCV nitration analyzed by proximity ligation assay (PLA, Olink Biosciences, Sweden). After LPS, MCV staining increased 4-, 3.4-, and 2-fold (vs. pre-LPS) in *C*, *A*, and *G*, respectively ($P < 0.05$, effect of T). By structure, MCV intensities (pixels/cell) were: HP < PT < CV ($P < 0.05$). With CV as the target structure, PLA demonstrated a 5-fold increase ($P < 0.05$) in colocalized pTN signals associated with MCV after LPS with decreasing ($P < 0.05$) nitration of MCV in samples where $G < A < C$. The data are consistent with MCV as a target for nitration after LPS and a protective effect of T against this nitration.

Key Words: endotoxin, mitochondria, vitamin E

W20 Reserpine-induced changes of the small intestinal histology and the expression of genes relative to mucosal immunity in rat. X. Zhu*[1], K. Guo[2], F. Liu[2,3], J. Yu[2], A. Lu[2], N. Zhang[1], G. Cheng[2,3], P. Yin[1], N. Wang[2], and J. Xu[1], [1]*TCVM Laboratory, CAU-BUA TCVM Teaching & Research Team, College of Veterinary Medicine, China Agricultural University*, *Beijing, China*, [2]*Department of Animal Science and Technology, Beijing University of Agriculture*, *Beijing, China*, [3]*Beijing Key Laboratory of TCVM, CAU-BUA TCVM Teaching & Research Team*, *Beijing, China*.

Clinical and experimental evidence indicates that damage to the intestinal surface structure can significantly impair intestinal epithelial integrity, as well as the stability of the mucosal immune system. The aim of this study was to investigate the changes of the small intestinal surface structure and the gene expression profile caused by reserpine treatment. Rats were randomly divided into two groups: the control groups (C) and the reserpine treated group (Res), 6 rats each group. The control rats and the Res rats were administered with Salt solution 0.9% and reserpine subcutaneously 0.5 mg/kg respectively for 7 days. At the end of the experimental period, the duodenum, jejunum and ileum were sampled for morphology structure examination and microarray analyses. Structural changes of the mucosa in Res included atrophy of villi and reduction in crypt size, indicating significant injury to the small intestinal mucosa. DNA microarrays were employed to examine the gene expression profile in the jejunum of Res versus C. According to the GeneSpring GX 10.0 analysis, twelve genes (Log2Ratio < −1.0) related to mucosal immunity were down-regulated and confirmed by real-time PCR. Genetic network of toll-like receptor 2 (Tlr2), toll-like receptor 4 (Tlr4), complement component 3 (C3), myxovirus (influenza virus) resistance 1 (Mx1) and myxovirus (influenza virus) resistance 2 (Mx2) was performed by GeneSpring GX 10.0 software. Results showed that genes associated with TLR2, TLR4 by a variety of mechanisms. The

lower levels of TLR2 protein in the jejunum of Res were in concert with previous findings that the mRNA levels of TLR2 were significantly lower in the Res. Immunohistochemistry results suggested that most TLR2 deposited from the epithelial cells of the rats jejunum brush border and submucosa. Rats treated with reserpine can induce down-regulation in gene expression relative to the innate mucosal immunity of the small intestine, as well as the TLR2 protein expression.

Key Words: reserpine, gene expression, small intestinal mucosa

W21 Gastrointestinal motility and gastrointestinal hormones VIP and GAS expression in reserpine-induced FGID rats. G. Jingyi[1], Z. Xiaoyu[1], C. Fei[1], C. Guilin[2,3], L. Fenghua[2,3], and X. Jianqin*[1], [1]*China Agricultural University China Agricultural University*, *Beijing, China*, [2]*Beijing University of Agriculture*, *Beijing, China*, [3]*CAU-BUA TCVM Teaching & Research Team*, *Beijing, China*.

The purpose of this study was to investigate effects of reserpine-induced rat functional gastrointestinal disorders (FGID) on the gastrointestinal motility, gastrointestinal hormones VIP and GAS expression. The rats were randomly assigned to 2 groups: Reserpine-treated group (RG) and Control group (CG), 12 rats each group. RG was intraperitoneally injected with reserpine 0.5 mL/kg; and CG with normal saline 0.5 mL/kg, once daily for 7 consecutive days separately. Six rats were chosen randomly from each group. Gastric emptying rate and intestinal propulsive ratio were detected by administration trophism semisolid. Collect serum and detect for the Amylase (AMS) and Lipase (LPS) activities were determined by kit manuals. Total RNA was isolated from stomach and small intestine using Trizol reagent. RT-PCR detected VIP and GAS mRNA expression. VIP and GAS protein contents were assayed by ELISA with according to the kit instructions. The surplus 6 rats of each group were determined gastric myoelectrical activity with Pclab-UE Systems. The statistic analysis were performed using ANOVA of SPSS 12.0. The results showed: compared with the control groups, serum amylase activity had significantly decreased ($P < 0.05$), while the lipase activity obviously increased ($P < 0.05$); gastric emptying rate was highly significantly lower ($P < 0.01$), and the intestinal propulsion ratio had improvement significantly ($P < 0.01$); both of the frequencies and amplitudes of gastric electrical ware had decreased obviously ($P < 0.05$). VIP mRNA expression in the reserpine-treated groups was significantly lower in the duodenum and jejunum ($P < 0.05$). GAS mRNA expression had improvement significantly in the stomach and ileum, and obviously decreased in the duodenum and jejunum ($P < 0.01$). VIP sharply decreased and GAS increased significant degree in the stomach ($P < 0.05$). The conclusion is, enzyme activities of serum and gastrointestinal motility were disordered as reserpine induced rat FGID. The stomach is a sensitive part of GI hormones VIP and GAS. The abnormal expression of GAS is one of the important factors.

Key Words: reserpine, gastrointestinal motility, GI hormones

W22 Effects of medicinal plants on broilers performance, organs weight, small intestine morphology and GIT microflora. A. Niknam, S. Rahimi*, J. Azimi, M. Hoseinzadeh, M. Moradi Nejad, and K. Seifi, *Tarbiat Modares University*, *Tehran, Iran*.

The objective of this study was to compare the effects of medicinal plants on some broilers characteristics. A total of 420, d-old male broilers (Arbor Acres) were randomly allocated into 7 groups with 5 replicates in a completely randomized design. The treatments were control, dry peppermint (*Mentha piperita*) (15kg/ton), thyme (*Thymus vulgaris*) (15kg/ton), basil (*Ocimum basilicum*) (15kg/ton) or garlic (*Allium sativum*) (15kg/ton), Virginiamycin (150g/ton) and Primalac (1kg/ton). On 42 d of experiment 15 birds from each group were sacrificed. The garlic increased ($P < 0.05$) body weight (BW) and feed conversion ratio (FCR) during d 0 to 28. There were no significant differences between groups in BW and FCR from d 28 to 42, total FCR and relative weights of gizzard, liver, neck and back muscle. However, the relative weight of the breast muscle and thigh were increased for peppermint and garlic-fed broilers, respectively ($P < 0.05$). Birds in the thyme and basil groups had highest villus height (VH) in duodenum and ileum, respectively ($P < 0.05$). Also, peppermint diet significantly increased duodenal absolute and relative length, and ileal villus width (VW), crypt depth and relative weight ($P < 0.05$). The only change found in the jejunum was an increase in the VW in birds given Primalac. Villus height to crypt depth ratio only increased at the ileum for virginiamycin-fed broilers ($P < 0.05$). Crop contents of garlic and peppermint treatments had highest and lowest number of lactobacillus (5.88 vs. 3.68 Log10 cfu/g), respectively ($P < 0.05$). There was no significant difference in coliforms number in crop, while highest number of total aerobic bacteria observed for control treatment (5.69 Log10 cfu/g), respectively ($P < 0.05$). Supplementation of diet with garlic increased number of lactobacillus in ileum (8.76 Log10 cfu/g) compare with other groups ($P < 0.05$), and Primalac increased both coliforms and total aerobic bacteria in ileum higher than other treatments ($P < 0.05$). In present study, effectiveness of medicinal plants in broiler performance demonstrates their use a potential alternative for antibiotic as growth promoters.

Key Words: medicinal plants, broiler performance, GIT microflora

W23 Identification of small heat shock proteins in the bovine genome. S. Schepis and M. Worku*, *North Carolina Agricultural & Technical State University*, *Greensboro*.

Protein-damaging stresses, including heat shock, cold, altered pH and oxygen deprivation induce the expression of a subgroup of molecular chaperones, called heat shock proteins (Hsp), which consist of several protein families designated by their molecular weight, such as the Hsp90, Hsp70, Hsp60, and the small Hsp (sHsp) families. Small heat shock proteins (sHsp) with a molecular mass of 15–30 kDa are ubiquitous and conserved. This large family of proteins is present within the prokaryotic and eukaryotic cell as large oligomeric complexes, ranging in size from 200 to 800 kDa. Unlike the high molecular weight Hsp, which are involved in protein folding in vivo, under normal conditions, sHsp play an important role in protecting organism from stress. The sHsp share an evolutionarily conserved sequence of 80–100 amino acids, located in the C-terminal region, and called "alpha-crystallin domain." Ten active genes for sHsp have been identified in the human genome. This project focused on 10 α-crystallin related Hsps belonging to the sHsp molecular chaperone family: HspB1- HspB10. It is anticipated that the recently completed annotated sequence of the cattle genome will lead to identification of genes for disease resistance and higher quality meat. The purpose of this project was to determine if genes coding for human sHsp are found in the bovine genome, and if so, how highly the sequences were conserved across the 2 species. The NCBI search engine, BLAST, and CLUSTALW on Biology Workbench were used. Homologs of 10 α-crystallin human small heat shock protein (sHsp) molecular chaperone family (HspB1- HspB10) were found within the bovine genome and single nucleotide differences identified in silico. The sequence for human sHspB9 expressed exclusively in the testis and cancerous tissue did not identify related sequences in the bovine.

Key Words: heat shock protein, bovine, human

W24 Use of partial least-square regression to predict SNP when some animals are genotyped with low density marker panels. C. Dimauro*, G. Gaspa, R. Steri, S. Sorbolini, E. Pintus, and N. P. P. Macciotta, *University of Sassari*, *Sassari, Italy*.

Genome wide selection exploits information from dense marker platforms (usually 50K-60K) to predict genomic breeding values (GEBV) for livestock. However, costs of analysis are expensive for high density marker (HDM) platforms, allowing the genotyping of only a few thousand animals. A decrease in costs could be reached by using low density marker (LDM) chips, but, in this case, a unavoidable reduction in GEBV accuracy is expected. An alternative could be the use of both reference (REF) and prediction (PRED) populations of animals genotyped with HDM and LDM chips, respectively. Missing genotypes in the PRED population could be reconstructed using a suitable mathematical model which exploits information from REF population. In this work the partial least square regression (PLSR) is used at this purpose. A data set, generated for the XII QTLs-MAS workshop, which simulated a genome with 6 chromosomes and 6,000 equally spaced biallelic SNP for 5,865 animals, was used. It was split into 2 data sets, the REF with 4,665 animals and 6,000 SNP and the PRED with 1,200 individuals and 3,000 SNP. The PLSR, applied separately for each chromosome, was used to predict the 3,000 missing SNP in the PRED population. Different scenarios of missing SNP sampling in PRED and decreasing size of REF population were tested. Goodness of prediction was evaluated by calculating correlations between actual and predicted data. Best results were obtained when unknown SNP were chosen evenly spaced along the chromosome and all 5,865 individuals in the REF population were used. In this case, the mean correlation between actual and predicted data was 97%. As the size of REF population decreased to 2,000 individuals, the mean correlation reached a value of 94%. Therefore, if an adequately large REF population is used, the PLSR technique is able to predict with high accuracy the missing SNP in other animals genotyped with a LDM platform. This research was funded by FAR 2008.

Key Words: PLSR, SNP

W25 Multiple trait genetic evaluation of linear type traits using genomic and phenotypic information in US Holsteins. S. Tsuruta*[1], I. Aguilar[1,2], I. Misztal[1], A. Legarra[3], and T. J. Lawlor[4], [1]*University of Georgia*, *Athens*, [2]*INIA*, *Las Brujas, Uruguay*, [3]*INRA*, *Castanet-Tolosan, France*, [4]*Holstein Association USA Inc.*, *Brattleboro, VT*.

Genetic evaluation was conducted for linear type traits using combined genomic and phenotypic data in US Holsteins. Single nucleotide polymorphism (SNP) markers from the Illumina BovineSNP50 genotyping Beadchip, consisting of 38,416 SNP on 30 chromosomes, were used available for 6,931 bulls. A unified approach proposed by Aguilar et al. (2010) was used to estimate genomic evaluations with single trait (ST) and multiple trait (MT) models. Three analyses of 5 linear type traits (stature, strength, body depth, dairy form, and rump angle with heritabilities 0.45, 0.27, 0.34, 0.30, and 0.34) were conducted, utilizing 8,865,120 records in 2009 and 7,715,925 records in 2004. The EBV were calculated using 2009 and 2004 data sets with phenotypes (traditional genetic evaluation) and a 2004 data set with phenotypes and genotypes (unified approach). Coefficients of determination (R^2) and regressions on 2004 genomic EBV were calculated for 1,307 young bulls with at least 50 daughters in 2009 using daughter deviations from 2009 MT traditional evaluations. The EBV for 2004 traditional evaluation were parent average (PA). The R^2 from regressing daughter deviations on ST PA, MT PA, ST genomic, and MT genomic predictions were 0.34, 0.34, 0.54, and 0.54, respectively, for stature. Corresponding R^2 for strength were 0.25, 0.29, 0.40, and 0.44, respectively. In general, R^2 for ST and MT genomic models were 13-19% and 14-18% higher, respectively, than those of PA (28-42%). The regressions with MT were slightly (0.01-0.02) higher than those with ST, indicating less bias. The genomic evaluation by MT is more accurate for selected traits than by ST. The improvement in accuracy from ST to MT in genomic predictions follows a similar improvement in PA. Preliminary results show that, with a small modification in the unified approach, bias can be essentially eliminated at the cost of a small reduction in R^2.

Key Words: genomic selection, linear type traits, US Holsteins

W26 Genotype by environment interaction: Effects of nutritional management on production traits. M. W. Dekleva*[1], C. D. Dechow[1], J. M. Daubert[1], S. Bauck[2], J. W. Blum[3], and G. A. Varga[1], [1]*The Pennsylvania State University*, *State College*, [2]*IGENITY Livestock Production Business Unit*, *Duluth, Georgia*, [3]*University of Bern*, *Switzerland*.

The objective of this study was to determine the effect of nutritional management factors on the level of genetic expression for milk, fat, and protein yield. Intakes of dry matter, crude protein and net energy of lactation (NE_L) in addition to 305 d yield were available for 970 cows from 11 tie-stall herds in Pennsylvania. All herds were visited monthly

to measure 24-h intake. Feed samples were collected on each visit and analyzed for dry matter percentage, crude protein percentage and NE_L (MCal/kg) content. Sire PTA for yield was available for all 970 cows, while 881 cows were genotyped and received an Igenity Profile Score (IS) for milk, fat, and protein where 1 corresponds to the lowest, and 10 corresponds to the highest genetic potential for yield. Multiple regression models were fit for 305 d milk, fat and protein yield. Fixed effects were herd averages for kg of dry matter refusals (DMR), ration crude protein percentage (CP), NE_L and the interactions of these herd averages with PTA or IS, herd-year-season, and lactation. Permanent environment was included as a random effect. For daughters of bulls that differed in PTA for milk by 500 kg, there was a 151.5 kg difference in milk yield at the tenth percentile for DMR compared with a 584.8 kg difference for cows at the ninetieth. A difference of 25 kg for sire PTA fat corresponded to a difference of 17.9 kg of fat yield for herds in the tenth percentile for CP and 51.5 kg for herds in the ninetieth. A change of one unit in Igenity Score corresponded to a difference of 1.87 kg of fat yield for cows at the tenth percentile for NE_L., compared with a 6.91 kg difference for cows at the ninetieth percentile. The results indicate that response to selection was reduced in herds that did not provide cows with adequate intakes of dry matter, crude protein and NE_L.

Key Words: genotype, environment, production

W27 Evaluation of the effect of inbreeding on age at first calving in Holstein cattle. J. Bezdicek* and J. Riha, *Agrovyzkum Rapotin s.r.o.*, *Rapotin, Czech Republic*.

The objective of this study was to examine the effect of inbreeding depression on age at first calving (d) in Holstein cows. The databases included cows (173,000) that calved in the years 1995–2006 at farms in the Czech Republic. Inbred cows were matched with their outbred contemporaries (n = 811) based on sire, farm of first calving, year and period of calving (±2 mo), and dam's breeding value for milk production (±5%). Inbred cows and their matched outbred contemporaries were subsequently divided according to inbreeding coefficients of the inbred cows (F_x = 1.25%; F_x = 12.5%; F_x = 25%, and other). The data were analyzed with StatSoft Inc. Statistica 8 using descriptive statistics and paired *t*-tests. The GLM procedure of SAS Inc. was used to analyze the effects of inbreeding depression. Age at first calving increased when the level of inbreeding increased. Within the observed groups (F_x = 1.25%; F_x = 12.5%; F_x = 25.0% and all animals), the average age at first calving for inbred cows (for their outbred contemporaries) was 820 (818); 835 (822); 844 (822) and 832 (820) d. In the groups F_x = 25% and other, differencies between inbred and outbred cows were highly significant ($P < 0.001$). There was also greater variability for groups of inbred cows (s_x = 83.2 d) compared with groups of outbred contemporaries (s_x = 63.4 d). Inbred cows also had significantly ($P < 0.01$) lower breeding values for milk (20.8 kg) than in outbred contemporaries (63.6 kg). Overall, this study confirmed an increase in age at first calving in inbred cows compared with their outbred cohorts.

Key Words: age at first calving, inbreeding, Holstein

W28 Age at first calving in Holstein cattle in the United States. J. Cole and D. Null*, *Animal Improvement Programs Laboratory, ARS, USDA*, *Beltsville, MD*.

Heifer rearing costs account for 15 to 20% of the total expense of milk production, and the decline in fertility of US Holsteins is well documented. Earlier age at first calving (AFC) may improve profitability and fertility. Records for 400,000 U.S Holstein cows born on or after January 1, 1997 were selected by random sampling of herd codes and used to estimate (co)variance components and breeding values. Phenotypic AFC averaged 788 ± 89 d, and ranged from 540 to 1095 d. The model included random animal and residual effects, and a fixed herd-year-season (HYS) of birth effect. Herd-year-season of birth was included to avoid confounding between sires and period-of-birth, and groups were required to include at least 10 observations. The 4 seasons were defined as: December to February, March to May, June to August, and September to November. Heritability averaged 0.027 ± 0.003 across the 6 data sets, which is lower than some literature estimates, and consistent with earlier, unpublished studies on US Holsteins. Predicted transmitting abilities for AFC of active bulls ranged from −13 to +14 d, and averaged −1.9 ± 3.6. Correlations were calculated among sire PTA for bulls with reliabilities of lifetime net merit (NM$) of at least 90%. Age at first calving had favorable (negative) correlations with milk (−0.22), fat (−0.18), and protein yield (−0.23), SCS (−0.05), productive life (−0.01), NM;(−0.18), heifer conception rate (HCR; −0.18), and persistency of milk (−0.12), fat (−0.13), and SCS (−0.02). Unfavorable (positive) correlations were found with cow conception rate (0.04) and protein persistency (0.04). Daughter pregnancy rate (DPR) was uncorrelated with AFC (0.001; $P > 0.05$). Excessive AFC has a negative effect on yield and lifetime profitability, which is reflected in these correlations. Genetic trend was estimated by regression of sire PTA for AFC on birth year, and was slightly negative, decreasing by −0.09 d per year ($P < 0.01$). Routine genetic evaluation of AFC is desirable because it provides dairy producers with an additional tool for managing reproduction in their herds.

Key Words: age at first calving, fertility, genetic evaluation

W29 Relationship of reason for lactation termination with genetic merit of Holsteins in the United States. H. D. Norman, J. R. Wright, and S. M. Hubbard*, *Animal Improvement Programs Laboratory, ARS, USDA*, *Beltsville, MD*.

Reasons that producers report to 4 dairy records processing centers for why individual cows exit the herd (lactation termination codes) were examined for 6.2 million US Holsteins with lactation records that ended in 2007 and 2008 to determine their relationship to genetic merit. The most frequent termination reasons were lactation ended normally and cow stayed in the herd (68%), cow died (5%), and cow was sold for low production (4%), reproductive problems (4%), or mastitis (4%) or for dairy purposes (3%); 9% of lactations had no reason specified. For cows with normally ended lactations, mean predicted transmitting ability (PTA) and standard deviations (SD) were 135 ± 271 kg for milk, 5 ± 10 kg for fat, 4 ± 8 kg for protein, 2.95 ± 0.38 for somatic cell score (SCS), 0.8 ± 1.4 mo for productive life (PL), 0.1 ± 0.9% for daughter pregnancy rate (DPR), and net merit (NM) was $115 ± 132; corresponding means and SD for parent averages (PA) were 117 ± 219 kg milk, 4 ± 8 kg fat, 4 ± 6 kg protein, 2.95 ± 0.37 SCS, 0.6 ± 1.3 mo PL, 0.1 ± 0.9% DPR, and $98 ± 111 NM. Mean PTA and PA for all yield traits and PL as well as NM generally were lower for cows that did not end their lactations normally; lowest means were 18 kg for PTA milk, 1 kg for PTA fat, 1 kg for PTA protein, 0.2 mo for PTA PL, $37 for NM, 74 kg PA milk, 3 kg PA fat, 2 kg PA protein, 0.3 mo for PA PL, and $62 for NM for cows sold for low production and –0.2% for PTA DPR and –0.1% for PA DPR for cows sold for reproductive problems. Cows that aborted had the highest mean PTA for all yield traits (159 kg for milk, 5 kg for fat, and 5 kg for protein) and PA milk (125 kg). For SCS, PTA and PA were highest for cows with normally ended lactations and lowest (2.80 for PTA SCS and 2.81 for PA SCS) for cows that died; cows sold because of mastitis had mean PTA SCS of 2.91 and mean PA SCS of 2.90. Across termination categories, SD were similar for each

trait except SCS. In general, cows with lactations that ended normally were genetically superior for all traits except SCS.

Key Words: lactation termination, genetic merit, Holstein

W30 Comparison of Holstein service-sire fertility for heifer and cow breedings with conventional and sexed semen. H. D. Norman*, J. L. Hutchison, and P. M. VanRaden, *Animal Improvement Programs Laboratory, ARS, USDA*, *Beltsville, MD*.

Sire conception rate (SCR), a service-sire fertility evaluation implemented in August 2008, is based on up to 7 conventional-semen breedings for parities 1 through 5 (C_{cow}). The same procedure was used to derive SCR for other types of breedings: sexed semen for cows (S_{cow}) and conventional semen and sexed semen for primiparous heifers (C_{hfr} and S_{hfr}, respectively). For all 4 breeding types, SCR were based on breedings from 2006 through 2009. Service-sire age groups were consolidated for sexed-semen breedings because of a limited number of bulls. Only artificial-insemination Holstein bulls with ≥ 300 breedings overall and ≥ 100 matings during the last 12 mo in ≥ 10 herds were included. Number of bulls evaluated was 2,309 for C_{cow} breedings, 270 for C_{hfr} breedings, 25 for S_{cow} breedings, and 114 for S_{hfr} breedings; respective mean SCR reliabilities were 79, 82, 73, and 75%. Mean SCR for all breeding types was near 0, and standard deviations were 2.21% for C_{cow}, 2.57% for C_{hfr}, 2.39% for S_{cow}, and 4.34% for S_{hfr} breedings. Correlation between C_{cow} and S_{cow} SCR was 0.18, which resulted in a genetic correlation (r_g) for true SCR of 0.24; corresponding correlations for heifer breedings also were low: 0.08 and 0.11, respectively. Correlation between C_{cow} and C_{hfr} SCR was 0.67 (r_g of 0.82); correlation between S_{cow} and S_{hfr} SCR was 0.75 (r_g of 1.02). Among artificial-insemination organizations, absolute differences between mean SCR for conventional and sexed-semen breedings ranged from 1.44 to 4.52% for cows and 0.87 to 6.78% for heifers. Bull age effects were quite large for conventional semen but small for sexed semen. Results suggest that fertility rankings for sexed semen differ markedly from those for conventional semen and separate SCR are needed. Combining cow and heifer inseminations together in some manner would seem to be advantageous.

Key Words: sire conception rate, bull fertility, sexed semen

W31 Derivation of factors to estimate daily, fat, protein, and somatic cell score from one milking of cows milked three times daily. M. M. Schutz*[1] and H. D. Norman[2], [1]*Purdue University*, *West Lafayette, IN,* [2]*USDA-ARS Animal Improvement Programs Laboratory*, *Beltsville, MD*.

The objective of this research was to derive factors to predict daily fat (F) and protein (P) yield and somatic cell score (SCS) when milk is sampled once per d for cows milked 3 times (3x) per d. Daily milk weights were recorded automatically and samples were collected from 8 herds for each milking on test-day by Dairy Herd Improvement personnel. Following edits, 1721 records of 1236 first lactation (L1) cows and 2704 records of 1940 later lactation (L2) cows remained. Factors currently in use to adjust single milking F and P for milking interval (MINT) were applied. No adjustments are currently in use for SCS. Also, 2 methods were compared with estimate factors or equations to predict daily F, P, and SCS. First, factors were estimated as the ratio of the sum of daily yield to the sum of partial yield within a parity-MINT class (13 intervals in 2 parities) [Method 1] or as the sum of the ratios of daily yield to partial daily yield for each cow-day divided by the number of cow-days within parity-MINT class [Method 2]. Resulting factors from both methods were smoothed, applied to data, and residuals were regressed on days in milk (DIM). Regression equations (n = 112) were also developed within parity-MINT-DIM classes (2 × 7 × 8) [Method 3] to jointly account for MINT and DIM. Separate factors were derived for milking 1, 2, and 3 for each trait in L1 and L2. Method 3 resulted in consistently strongest correlations between estimated and actual yields, and smallest variances of estimates, and root mean squared errors (rMSE) for all components in milkings 1, 2, and 3 in L1 and L2. Method 3 resulted in rMSE of 0.14 (F, L1), 0.22 (F, L2), 0.09 (P, L1), and 0.14 (P, L2) kg for milking 1; compared with rMSE of 0.18, 0.27, 0.12, and 0.16 kg from current factors for the same traits in L1 and L2. Differences in rMSE were similar for F and P for milking 2 and 3 and for SCS for all milkings. Work is ongoing to determine whether equations from Method 3 will allow accurate estimation of daily milk, F, P, and SCS when applied to other herds.

Key Words: milking interval, adjustment factor, milking frequency

W32 Derivation of factors to estimate daily milk yield from one milking of cows milked three times daily. M. M. Schutz*[1], J. M. Bewley[2], and H. D. Norman[3], [1]*Purdue University*, *West Lafayette, IN,* [2]*University of Kentucky*, *Lexington,* [3]*USDA-ARS Animal Improvement Programs Laboratory*, *Beltsville, MD*.

The objective of this research was to derive factors to predict daily milk yield when milk is sampled once per d for cows milked 3 times (3x) per d. Milk weights for all 3 milkings were recorded automatically by 8 herds and collected by Dairy Herd Improvement supervisors on test-day. Following edits, 196,725 daily milk weight records of 2235 first lactation (L1) cows and 346,508 records of 3385 later lactation (L2) cows remained. Factors currently in use to adjust single milking yields for milking interval (MINT) were applied. Also, 3 methods were compared with estimate factors or equations to predict daily milk yield. First, factors were estimated as the ratio of the sum of daily yield to the sum of partial yield within a parity-MINT class (13 intervals in 2 parities) [Method 1] or as the sum of the ratios of daily yield to partial daily yield for each cow-day divided by the number of cow-days within parity-MINT class [Method 2]. Resulting factors from both methods were smoothed, applied to data, and residuals were regressed on days in milk (DIM). Regression equations (n = 112) were also developed within parity-MINT-DIM classes (2 × 7 × 8) [Method 3] to jointly account for MINT and DIM. Separate factors were derived for milking 1, 2, and 3 for each trait in L1 and L2. Method 3 resulted in consistently strongest correlations between estimated and actual yields, and smallest variances of estimates, and root mean squared errors (rMSE) for milkings 1, 2, and 3 in L1 and L2. Method 3 resulted in rMSE of 3.12 (Milking 1, L1), 3.26 (Milking 2, L1), 3.25 (Milking 3, L1), 4.52(Milking 1, L2), 4.72 (Milking 2, L2)and 4.57 (Milking 3, L2) kg; compared with rMSE of 3.58, 3.66, 3.59, 5.13, 5.41, and 5.09 kg, respectively, from current factors for the same milkings for L1 and L2. The multiple regression methodology (Method 3) appears to provide the most accurate prediction of daily milk weight from a single milking for herds milking 3x daily.

Key Words: milking interval, adjustment factor, milking frequency

W33 Genetic relationship between milk urea nitrogen and milk constituents in Holstein dairy cows. N. Ghavi Hossein-Zadeh*[1] and M. Ardalan[2], [1]*Department of Animal Science, Faculty of Agriculture, University of Guilan*, *Rasht, Iran*, [2]*Department of Animal Science, University College of Agriculture and Natural Resources, University of Tehran*, *Karaj, Iran*.

The objectives of this study were to estimate the heritability of milk urea nitrogen (MUN) concentration and describe the genetic and phenotypic relationship between MUN and other milk constituents in Iranian

Holstein dairy cows. Lactation records including MUN data obtained from 57301 dairy cows on 20 large dairy herds in Iran between January 2005 and June 2009. Genetic parameters were estimated using an animal model with covariates for days in milk and age at first calving, fixed effects for season of calving and effect of lactation number, and random effects for herd-test day, animal, permanent environment, and residual error. Coefficient of variation for MUN was 38.76%. Estimated heritability for MUN was 0.14. Phenotypic trend of MUN increased significantly over the years. Also, phenotypic correlations of MUN with milk production traits were close to zero. The genetic correlation was close to zero for MUN and lactose percentage (- 0.07); was moderately positive for MUN and net energy concentration of milk (0.24), fat percentage (0.23), protein percentage (0.34), total solids (0.29), solids-not-fat (0.31), and milk yield (0.25), and was negative for MUN and somatic cell score (- 0.14). Herd-test day explained 52% of the variation in MUN, which suggests that management adjustments at herd-level can reduce MUN. This study shows that it is possible to influence MUN by herd management and by genetic selection.

Key Words: milk urea nitrogen, dairy cattle, milk traits

W34 Genetic relationship between milk urea nitrogen and reproductive performance in Iranian Holsteins. N. Ghavi Hossein-Zadeh*[1] and M. Ardalan[2], [1]*Department of Animal Science, Faculty of Agriculture, University of Guilan, Rasht, Iran*, [2]*Department of Animal Science, University College of Agriculture and Natural Resources, University of Tehran, Karaj, Iran*.

The objective of this study was to describe the genetic and phenotypic relationship between milk urea nitrogen (MUN) and reproductive traits in Iranian Holstein dairy cows. Lactation records including MUN data obtained from 57301 dairy cows on 20 large dairy herds in Iran between January 2005 and June 2009. Genetic parameters for MUN and reproductive traits were estimated with an animal model using ASREML. Herd-test-day or herd-year-season along with age at calving and days in milk were included as fixed effects in all models. Heritabilities for MUN and reproductive traits were estimated separately for first lactation, second lactation, and third lactation. Estimated heritabilities for MUN varied from 0.18 to 0.21. Heritability estimates were low for reproductive traits and ranged from 0.02 to 0.06 for different traits across parities. Except for days open, phenotypic and genetic correlations of MUN with reproductive performance traits were close to zero. Genetic correlations between MUN and open days were 0.22 in first lactation, 0.33 in second lactation, and were 0.46 in third lactation. On the other hand, phenotypic correlations between MUN at different parities were moderate (0.29 to 0.34), but genetic correlations between MUN at different parities were high and ranged from 0.84 to 0.97. This study shows that it is possible to influence MUN by genetic selection.

Key Words: milk urea nitrogen, dairy cow, reproductive traits

W35 Adjusted phenotypic trend estimation for peak milk yield of Iranian Holsteins milked three times daily. H. Farhangfar*[1], M. Bashtani[1], and J. Modarresi[2], [1]*University of Birjand, Birjand, Iran*, [2]*Agricultural Jihad Organisation, Birjand, Iran*.

The main aim of this study was to estimate adjusted phenotypic trend for sample milk yield at peak time of thrice a day milking Iranian Holstein cows. A total of 212,889 sample milk yields (at third month of lactation) collected from 70,963 Iranian first lactation Holstein cows calving from 1997 to 2008 were used. All cows were milked 3 times a day: morning, noon and night. The number of herds was 739. The average milk samples were 10.792, 10.366 and 10.310 kg for morning, noon and night milking respectively. To analyze the data, a fixed statistical linear model was used. In the model, fixed effects of herd, year and season of calving, time of milking as well as covariables of Holstein gene percentage, first calving age and days in milk were included. In the model, 2-way interactions between season of calving and time of milking and between year of calving and time of milking were also taken into account. For fitting the model General Linear Model (GLM) procedure of SAS program was applied. Results indicated that all effects except days in milk had statistically significant ($P < 0.01$) influences on milk samples at peak time. Morning sample milk yield was revealed to be significantly different from night sample ($P < 0.05$) while no significant difference were found between morning and noon and between noon and night milk samples. Linear regression analysis of adjusted milk sample yields on year of calving ($R^2 = 0.974$) showed a positive significant ($P < 0.001$) phenotypic trend of 0.168 kg for sample milk yield over the period of time. As the phenotypic trend consisted of genetic (resulted from genetic selection for high producing cows) and environmental trends (good dairy herd management practices such as appropriate ration formulation, and good animal health), further research is needed in future to be carried out to estimate genetic part of phenotypic improvement of sample milk yield in Iranian Holsteins.

Key Words: Iranian Holsteins, phenotypic trend, milk sample

W36 REML estimates of heritability and repeatability for monthly test day milk yield of primiparous Iranian Holsteins. A. Seyed Dokht*[1], H. Farhangfar[2], A. A. Aslami Nezhad[1], and M. Tahmorespour[1], [1]*Ferdowsi University of Mashhad, Mashhad, Iran*, [2]*Birjand University, Birjand, Iran*.

In this research, a total of 634,949 monthly test day milk records collected from 72,523 Iranian Holstein first lactation cows calving between 1999 and 2008 were utilized to estimate heritability and repeatability using restricted maximum likelihood (REML) statistical approach. The records were obtained from 724 herds over 19 provinces in the country. All monthly test day records were obtained from 3-times a day milking cows. The average monthly test day milk yield in the whole data set was 29.11 kg (SD = 7.07 kg). A repeatability test day animal model was used. In the model, fixed contemporary group (combining province-herd-year of recording-season of recording), stage of lactation (10 stages), and covariables of Holstein gene percentage, days in milk nested in the stage of the lactation, and age of cow at recording (in month) were included. The random part of the model consisted of additive genetic, permanent environment and residual effects. The total number of animals (including daughters, sires and dams) in the pedigree was 101,601. DMU software was run in a Pentium 4 computer with 4 gigabyte memory to fit the animal model. Additive genetic, permanent environment and residual variance estimates were 4.352, 13.494 and 15.335 kg2 respectively. The results revealed that heritability and repeatability of monthly test day milk yield were 0.131 and 0.537 respectively. Low heritability of monthly test day milk yield obtained in this study indicates major part of the phenotypic variation for the trait under consideration is resulted from the temporary environment and model unexplained variation revealing that genetic selection based upon test day milk records may not be as cost effective as the traditional lactation model for which there is usually a higher heritability.

Key Words: Iranian Holsteins, genetic parameters, test day milk yield

W37 Correlation between milk components with regard to the season in Iranian dairy herds. A. Laki*, S. Babaei, N. Hedayat-

Evrigh, M. Dehghan-Banadaky, and K. Rezayazdi, *Department of Animal Science, Campus of Agriculture, University of Tehran*, *Karaj, Tehran, Iran*.

Previous studies showed a positive correlation between somatic cell count (SCC), fat and protein, and a highly significant negative correlation between SCC and lactose content. The aim of this study was to determine the correlation between milk components in different seasons in Iranian dairy herds. All test-day data (n = 126,357), including milk composition measured by infrared test method at the Tehran milk quality laboratory, were collected from 124 commercial Holstein dairy herds in the State of Tehran during a 4-year period (2004–2008). Overall means for fat, protein, SCC, lactose, total solids, solids-not-fat, and milk urea nitrogen were 3.54%, 3.15%, 424,370 cells/ml, 4.54%, 11.52%, 9.12% and 17.43 mg/ml respectively. The data showed a statistically significant ($P < 0.01$) positive correlation between SCC and fat (0.04) and protein content (0.11), and between fat and protein (0.17); and a highly significant negative correlation between SCC and lactose content (−0.26). With regard to season, the correlation between fat and protein was lowest in spring (0.11) and highest in fall (0.188). Also the correlation between lactose and SCC was lowest in summer (−0.23) and highest in fall (−0.28). The correlation between protein and SCC was the lowest in spring and the highest in fall (Table 1).

Table 1. Correlation coefficients between milk components in different season

Season	Fat & Protein	Fat & Lactose	Fat & SCC	Protein & Lactose	Protein & SCC	Lactose & SCC
Spring	0.11[b]	–0.02 [a]	0.05 [b]	0.04 [b]	0.09 [b]	–0.26 [b]
Summer	0.187 [b]	–0.08 [b]	0.06 [b]	–0.08 [b]	0.11 [b]	–0.23 [b]
Fall	0.188 [b]	–0.10 [b]	0.04 [b]	–0.14 [b]	0.13 [b]	–0.28 [b]
Winter	0.16 [b]	–0.03 [b]	0.03 [b]	–0.05 [b]	0.11 [b]	–0.27 [b]

[a]significant at ($P < 0.05$); [b]significant at ($P < 0.01$).

Key Words: correlation coefficient, milk composition, season

W38 Comparison of fixed and random regression test day models in genetic evaluation of Iranian Holsteins for protein yield. M. Bashtani*, H. Farhangfar, H. Naeemipour, M. R. Asghari, A. Arab, and M. Jafari Tarbaghan, *Birjand University*, *Birjand, Iran*.

The main objective was to compare 2 test day models (with fixed or random regressions) applied for genetic evaluation of protein yield trait in Iranian Holsteins. The data were 57,551 protein test day records from 7036 first parity Holstein cows calved between 2003 and 2006. Total number of herds (located in Razavi Khorasan province), sires, dams and animals in pedigree file were 138, 590, 6091 and 13117 respectively. Contemporary groups were defined based on combining herd - year - season of production - milking times (HYSM). The response variable was test day protein yield for which there was an average 918 gr (SD = 225.8 gr) in the whole data set. In fixed and random regression test day models, HYSM (fixed effect), calving age (linear and quadratic covariables), Holstein gene percentage (linear and quadratic covariables), and random effects of additive genetic and permanent environment were included. To take account of the shape of the lactation curve at phenotypic, genetic and environmental levels, orthogonal Legendre polynomials were also included in the models so that the order of the Legendre fit was level and cubic for fixed and random regression test day models, respectively. Fixed and random regression test day models were run using WOMBAT and DXMRR software, respectively. The results indicated there was a very high rank correlation coefficient (0.936) between predicted breeding values (PBV) which was statistically significant ($P < 0.001$). Averages PBV of progeny were found to be −0.209 and −0.037 gr for fixed and random regression test day models, respectively which were not significantly different from each other. It can therefore be concluded that fixed regression test day model could be used instead of random regression test day model in genetic evaluation of Iranian Holsteins for protein test day records in particular where computational capacity is limited for running a random regression test day model at the national scale.

Key Words: Iranian Holsteins, test day protein yield, random regression

W39 Estimation of udder composite in the Holstein population of Iran. M. R. Bakhtiarizadeh*, M. Moradi Shahr Babak, and A. Pakdel, *University of Tehran*, *Karaj, Tehran*.

The objective of the present study was to estimate the weights of udder type traits in udder composite (UC) of Holstein cattle in Iran. Records generated for first lactation Holstein dairy cows from 1991 to 2007 over 220 herds. The genetic parameters and relationships between udder traits and functional traits (milk yield, longevity, and somatic cell score (SCS)) were estimated and data (included udder type traits (udder depth (UD), fore udder attachment (FU), rear udder width (RUW), rear udder height (RUH), fore teat placement (FTP), rear teat placement (RTP), suspensory ligament (SL)), milk production, SCS and pedigree) were used by Animal Breeding Center in Iran. The genetic parameters were estimated by ASREML software and also SelAction software was used for estimating coefficient importance of functional traits. The equation Y = Rg*v was used for estimating UC. In this equation, Y is weight of udder type traits in UC trait, Rg is the genetic correlation between the udder type traits and functional traits and v is importance coefficient of functional traits that were estimated from SelAction software. Heritability estimates for the udder type traits ranged from 0.1 (FU) to 0.19 (RTP). Heritabilities were 0.05, 0.07, and 0.28 for longevity, SCS and milk production, respectively. The genetic correlation among udder type traits and longevity ranged from 0.41 (UD) to −0.33 (RTP), among udder type traits and SCS ranged from 0.85 (RUW) to −0.6 (FU), among udder type traits and production ranged from 0.34 (RUW) to −0.31(UD). The importance coefficient of functional traits were 0.55, 0.38 and −0.07 for milk production, longevity and SCS, respectively. Finally the UC trait has been shown as follows (PTA is predicted transmitting ability):
UC= (−0.091*PTAfu)+(0.015*PTAruh)+(−0.035*PTAruw)+(−0.015*PTAsl)+(0.134*PTAud) +(0.69*PTAftp) +(−0.015*PTArtp).
In this study breeding goal was to decrease SCS and increase milk production and longevity by applying the UC trait. Consequently, each trait that has a desirable relationship with functional traits in the breeding goal has a higher coefficient in UC trait.

Key Words: udder composite, type traits, genetic parameters

W40 Bayesian estimates of genetic parameters for cystic ovarian disease, displaced abomasum and foot and leg diseases in Iranian Holsteins via Gibbs sampling. N. Ghavi Hossein-Zadeh*[1] and M. Ardalan[2], [1]*Department of Animal Science, Faculty of Agriculture, University of Guilan*, [2]*Department of Animal Science, University College of Agriculture and Natural Resources, University of Tehran*.

The objective of this study was to estimate heritability and genetic correlations between cystic ovarian disease (COD), foot and leg diseases (FLD), and displaced abomasum (DA) within the first 3 lactations of

Holstein dairy cows. The records of 57,301 dairy cows on 20 large dairy herds in Iran between January 2005 and June 2009 were analyzed with univariate and bivariate threshold animal models, using Gibbs sampling methodology. The final model included the fixed class effects of herd-year, season of calving, parity of dam, the linear covariate effect of age at calving, and additive direct genetic effect of animal. Posterior means of heritability in first, second, and third lactations were 0.14, 0.18, and 0.20, respectively, for FLD; 0.08, 0.10, and 0.11 for COD; 0.05, 0.06, and 0.08 for DA. Posterior means of genetic correlations between diseases were low (from 0.02 to 0.12), within lactations; the largest estimates were for FLD and DA, and the lowest involved FLD and COD. Positive genetic correlations between diseases suggest that some general disease resistance factor with a genetic component exists. The results of this study indicated the importance of health traits for considering in the selection index of Iranian Holstein dairy cows.

Key Words: Bayesian methods, cystic ovarian disease, displaced abomasum

W41 Bayesian estimates of genetic parameters for metritis, retained placenta, milk fever, and clinical mastitis in Holstein dairy cows via Gibbs sampling. N. Ghavi Hossein-Zadeh*[1] and M. Ardalan[2], [1]*Department of Animal Science, Faculty of Agriculture, University of Guilan*, [2]*Department of Animal Science, University College of Agriculture and Natural Resources, University of Tehran*.

The objective of this study was to estimate heritability and genetic correlations between the liabilities of clinical mastitis (CM), milk fever (MF), metritis (MET), and retained placenta (RP) within the first 3 lactations of Holstein dairy cows. The records of 57,301 dairy cows from 20 large dairy herds in Iran between January 2005 and June 2009 were analyzed with univariate and bivariate threshold animal models, using Gibbs sampling methodology. The final model included the fixed class effects of herd-year, season of calving, parity of dam, the linear covariate effect of age at calving, and the random direct genetic effect of animal. Posterior means of heritability for liabilities in first, second, and third lactations were 0.06, 0.08, and 0.09, respectively, for CM; 0.10, 0.12, and 0.11 for MF; 0.09, 0.07, and 0.10 for MET, and 0.07, 0.08, and 0.08 for RP. Posterior means of genetic correlations between disease liabilities were low or moderate (from −0.01 to 0.26). The results of this study indicated the possibility of considering health traits in the selection index of Iranian Holstein dairy cows.

Key Words: Bayesian methods, clinical mastitis, metritis

W42 Genetic relationships between somatic cell count, milk production and udder conformation traits in Iranian Holsteins. M. R. Sanjabi*[1], A. Gholibaigi Fard[2], R. Vaez Torshizi[2], A. Lavaf[2], and A. H. Ahadi[1], [1]*Iranian Research Organization for Science and Technology, Tehran, Iran*, [2]*Azad University, Karaj, Iran*.

Heritabilities and genetic correlations between milk yield (MY), fat percentage (FP), protein percentage (PP), somatic cell count (SCC) and udder type traits in 10 dairy Holstein herds near Tehran on 3500 lactations were evaluated. The DFREML software was used for calculation of variance components and heritabilities of individual traits, and genetic correlations were estimated using Harvey's software. Heritabilities were low for SCC (0.04), moderate for MY (0.19) and FP (0.24), and high for PP (0.48). For type traits, heritability estimates ranged from 0.04 to 0.55. The estimated genetic correlation between SCC and udder type traits varied from −0.78 to 0.51 and estimated genetic correlations between SCC and MY, FP and PP were 0.15, 0.03, and 0.04, respectively. In general, the cows with shallow and tightly attached udders and closer teat placement had lower somatic cell count and lower risk of mastitis. In summary, it appears that selection for improved udder conformation will reduce SCC and clinical mastitis among cattle selected for high milk production.

Key Words: dairy cattle, genetic parameters, somatic cell count

W43 Microbiological quality of pasteurized milk from Minas Gerais state, Brazil. E. H. P. Andrade, M. O. Leite*, M. R. A. Moura, T. Roza, C. F. A. M. Penna, M. M. O. P. Cerqueira, L. M. Fonseca, and M. R. Souza, *Federal University of Minas Gerais*, *Belo Horizonte, Minas Gerais, Brasil*.

The objective of this work was to evaluate the microbiological quality of pasteurized milk from different regions of Minas Gerais state, Brazil, from 2006 to 2008, to verify compliance with Brazilian standards. This state is the largest dairy producer region in Brazil, with about 7 million metric tons of milk production for the year 2008. The analyzed parameters were: aerobic mesophilic microbial counting, total and thermotolerant coliforms, *Salmonella* spp. presence and *Staphylococcus* coagulase positive counting. It was observed that 42 (70%) of the 60 samples were in disagreement with Brazilian microbial standards with at least one parameter not in compliance with the requirements. Only 18 (30%) was in accordance to the legal requirements for all parameters evaluated. Of the total of samples used in this study, 18 samples (30%) presented more than the maximum allowance for aerobic mesophilic microbial counts, 35 (58.3%) were in disagreement for total coliforms, with 23 samples (38.3%) above the limit for thermotolerant coliforms, and 2 samples (3,3%) with *Salmonella* contamination.

Key Words: milk quality, microbiology

W44 The relationships between somatic cell count and bacteriology on milk quality and production in dairy goats. K. N. Baker*, S. D. Horner, D. K. Rucker, L. C. Nuti, and G. R. Newton, *Prairie View A&M University*, *Prairie View, TX*.

Somatic cell count (SCC) in milk is an indicator of mammary infections and a barrier for production of grade A milk. The relationships between mammary infection and SSC are not clear in goats. Two experiments were conducted to evaluate the incidences of sub-clinical mastitis on mammary health and milk production. The effects of a protective teat dip and intra-mammary infusion of antibiotics on milk production, composition, SCC and bacteriology were evaluated in a 2 by 2 factorial design. At dry-off and on d 3–5 of the next lactation, goats (n = 50) were screened for the presence of intra-mammary infections. At dry-off 80% of the halves sampled were negative for bacteria. This percentage increased to 84% at the start of the next lactation. Mammary treatments did not influence the incidence of mammary infection at the start of lactation when compared with halves receiving no treatments. Content of milk fat (5.77 ± 0.5%), protein (3.92 ± 0.04%), lactose (6.06 ± 0.07%) and SCC (721 ± 302/ml) were not affected by mammary treatments. Next, milk was collected from goats (n = 65) once a month from March through November to evaluate the relationships between milk production, SCC and bacteriology. SCC in uninfected halves displayed a curvilinear increase ($P < 0.01$) with lowest values recorded in March (260 ± 11.1/ml) and highest values observed in November at the end of lactation (2075 ± 11.1/ml). SCC in infected halves did not differ during the sampling period ($P > 0.1$) and was consistently higher than samples from uninfected halves. In March SCC was 1242 ± 556/ml in infected halves. Values remained elevated through out the sampling period, reaching a peak in November (3158 ± 556/ml). Milk production by infected and uninfected halves did not differ. Production was highest in March (1.18 ± 0.03 L/half) and steadily declined to a nadir in November (0.48 ± 0.03 L/half; $P < 0.01$). Therefore, sub-clinical mastitis contributes to elevated SCC levels through out lactation. However, elevated SSC in uninfected halves late in lactation may also influence the ability to produce and market grade A milk.

Key Words: milk, bacteriology, quality

W45 Biodiversity of enterococci in Egyptian dairy products. S. Awad*[1], C. Snauwaert[2,3], P. Vandamme[3], A. El Attar[1], and M. El Soda[1], [1]*Department of Dairy Science and Technology, Faculty of Agriculture, Alexandria University*, *Alexandria, Egypt*, [2]*BCCM/LMG Bacteria Collection, Ghent University, K.L. Ledeganckstraat 35, 9000 Ghent, Belgium*, [3]*Laboratory of Microbiology, Ghent University*, *K.L. Ledeganckstraat 35, 9000 Ghent, Belgium*.

Egyptian dairy products are generally produced under artisan conditions from raw milk without using industrial starter cultures. The main traditional cheeses are Ras (hard type), Domiati (soft type), and Mish; and the main fermented milk products are Zabady and Laban Rayeb. The quality of these products is strictly dependent on the microbial associations responsible for the fermentation, and the biodiversity of lactic acid bacteria. Enterococci are ubiquitous bacteria present in the environment and in the gastrointestinal tract of healthy animals and humans. To study the biodiversity of enterococci strains of the Egyptian Dairy products, 364 samples (raw & fermented milk and cheeses) were collected from farm houses, traditional cheese making factories and local markets in the Delta region, Egypt, and enterococci were isolated. All isolates were tested for their Gram reaction, catalase activity, and morphology. API and SDS-PAGE were used for identification of 784 isolates. Rep-PCR fingerprinting technique with the (GTG)5 primer and, in some cases pheS and 16S rRNA genes sequencing were also used to confirm the identification. These results confirm the importance of using molecular methods for exhaustive and precise identification of the microbial flora occurring in artisanal cheeses.

Key Words: Egyptian dairy products, (GTG)5-PCR, lactic acid bacteria

W46 Identification, characterization, and differentiation of bifidobacteria obtained from Ukraine. L. Tmanova*, A. Onyenwoke, and R. F. Roberts, *The Pennsylvania State University*, *University Park*.

Speciation of bifidobacterial isolates using traditional biochemical and phenotypic methods is tedious and often provides inconclusive results. DNA-based methods often yields clearer results. Ten freeze-dried bifidobacterial strains used as probiotics in Ukraine and identified by the supplier as *Bifidobacterium adolescentis* (2), *Bifidobacterium bifidum* (2), *Bifidobacterium longum* (4), *Bifidobacterium animalis* (1), and *Bifidobacterium infantis* (1) were characterized using polymerase chain reaction (PCR), pulsed field gel electrophoresis (PFGE) and allelic profiling. After anaerobic growth on MRS-cysteine (MRS) at 37°C for 72 h, single colony isolates were picked and evaluated using PCR primers specific for the genus, relevant species and for *B. animalis* ssp. *lactis*. All 10 isolates were identified as members of the genus *Bifidobacterium*. However, species-specific PCR revealed all 10 isolates were *B. animalis* ssp. *lactis*. Further evaluation using PFGE to assess strain relatedness showed all 10 isolates gave PFGE patterns identical to the type strain DSMZ 10140^T when digested with *Spe*I. When digested with *Xba*I, 9 of the isolates gave patterns identical to DSMZ 10140^T. One strain, RT09, had one extra band when digested with *Xba*I. Allelic profiling of the Ukrainian bifidobacterial strains, revealed 4 distinct groups.

Interestingly, 6 (60%) of the isolates fell into the same cluster as that containing the common commercial probiotic strain BB-12. Our results demonstrate the conventional phenotypic methods used to characterize these isolates were sufficient to assign the correct genus, but not the correct species. These findings highlight the importance of employing molecular methods when typing bifidobacterial isolates.

Key Words: *Bifidobacterium animalis* ssp. *lactis*, allelic profiling, probiotics

W47 Buffering capacity affects starter bacteria in nonfat probiotic yogurt. M. Michael, R. K. Phebus, and K. A. Schmidt*, *Kansas State University*, *Manhattan*.

Sodium acetate has been reported to increase acid production and growth yield of some lactic acid bacteria in the growth medium predominately due to its buffering capacity. A buffering agent in yogurt mix may counteract the lethal effect of acid accumulation on starter and probiotic bacteria resulting in greater microbial counts at the end of fermentation. The objective of this study was to determine if changes in yogurt mix's buffering capacity could enhance starter and/or probiotic counts at the end of fermentation. Four nonfat yogurt mixes were prepared with 0.25% sodium acetate (SA) and 4 with no supplement (NS). Mixes were inoculated with yogurt starter alone or yogurt starter and *B. animalis*, *L. acidophilus* or both probiotics, and fermented in a bioreactor at 40°C until pH 4.50. Buffering curves of mixes were generated and pH, titratable acidity (TA) and microbial enumeration were done on an hourly basis during fermentation. Two replications were done and differences in means were determined using LSD at $\alpha = 0.05$ with SAS. Results showed that SA-supplemented mixes had greater buffering capacity at pH <6.00 than that of NS mixes. At the end of fermentation, SA supplementation resulted in greater S. thermophilus counts (~4 to 5%) in yogurts fermented with starter and *B. animalis* or *L. acidophilus*, and greater *L. bulgaricus* counts (~6%) in yogurts fermented with starter and *B. animalis* as compared with NS yogurts. *B. animalis* growth was not affected by the supplementations or fermentation bacteria. No significant differences in *L. acidophilus* counts were observed at the end of fermentation based on supplementation or fermentation bacteria. At pH 4.50, SA-supplemented yogurts had greater TA compared with NS yogurts. In general, fermentation time was longer for SA-supplemented mixes or mixes fermented with *L. acidophilus*. These results suggest that SA supplementation increased the buffering capacity of yogurt mix which improved the starter bacteria counts at the end of fermentation; however, further research should address if SA supplementation of yogurt mix could improve the viability of starter and/or probiotic bacteria in yogurt during storage.

Key Words: yogurt, probiotics, buffering capacity

W48 Identification of lactic acid bacteria in Taiwanese ropy fermented milk and evaluation of their microbial ecology in different milk. K. N. Chen[1], S. Y. Wang[2], and M. J. Chen*[2], [1]*Tungnan University*, *Taipei, Taiwan*, [2]*National Taiwan University*, *Taipei, Taiwan*.

Taiwanese ropy fermented milk (TRFM) is a domestic fermented milk. Its real original is unknown, but it has spread from family to family in northern Taiwan. TRFM has a stringy texture, a good diacetyl flavor and a pleasant taste. The purpose of this study was to identify species of lactic acid bacteria (LAB) in TRFM and to study their microbial dynamics during the fermentation process. The effects of different type of milk on the microbial ecological profiles were also investigated in this study. Ten grams of TRFM starters were homogenized in a laboratory blender. Concentrations of the viable LAB and yeasts in suspensions were obtained by serial plating dilutions. A combination of conventional microbiological cultivation, polymerase chain reaction-denaturing gradient gel electrophoresis and DNA sequencing was used to identify microorganisms and study their microbial dynamics. Identification results indicated that *Lactococcus lactis* ssp. *cremoris* and *Leuconostoc mesenteroides* ssp. *mesenteroides* were the major LAB in TRSM. Interestingly, three groups were identified as *Lactococcus lactis* ssp. *cremoris* using r16S DNA sequencing, but they showed different DGGE patterns and assimilation of carbohydrates. In addition, the microbial dynamics study in different fermentation stages demonstrated that *Lc lactis* ssp. *cremoris* was the most dominant bacterial species in the samples, followed by *Leu. mesenteroides* ssp. *mesenteroides* with no differences among the fermentation stages. Finally, the microbial distribution profiles showed that the microbial ecology was different in bovine, caprine and reconstituted milk, which might further affect the characteristics of the product. In this study, we demonstrated that *Lc lactis* ssp. *cremoris* and *Leu. mesenteroides* ssp. *mesenteroides* were the major LAB in Taiwanese ropy fermented milk. The percentages of the prevalent LAB populations present at different stages during the sample fermentation were similar. we also showed that the type of milk had a great influence on the microbial ecology.

Key Words: ropy fermented milk, microbial ecology, DGGE

W49 Summary of a 2-year study involving screening, characterization, and environmental scanning of bacteria with the potential to produce ropy milk in a farm. A. Laubscher*[1], H. Guo[1], K. White[1], B. Rossi Paneto[1], A. Cano[1], R. Cano[2], and R. Jiménez-Flores[1], [1]*Dairy Products Technology Center, California Polytechnic State University*, *San Luis Obispo,* [2]*Biological Sciences Department, California Polytechnic State University*, *San Luis Obispo*.

Prevention of microbial contamination in raw milk is an important objective in farms where value added is tied with quality. Recent reports of ropy milk have made us aware again of the problem. Ropy milk is characterized by its viscosity and tendency to form a slimy thread. The viscous character of the milk is produced by a complex oligosaccharide present in the capsule of different microorganisms. Over 250 raw milk samples were received from plants throughout the southern states. Of the 5 types of colonies observed, only one appears to have the "ropy" characteristic of mucoid. Isolated mucoid strains were tested for ropy milk production by inoculation in UHT milk and incubation at 25°C for 36 h. The "ropy test" proved successful with 100% reproducibility, but it was discovered that not all mucoid isolates produce a positive RM test. Using API biochemical identification tests, over 80% of the 160 positive "ropy tests" are in the *Klebsiella* species. This result gives us the belief that the presence of ropy milk can be correlated to coliform counts. The objectives were to identify high-risk areas for contamination of the responsible bacteria, the correlation with coliform and *Escherichia coli* (E/C) counts, and development of a subjective or quantitative method to evaluate the risk of finding ropy milk producing bacteria. Ten locations were examined on the Cal Poly Dairy Farm, with bedding having the highest E/C counts and the most probable source for ropy-causing bacteria contamination on the farm. The threshold for the enumeration of ropy-causing bacteria was determined to be only 2.5 CFU/10 mL in a sterile milk sample was enough to turn the milk ropy. With tests performed in triplicate, the threshold of the ropy-causing bacteria is much higher in the presence of typical raw milk microorganisms, suggesting a poor competitive nature. Our results indicate that "ropyness" is a result of a presumptive *Klebsiella oxytoca/pneumoniae* (coliform) a poor-competing bacteria and ubiquitous under poor sanitary conditions, in particular those associated with biofilm formation.

Key Words: milk quality, *Klebsiella*, ropy milk

W50 Screening of *Lactobacillus casei* strains for the application of yogurt starter and probiotics. J. K. Choi*, J. H. Im, and G. B. Kim, *Department of Animal Science & Technology, Chung-Ang University*, *Anseong 456-756, South Korea*.

Lactobacillus casei is one of the most important probiotics, and it is widely used in functional foods and dairy products. As a trial for the development of a new starter culture, more than 200 lactic acid bacteria strains were isolated from raw milk and healthy human feces. The strains showing excellent growth and acid production ability in the 10% skim milk media were selected and identified as *Lactobacillus casei* by the result of API carbohydrate fermentation pattern and 16S rDNA sequence analysis. Among the selected strains, *L. casei* CU2604 and CU3204 were further investigated for their physiological characteristics as a starter culture comparing them with a commercial strain, *L. casei* Shirota. Both CU3204 and CU2604 strains showed good acid production and growth characteristics in milk, which are comparable with those of *L. casei* Shirota strain. However, *L. casei* CU2604 was the only selected strain that had a similar sugar fermenting pattern and PFGE band pattern compared with *L. casei* Shirota. Furthermore, CU2604 showed better tolerance to bile and to pH than *L. casei* Shirota. In addition, to assess the effect of *L. casei* strains in irritable bowel syndrome (IBS), the inhibitory effect of the selected strains against nitric oxide (NO) production of lipopolysaccharide (LPS)-stimulated RAW 264.7 cells was measured. Among the tested *L. casei* strains, *L. casei* MCL was observed to have the greatest NO inhibitory activity. Based on these results from this study, we anticipate the possible use of *L. casei* MCL strain as a new probiotic and CU2604 as a new starter culture.

Key Words: *Lactobacillus casei*, yogurt starter, probiotics

W51 Effect of yogurt consumption on the human intestinal microbiota. H. J. Kim*[1], S. J. Eom[1], Y. T. Ahn[2], J. H. Lee[2], C. S. Huh[2], and G. B. Kim[1], [1]*Department of Animal Science and Technology, Chung-Ang University*, *Anseong 456-756, South Korea*, [2]*Research and Development Center. Korea Yakult Co. Ltd.*, *Yongin 449-901, South Korea*.

In this study we investigated the effect of consumption of yogurt on the fecal microflora of 40 healthy volunteers. The subjects were randomly divided into experimental (n = 20) and control (n = 20) groups for a double-blind placebo-controlled clinical study. The experimental group consumed yogurt 2 times a day (150mL each) for 3 weeks and the control groups consumed the same amount of milk acidified with lactic acid. Fecal samples at defined time points before, during, and after the period of yogurt ingestion were collected and analyzed. The fecal population of lactobacilli and bifidobacteria was determined by culture-based methods using Rorosa SL agar and TOS-propionate agar media, respectively, and subsequent colony PCR for the confirmation of the target Genus. The comprehensive dynamics of intestinal microbiota in response to yogurt consumption was analyzed using a bacterial barcoded pyrosequencing.

The population of bifidobacteria in the fecal sample of experimental group increased from 9.65±0.56 to 10.20±0.41 (log_{10} cells/g wet feces, mean ± SD) during the ingestion of yogurt, but it tended to be normalized (9.67±0.84) when they stopped the ingestion. The similar tendency was observed in the population of lactobacilli during the experiment; however, there were no significant changes in the control group. Molecular analysis of the human fecal bacterial populations by pyrosequencing of 16S rRNA tags revealed that yogurt consumption induced significant alterations of the gut microbiota. The ratio of *Firmicutes* to *Bacteroidetes* was 1.23, 0.59, and 2.01 at the time points before, during, after the period of yogurt ingestion, respectively. This study provides evidence that the gut microbiota could be modulated by dietary intenvention such as yogurt ingestion and further studies should be done to better understand the modulation of the gut microbiota associated with health attributes in well-defined human clinical studies.

Key Words: yogurt, pyrosequencing, microbiota

W52 The effect of fermented yogurt on the prevention and treatment of diarrhea in animal models. J. H. Im*[1], J. K. Choi[1], M. H. Lee[2], J. H. Sim[2], C. S. Huh[2], and G. B. Kim[1], [1]*Department of Animal Science & Technology Chung-Ang University*, *Anseong 456-756, South Korea*, [2]*Research and Development Center. Korea Yakult Co., LTD.*, *Yongin 449-901, South Korea*.

Constipation is the most prevalent health condition in the world. Common symptoms are difficult stool passage, infrequent stools, or both. Dairy products such as milk and yogurt improve intestinal function. The objective of this study was to investigate the improvement of intestinal function, the prevention of constipation, and the curative value of supplying fermented milk products to mice and rats. Constipation was induced by oral administration of loperamide and experiments were executed for 5 consecutive days. All experiments separated research subjects into 3 groups; the control, the treatment of loperamide alone, and the treatment of low, medium, and high levels fermented milk. The results showed that the effects varied significantly among different levels of doses in that: 1) The digestive tract transfer rate showed that the control 44.2%, low levels 51.7%, medium levels 67.4%, high levels 67.7%; 2) Constipation preventive effect showed that the water and food intake, and the amount and number of feces decreased significantly with loperamide alone, low, medium levels ($P < 0.001$, $P < 0.05$, $P < 0.01$). However the treatment of loperamide with fermented milk increased the number of feces significantly at high level ($P < 0.05$), amount of feces increased significantly at low, high levels ($P < 0.05$, $P < 0001$), also water contents increased. 3) Effective treatment of constipation showed that the water and food intake decreased significantly; the number of feces increased significantly at medium level ($P < 0.001$), weight of feces showed similar results. Water contents increased significantly at medium, high levels ($P < 0.05$, $P < 0.001$). These results suggest that the repetitive ingestion of fermented yogurt is effective to prevent and treat constipation in animal models.

Key Words: animal trials, fermented yogurt, constipation

W53 Effect of milk fermented by *Lactobacillus rhamnosus* on an experimental infection with *Salmonella enterica* ssp. *enterica* serov. Typhimurium in gnotobiotic and conventional mice. A. H. Mendonça[1], M. M. O. P. Cerqueira*[2], J. R. Nicoli[2], M. O. Leite[2], M. R. Souza[2], L. M. Fonseca[2], R. M. N. Drummond[2], R. M. E. Arante[2], and C. F. A. M. Penna[2], [1]*Ministry of Agriculture*, *Brasília, Distrito Federal, Brasil*, [2]*Federal University of Minas Gerais*, *Belo Horizonte, Minas Gerais, Brasil*.

An experimental infection with *Salmonella enterica* ssp. *enterica* serov. Typhimurium was evaluated in gnotobiotic (GN) and conventional (CV) mice previously treated or not with milk fermented by a *Lactobacillus rhamnosus* strain isolated from healthy human newborn. Conventional mice received 0.1 mL probiotic milk (8.0 log CFU) daily, 10 d before the oral pathogenic challenge (5.0 log CFU). Then, probiotic treatment was continued until the end of the experiment. Probiotic treatment in germ-free mice consisted of a single dose at the beginning of the experiment

and a challenge 10 d later (3.0 CFU). Protective effect was observed in both GN and CV animals in terms of histopathology and morphometric data but in different anatomical site. This protection was observed in liver and intestines, respectively for GN and CV mice. However, *Salmonella enterica* ssp. *enterica* serov. Typhimurium populations were similar in the feces of both treated and control GN mice. Concluding, a protective effect by *L. rhamnosus* against experimental *Salmonella enterica* ssp. *enterica* serov. Typhimurium was observed. This protection was not due to the reduction of the population of pathogens in the intestine.

Key Words: fermented milk, *Lactobacillus rhamnosus*, probiotic

W54 Influence of bovine and caprine caseinomacropeptide on the viability of *E. coli* and *L. rhamnosus* in acidic conditions. G. Robitaille*, C. Lapointe, D. Leclerc, and M. Britten, *Food Research and Development Centre, Agriculture and Agri-Food Canada*, *St-Hyacinthe, QC, Canada*.

Caseinomacropeptide (CMP) is a 7-kDa phosphoglycopeptide fragment released from κ-casein during chymosin-induced renneting of milk. Bovine CMP differs from caprine CMP by 19 substitutions, 2 insertions, by glycosylation extent and the level of phosphorylation. The objective of the study was to analyze the effects of pepsin-treated CMP (CMPpt) on the survival of *E. coli* and *L. rhamnosus* in acidic conditions. To induce acid shock, bacterial cells were incubated at 37°C in PBS with or without additive (CMPpt, non-glycosylated CMPpt (aCMPpt) and glycosylated CMPpt (gCMPpt) isoforms) from bovine and caprine. Viability (CFU/mL) was determined at 0, 15, 30, 60 and 90 min. As expected, *E. coli* was sensitive to low pH. The bacterial viability decreased by more than 1.5 log within 15 min at pH ≤3.0. At pH 3.5, it took about 90 min to reach a similar decrease. When added to the media, CMPpt was bactericidal in a dose dependent manner, reducing survival by more than 90% within 15 min at ≥0.25 mg/ml. This indicates that the encrypted bioactive peptides within CMP are released by pepsin proteolysis and are bactericidal against *E. coli* at low pH. Moreover, the effectiveness of CMPpt to kill *E. coli* at pH 3.5 was not significantly affected by the presence of linked oligosaccharides or by the origin of the milk. This suggests that the active peptide is located in the N-terminal portion of the polypeptide, a region of high homology between species that does not carry any phosphate or oligosaccharide. Survival of *L. rhamnosus* at pH 2.9 decreased to about 5% within 60 min. Supplementation with bovine or caprine CMPpt has an inverse effect. It increased viability to values as high as 50%, with similar efficiencies for aCMPpt and gCMPpt. These results suggest that peptic digests of bovine and caprine CMP may act as antimicrobial agents against *E. coli* in a gastric context without any deleterious effect on the resistance of a probiotic to gastric pH.

Key Words: caseinomacropeptide, bacterial growth, gastric pH

W55 Screening of β-galactosidase-containing probiotic for the production of galacto-oligosaccharides and its optimal preparation conditions. Y. Gao, X. Mi, L. Feng, R. Zhong, B. Qian, and S. Zhang*, *Department of Food Science and Technology, School of Agriculture and Biology, Shanghai Jiao Tong University*, *Shanghai, China*.

As β-galactosidase carriers, whole probiotic cells were screened out for the production of galacto-oligosaccharides (GOS) and the optimal production conditions were investigated in this study. In this process, probiotics including 2 strains of *Bifidobacterium bifidum*, 2 strains of *Lactobacillus helveticus* and one strain of *Lactobacillus delbrueckii* ssp. *bulgaricus* were employed. A high-performance anion exchange chromatography with pulsed amperometric detection (HPAEC-PAD) was utilized for the sugar composition analyses in the prepared products. Results showed: top 3 GOS production prebiotics were *Bifidobacterium bifidum* BB03, *Bifidobacterium bifidum* BB02 and *Lactobacillus delbrueckii* ssp. *bulgaricus* with the production of GOS at 201.8 g/L100g, 160.1 g/L and 129.4 g/L, respectively. The optimal production conditions of *Bifidobacterium bifidum* BB03 were as follows: 0.20 g freeze-dried cells were transferred into a flask with 50 mL of lactose aqueous solution (473.4 g/L), shaken at the speed of 150 rpm and cultured at 37 centigrade for 8h. The fractions of GOS in this product were proved to be with 197.7 g/L dimer GOS and 4.1 g/L tetramer GOS. In addition, the production of galactose, glucose and the residual lactose in the product were presented to be 1.9 g/L, 94.3 g/L and 1.3 g/L, respectively.

Key Words: galacto-oligosaccharides, probiotic, HPAEC-PAD

W56 Characterization and partial purification of antimutagenic peptide produced by *Lactobacillus plantarum* CNU 2116. J. W. Jeong*[1], B. H. Yoon[1], D. J. Park[3], Y.-S. Son[2], and S. Oh[1], [1]*Division of Animal Science, Chonnam National University*, *Gwangju, South Korea*, [2]*Division of Bioscience & Technology, Korea University*, *Seoul, South Korea*, [3]*Korea Food Research Institute*, *Gyeonggi-do, South Korea*.

Intestinal lactic acid bacteria (LAB) are closely associated to the host's health because the presence of LAB are an important bio-defense factor in preventing colonization and subsequent proliferation of pathogenic bacteria in the intestine. Some probiotics such as *Lactobacillus* species can intoxicate the carcinogens including chemical mutagens. The antimutagenic activity of 24 LAB strains was investigated using 3 mutagens (4-nitroquinoline-N'-oxide, 4-NQO; N-methyl-N'nitro-N-nitrosoguanidine, MNNG; and 2-amino-3- methylimidasol quinoline, IQ). In the Ames test, dose-dependent activity was exhibited significantly against 4NQO, MNNG, and IQ. *Lactobacillus casei* KCTC 13086 and *L. plantarum* strains showed the highest anti-4NQO activity (62.1%) among the tested strains of LAB. The active substance was found to be sensitive to trypsin (71500 units/mL). This indicates that antimutagenic substance is proteinaceous in nature. The molecular weight of the antimutagenic peptide was estimated as an approximately 762 Da using tricine-SDS-PAGE. N-terminal amino acid residue sequence from the purified peptide was identified as NH_2 -Xaa-Leu-Glu-Xaa-Lys-Lys-Ala-Glu-Xaa-Ile-Thr-Thr. Compared with other sequences in the NCBI database using Blast program, we found no significant sequence similarity to previously reported antimutagenic peptides.

Key Words: antimutagenic activity, lactic acid bacteria, characterization

W57 Characterization of microorganisms isolated from biofilms formed on whey reverse osmosis membranes. A. C. Biswas*, M. Avadhanula, S. Anand, and A. Hassan, *Midwest Dairy Foods Research Center, Dairy Science Department, South Dakota State University*, *Brookings*.

Microbial biofilm is a complex structure made up of organisms embedded in polymeric matrices of biological origin attached to a substratum. The present investigation was undertaken to characterize the multispecies microbial consortia isolated from reverse osmosis (RO) membranes drawn from active industrial whey filtration process at 2, 4, 6, 8, 10, 12, and 14 mo of age. The ability of the different bacterial isolates to produce capsule and slime, and increase whey viscosity as indications of exopolysaccharides (EPS) production was also studied. Results showed that *Bacillus* sp. was present on almost all RO membranes from 4 to 12 mo. *Enterococcus*, *Streptococcus*, *Staphylococcus*, *Micrococcus*, *Aeromonas*, *Corynebacterium*, and *Pseudomonas* species were also

encountered frequently. *Escherichia coli* and *Klebsiella oxytoca* were detected only on 8, 12 and 14 mo old membranes. Among all isolates, about 25% did not produce capsules or slime, or increased viscosity of whey, which indicated lack of EPS production. This reflects that strains not producing EPS can also be involved in biofilm formation. However, since the EPS production was only tested in planktonic cells, there is still a possibility that they produce EPS in biofilm matrices. Interestingly, the EPS production was more pronounced in isolates from older (8 to 14 mo old) as compared with newer (2 to 6 mo old) membranes. Studies also confirmed the ability of individual isolates to form biofilms under static in vitro conditions. Predominance of *Escherichia coli* and *Bacillus sp*. was observed during the reproduction of mixed species biofilms. The study provides useful information on the predominant bacterial species in biofilms formed on whey processing membranes. This will help in developing more effective cleaning and sanitation regimens.

Key Words: biofilm, exopolysaccharides (EPS), RO membrane

W58 Transcriptional analysis of a very broad spectrum lantibiotic produced by *Bifidobacterium longum* DJO10A. J. H. Lee*, X. Li, and D. J. O'Sullivan, *University of Minnesota*, *St Paul*.

Lantibiotics are bacteriocins produced by some gram-positive bacteria with a very broad antimicrobial spectrum. A reverse genomic analysis of *B. longum* ssp. *longum* DJO10A revealed the potential to produce a lantibiotic and subsequent analysis revealed it produced a small (<5 kDa) peptide, only on agar media, with an antimicrobial spectrum that included gram-negative bacteria. To further understand the regulation for production of this lantibiotic a full-genome microarray analysis with total RNA from both agar and broth cultures was conducted. This revealed a very different expression pattern between agar and broth cultures, including the lantibiotic-producing genes which were expressed much higher in agar. Interestingly, the expression of the 2-component regulatory genes in this operon, were relatively constant in both conditions, suggesting it should be functional in broth cultures. To further investigate this, a real-time PCR procedure, with a specific TaqMan probe targeting the lanA gene, was developed. This confirmed the broth and agar differential expression of *lanA* in different media, with MRS agar showing the highest gene expression. To obtain some crude lantibiotic compound, it was extracted from MRS agar using 95% methanol and partially purified via size fractionation with filtration systems. Different concentrations of this partially purified lantibiotic were used to investigate the expression of *lanA* in broth cultures. Strikingly, *lanA* gene expression was drastically increased in a dose dependant fashion in broth cultures, confirming that increasing the external signal in broth cultures allows the expression of the lantibiotic production genes, thus facilitating lantibiotic production in broth.

Key Words: bifidobacteria, lantibiotic, microarray

W59 Comparison of the Baird-Parker agar, Baird-Parker-RPF and Petrifilm Staph Express in the detection and enumeration of *Staphylococcus* coagulase positive in raw milk. A. K. R. Santos, M. O. Leite*, L. M. Fonseca, M. O. P. Cerqueira, M. R. Souza, C. F. A. M. Penna, and M. R. A. Moura, *Federal University of Minas Gerais*, *Belo Horizonte, Minas Gerais, Brasil*.

The reference methodology for *Staphylococcus* spp. enumeration recommends the use of Baird-Parker agar (BP); however, other culture media may produce results in shorter time, as Baird-Parker - RPF agar (bioMérieux, Marcy l'Etoile, France) and Petrifilm™ Staph Express Count Plate - PSE - (3M Microbiology Products, St. Paul, USA). Thus, this work was carried out to compare the efficiency of the forecited culture media for the enumeration of *Staphylococcus* spp. in 36 samples of raw milk. The experiment was designed in random blocks and the media were compared by the *t*-test. Mean *Staphylococcus* spp. count obtained by PSE (2.50 Log10 CFU/mL) was lower ($P < 0.05$) than those by BP (4.12 Log10 CFU/mL) and RPF (3.86 Log10 CFU/mL), being the latter 2 values considered similar ($P > 0.05$). The results showed viable the use of RPF, but not PSE, replacing BP for *Staphylococcus* spp. enumeration without altering the accuracy of the analysis.

Key Words: *Staphylococcus*, culture media, raw milk

W60 Influence of low pressure homogenization on growth of *Streptococcus thermophilus*. T. Muramalla[1] and K. Aryana*[1,2], [1]*Louisiana State University*, *Baton Rouge,* [2]*Louisiana State University Agricultural Center*, *Baton Rouge*.

The objective was to study the effect of low pressure homogenization on growth of *Streptococcus thermophilus*. Fat free milk was sterilized by autoclaving, chilled to 4°C, inoculated with *Streptococcus thermophilus* and homogenized at 0, 3.45, 6.90, 10.35, 13.80 MPa for 5 continuous passes. The control (0 MPa) and homogenized (3.45, 6.90, 10.35, 13.80 MPa) samples were individually inoculated in Lactobacilli MRS broth. Samples were plated in duplicate at 0, 2, 3, 4, 5, 6, 8, and 10 h using the pour plate technique. During 10 h incubation period the broth samples were kept at 37°C and plates were incubated aerobically at 37°C for 3 d. Entire experiments were replicated 3 times. Data were analyzed using proc mixed of SAS. The interaction effect of pressure x time was not significant. Both main effects pressure and time were significant ($P < 0.0001$). The homogenized samples (6.90, 10.35, 13.80 MPa) were not significantly ($P < 0.05$) different from each other but exhibited counts significantly ($P < 0.05$) higher than control (0 MPa). The homogenized samples treated to pressures of 6.90, 10.35, 13.80 MPa exhibited average counts of 11.84, 11.85, 11.83 log CFU/ml and control (0 MPa) had an average count of 11.70 log CFU/ml. The low pressure homogenization at 6.90, 10.35, 13.80 MPa had a slight yet positive significant effect on growth of *Streptococcus thermophilus*.

Key Words: dairy, culture, bacteria

W61 Influence of mild pulsed electric field conditions on the growth of *Streptococcus thermophilus*. N. Najim[1] and K. Aryana*[1,2], [1]*Louisiana State University Agricultural Center*, *Baton Rouge,* [2]*Louisiana State University*, *Baton Rouge*.

Pulsed electric field (PEF) processing involves the application of pulses of voltage for less than one second to fluid products placed between 2 electrodes. *Streptococcus thermophilus* is an important bacterium used for the production of fermented dairy products. Objective of this study was to determine the influence of a mild PEF condition on the growth of *Streptococcus thermophilus*. A range of mild pulsed electric field conditions were earlier screened by the authors to arrive at an optimum overall mild pulsed electric field condition for various probiotic characteristics. Freshly thawed *Streptococcus thermophilus* was suspended in 0.1% w/v sterile peptone water and treated in a pilot plant PEF system. The treatment was a mild PEF condition of positive square unipolar pulse of 3 µs, pulse period of 0.5 s and voltage of 1kv/cm. Control was run through PEF system but without receiving any pulsed electric field condition. Control and treated sample flow rates were kept constant at 60 mL/min. Samples were individually inoculated in lactobacilli MRS broth. Samples were plated in duplicate. Pour plates were incubated aerobically at 37°C for 3 d. Growth was determined hourly for 20 h. Experiments were replicated 3 times. The control and mild PEF treated samples had the same counts of 10.97 (+/− 0.25) log cfu/mL at 0 h. The

mild PEF treated samples reached the log phase an hour earlier than control. Although at most time points, counts were within the same log cfu/mL for the control and treated samples, the mild PEF treated samples had significantly ($P < 0.05$) higher counts compared with control for most of the time points over the 20 h of growth. The mild PEF condition enhanced growth of *Streptococcus thermophilus*.

Key Words: pulsed electric field, nonthermal, culture

W62 Effect of mild sonication on the growth of *Streptococcus thermophilus*. M. Moncada*[1,2] and K. Aryana[1,2], [1]*Louisiana State University Agricultural Center*, *Baton Rouge,* [2]*Louisiana State University*, *Baton Rouge*.

Mild sonication (20–40% amplitude) conditions have been reported to increase the transport of small molecules in solution enabling bacterial cell growth. *Streptococcus thermophilus* is an important lactic acid bacterium used for the production of some fermented dairy products. The objective was to study the influence of mild sonication on the growth characteristics of *Streptococcus thermophilus*. Freshly thawed culture was suspended in 0.1% peptone water and 18 mL of sample was sonicated using horn (diameter 13 mm) set at a maximum acoustic power output of 750 W, frequency 24 kHz. The treatments were amplitudes of 21, 27, 33 and 39%. In all treatments energy input into the system was kept constant at 1500 J. The control was sample not treated with mild sonication. Samples were inoculated in lactobacilli MRS broth. Samples were pour plated in duplicate. During 12 h incubation period the samples were kept at 37°C. Pour plates were incubated aerobically at 37°C for 3 d. Growth of control and treated samples were determined hourly over 12 h. Three replications were conducted. Data were analyzed using the PROC GLM of the Statistical Analysis Systems (SAS). The control and samples treated with 21% amplitude exhibited average counts of 14.55 and 15.01 log CFU/mL respectively at the end of the 12-h incubation. Similar increases in counts were observed in samples treated with 33% amplitude compared with control in which average counts at the end of the 12 h were 14.58 and 14.26 log CFU/mL respectively. With an increase in amplitude of mild sonication the counts declined but maintained higher than the control. It is concluded that the lowest sonication intensity studied (amplitude of 21%) had the best effect on increasing *Streptococcus thermophilus* counts.

Key Words: sonication, culture, growth

W63 Low pressure homogenization effects on bile tolerance of *Streptococcus thermophilus*. T. Muramalla*[1] and K. Aryana[1,2], [1]*Louisiana State University*, *Baton Rouge,* [2]*Louisiana State University Agricultural Center*, *Baton Rouge*.

The goal was to determine the influence of low pressure homogenization on bile tolerance of *Streptococcus thermophilus*. Fat free milk was autoclaved, chilled to 4°C, inoculated with *Streptococcus thermophilus* and homogenized at 0, 3.45, 6.90, 10.35, 13.80 MPa for 5 continuous passes. The control (0 MPa) and homogenized (3.45, 6.90, 10.35, 13.80 MPa) samples were individually inoculated in Lactobacilli MRS broth with oxgall bile. Samples were plated in duplicate at 0, 2, 3, 4, 5, 6, 8, and 10 h. During 10 h incubation period the broth samples were kept at 37°C. Pour plates were incubated aerobically at 37°C for 3 d. Entire experiments were replicated 3 times. Data were analyzed using proc mixed of SAS. The interaction effect of pressure × time was not significant while both the main effects pressure and time were significant ($P < 0.0001$). The homogenized samples (3.45, 6.90, 13.80 MPa) were not significantly ($P < 0.05$) different from each other but exhibited counts that were significantly ($P < 0.05$) higher than control (0 MPa). The homogenized samples treated to pressures of 3.45, 6.90, 13.80 MPa exhibited average counts of 10.72, 10.79, 10.81 log CFU/mL compared with control (0 MPa) which had an average count of 10.60 log CFU/mL. The low pressure homogenization at 3.45, 6.90, 13.80 MPa had a slight yet positive significant effect on bile tolerance of *Streptococcus thermophilus*.

Key Words: culture, homogenization, bacteria

W64 Acoustical emissions generated by bacteriophages sk1 and ml3 using *Lactococcus lactis* ssp. *lactis* C2 host. A. K. Wardani[1], C. L. Hicks*[2], and J. M. Stencel[3], [1]*University of Brawijaya*, *Malang, Indonesia*, [2]*University of Kentucky*, *Lexington,* [3]*Tribo Flo Separations*, *Lexington, KY*.

Lactococcus lactis ssp. *lactis* C2 bacteria in M17 medium, at 26°C for 8 h were infected with phages sk1 or ml3, and monitored using contact piezoelectric sensors attached to the sides of the growth vessel. The 2 sensors (5 to 50 kHz range) had individual characteristic and internal amplification mechanisms that were calibrated and adjusted to minimize background noise. After the sensors had been calibrated, the M17 medium was inoculated with *L. lactis* ssp. *lactis* C2 culture (1×10^9 cfu/mL), stirred for 1 min, and allowed to grow for approx. 90 min before infection (stirred for 1 min) with phages sk1 or ml3. Infection time was set to correspond with the start of the log growth phase. Infection level was 10^5 pfu/mL for both phages sk1 and ml3. Sound intensity from the growth chambers was measured in attojoules (aJ = 10^{-18} Joules) and plotted as the energy rate-per-detected acoustic wave. Acoustic peaks considered significant and beyond internal or external generated noise were those having greater than ± 3 times the sigma value of the general variation in acoustic intensity over the entire data set of each test. Energy rate data from control tests in which *L. lactis* ssp. *lactis* C2 was grown without phage sk1 or phage ml3 infections contained no acoustic peaks with intensities that exceeded the ± 3 sigma standard whereas phage sk1 or ml3 infected *L. lactis* ssp. *lactis* C2 culture contained multiple acoustic peaks with intensities that exceeded ± 3 sigma. The first peak for phage sk1 appeared at 33.2 ± 4.4 min whereas the first peak for phage ml3 appeared 40 min. Thus, the acoustic data from phage sk1 or phage ml3 infected *L. lactis* ssp. *lactis* C2 were considered to be the result of phage infection. The timings of the acoustic peaks from phage sk1 were sufficiently different from phage ml3, that these 2 phage could probably be distinguished by acoustic emission monitoring during phage infection of the bacteria.

Key Words: acoustic emission, bacteriophage, *Lactococcus*

W65 Viability of bifidobacteria and lactobacilli in skim milk with shiitake mushroom extract during refrigerated storage. O. Hassan*[1], O. S. Isikhuemhen[1], S. A. Ibrahim[1], A. AbuGhazaleh[2], and D. Song[1], [1]*North Carolina A &T State University*, *Greensboro,* [2]*Southern Illinois University*, *Carbondale*.

Probiotics, such as bifidobacteria and lactobacilli, have been demonstrated to help establish and support strong immune systems. A key growth source for these bacteria are certain carbohydrates, so food rich in these food components would presumably help probiotics to thrive. Shiitake mushroom (*Lentinus edodes*) contains antitumor oligosaccharides and polysaccharides which could enhance probiotics growth. The objective of this study was to exam the viability of selected probiotic cultures in skim milk in the presence of different levels of Shiitake mushroom extract during refrigerated storage. *Lactobacillus reuteri* CF2–7F, *L. reuteri* DMS 20016, *Bifidobacterium breve* and *B. adolescentis* were individually inoculated into skim milk supplemented with

different concentrations of mushroom extract (0%, 1%, 2%, and 4%) and stored immediately at 4°C for 4 weeks. Aliquots were withdrawn at one-week interval to determine bacterial population, pH and titratable acidity of the milk samples. Results showed that the viability of tested strains was significantly higher in milk supplemented with Shiitake mushroom extract ($P < 0.05$) compared with the control sample. All tested strains demonstrated culture stability upon refrigerated storage and exhibited no significant loss of viability during storage conditions for 2 weeks. After 4 weeks of storage, 2 log reduction of viable cells from an initial mean of 109/ml was observed. Samples had a mean initial pH of 6.5 and titratable acidity of 0.16. Both pH and titratable acidity showed negligible change at 4°C during 2-week storage. Our results suggest that shiitake mushroom extract can be used as a natural additive in dairy products to improve the viability of probiotics during refrigerated storage and to improve consumer health.

Key Words: bifidobacteria, lactobacilli, mushroom

W66 Microbiological quality of dairy protein supplements sold in Saudi Arabia markets. S. O. Aljaloud*[1], D. Song[2], A. M. Fraser[1], and S. A. Ibrahim[2], [1]*Clemson University*, *Clemson, SC*, [2]*North Carolina Agricultural and Technical State University*, *Greensboro*.

Whey proteins are becoming popular dietary supplements here in the US and around the world. However, these ingredients are typically not sterile. There is need to investigate the microbiological safety of these products. The objective of this study was to determine the microbiology quality of whey protein supplements sold in Saudi Arabia. Twenty different dairy protein supplements were purchased from local stores in Riyadh, the capital of Saudi Arabia. These products ranged from whey protein concentrate (5), whey protein isolate (4), why protein hydrolyzed (2), whey protein concentrate lactose free (3), whey protein concentrate mineral free (2) and casein isolates (4). Samples were analyzed for several microbial quality attributes including aerobic total plate count (ATPC), psychrotrophs (PC), *Enterobacteriaceae*, total coliforms, and fecal coliforms. The presence of selected pathogens such as *Staphylococcus aureus* and *Salmonella* were investigated. Our results showed that the average bacterial population for ATPC, PC and *Enterobacteriaceae*, were 4.1, 2.1, and 1.2 log cfu/mL, respectively. Coliform groups were found in 29% of samples while 10% were fecal coliform positive as revealed by the MPN method. *S. aureus* was located in at least 25% of samples, with a mean count of 2.1 log cfu/mL. Our results confirmed that there is potential health risk with the consumption of dairy protein supplements sold in Saudi Arabia. There is a need to develop a monitoring system to check the microbiological quality of dairy protein supplements on market to assure them safe to use.

Key Words: microbiological quality, dairy protein supplements

W67 Antimicrobial activity and composition of oregano essential oils from different climate zones of Colombia. L. Betancourt*[1,3], R. Patiño[2], V. Phandanauvong[2], C. Ariza-Nieto[2], and G. Afanador-Téllez[3], [1]*Universidad de La Salle*, *Bogotá, Colombia*, [2]*CORPOICA*, *Bogotá, Colombia*, [3]*Universidad Nacional de Colombia*, *Bogotá, Colombia*.

The antimicrobial activity of oregano essential oils has been showed in the literature; however, composition and antibacterial activity of oregano essential oils (OEO) from different climatic zones of Colombia have not been studied. The aim of this study was to characterize 4 chemotypes of OEO, *Origanum majorana* (OM), *Origanum vulgare* L (OVL), *Lippia origanoides* (LO) and *Origanum vulgare* H. (OVH, from Greece). Composition was analyzed by GC/Ms and its antibacterial activity through minimum inhibitory concentration (MIC) against *Lactobacillus acidophilus*, *Bifidobacterium breve*, *Salmonella enteritidis*, *Salmonella typhimurium* and *Escherichia coli* by broth dilution method. OVH from Greece presented the highest carvacrol content (90%), while the highest thymol was found in LO from Colombia (79%). OM was rich in Sabinyl compound (24%). OVL presented high thymol content (21%) and low carvacrol (4%). The best carvarol: thymol ratio was for OVH (25) and LO present the most very low (0.01). The amount of lowest precursors (gamma terpinene+para-cymene) was for LO (9%), but varieties of oregano produced in greenhouse conditions at high altitude (Savannah of Bogotá, 2650 AMSL)) had highest precursors content, 17% for OM and 41% for OVL. Carvacrol, OVH and LO showed the same MIC values against *S. enteritidis* (0.098 mg/ml). Carvacrol had better MIC against both *S. typhimurium* (0.098 mg/mL) and *E. coli* (0.0061 mg/mL), followed by OVH and LO. The lowest MIC against beneficial bacteria was for OM (6.25 mg/mL) against *L. acidophilus* and LO (50 mg/mL) against *B. breve*. These results clearly showed that OEO rich in thymol could have a desirable antibacterial effect on gastrointestinal tract.

Key Words: *Lactobacillus*, *Bifidobacterium*, *Salmonella*

W68 Effect of processing on the milk fat globule membrane constituents. X. Elías-Argote* and R. Jiménez-Flores, *California Polytechnic State University San Luis Obispo*.

The milk fat globule membrane (MFGM) proteins have been studied extensively using proteomic techniques to characterize them and to find out their structure within the membrane. The MFGM constituents have the potential to offer excellent health benefits; however, few studies have highlighted the effects of processing on the MFGM constituents and the repercussion it may have on their functionality. In this study, we have analyzed milk throughout traditional processing. These include collection, refrigeration, and 2 types of commercial pasteurization. In addition, this work also includes a potential pasteurization method using pulsed light treatment. Milk was collected before reaching the storage unit and kept at 37°C. Samples were processed at storage temperature (4°C), batch and high temperature short time (HTST) pasteurizations, and by pulsed light treatment. The cream was separated, and milk fat globule size distribution was determined using laser light scattering in the skim milk and cream fractions of the 4 treatments. The MFGM was then extracted and analyzed using 2D-PAGE and LC-MS. Microscopic evaluations were performed using confocal microscopy. As the heat treatment increased, more casein and whey proteins were absorbed onto the membrane and observed in the final product. The particle size reflects small diameter globules remaining in the skim milk and greater variability in the size distribution with heat treatments. We observed that MFGM proteins, especially adipophilin and butyrophilin, are affected differently by processing. Their concentration in the MFGM decreases as pasteurization temperature increases.

Key Words: MFGM, proteomics, protein interactions

W69 Evaluation of vacuum packaging on particle size, particle density and solubility of dry dairy powders. H. Eshpari* and P. S. Tong, *California Polytechnic State University*, *San Luis Obispo*.

Dry dairy ingredients can have a long shelf life if packaged and stored properly. Vacuum packaging can be an attractive method for keeping quality and provides added value; because of the inherent compactness of the products. Vacuum packaged dry dairy ingredients may also have added ease of handling for end users. However little is known about the impact of vacuum packaging on the properties of dry dairy ingredients. The objective of this study was to determine the effects of vacuum packaging on particle size, particle density and solubility of 4 types of dry dairy ingredients. Commercial samples of nonfat dry milk powder, whole milk powder, buttermilk powder, and milk protein Isolate were repackaged in duplicate using multi-wall foil side gusseted bags under varying degrees of vacuum (1, 0.7, 0.4 bar) and a control with no vacuum, and then stored for 3 mo at 37°C and 60% relative humidity. Each powder was sampled and analyzed in duplicate for particle size, particle density and solubility upon receiving and after 3 mo storage. After 3 mo storage there were no significant differences in solubility and particle density of the powders, regardless of the vacuum level, but some significant differences in particle size of the powders (Table 1). Moreover, the trend of change in particle size is different for different powders. The data suggest that the proposed vacuum packaging method may be beneficial to maintain the quality of the powders studied.

Table 1. Significant changes observed in the particle size of the samples after 3 months storage

Powder	Changes observed	P-value
Nonfat dry milk	no vacuum > before packaging	0.03
Whole milk	1 bar vacuum > before packaging	0.02
Whole milk	0.7 bar vacuum > before packaging	0.00
Whole milk	0.4 bar vacuum > before packaging	0.00
Whole milk	no vacuum < before packaging	0.00
Whole milk	no vacuum < 1 bar vacuum	0.00

Key Words: vacuum packaging, dry dairy powders, physical properties

W70 A new cold gelation method for producing calcium-fortified whey protein gels. Y. C. Tseng and C. L. Hicks*, *University of Kentucky*, *Lexington*.

Whey proteins, with versatile functionalities and excellent nutritional values, are widely utilized in food applications. In the presence of calcium ions or an acidulating agent, preheated whey proteins form gels at ambient temperature. However, to obtain a good texture, currently cold-set calcium-induced whey protein gels are prepared by introducing Ca^{2+} into a whey protein solution through dialysis, which is an inconvenient and time-consuming process. Thus, the objective of this research was to develop a new procedure for making homogeneous calcium-fortified cold-set whey protein gels. Whey protein isolate suspensions (7% w/v, pH 7) were prepared with distilled water and heated at 80°C for 30 min. After cooling to room temperature, calcium carbonate was added to the protein solutions at various concentrations (0, 5, 10, 15 m*M*). Gelation was induced by adding 30 m*M* glucono-delta-lactone (GDL) to the protein solutions at 24°C. The kinetic profile of the gelling system was studied using a Bohlin VOR rheometer. Finished gels were subjected to textural profile analysis and measurements of water holding capacity, pH and color. Within 2 h after the addition of GDL, all samples were shown to have significant increase in storage modulus (G'), indicating the formation of a viscoelastic gel network. Homogeneous cold-set gels were obtained from all treatments 5h after the initiation of gelation. Calcium level (0–15 m*M*) was shown to affect ($P < 0.05$) the pH, L value (lightness), and textural profile of the final gels. As Ca^{2+} increased, final pH values of the gels increased from 4.7 (calcium free samples) to 5.8 (samples w/ 15 m*M* $CaCO_3$) while the respective L values reduced from 72.4 to 70.8. Gel breaking strength was greatly reduced as calcium level increased, with values ranging from 595g to 349g, respectively. Results indicate that GDL combining with calcium carbonate can be utilized as an effective coagulating agent for making cold-set whey protein gels having fortified calcium levels, less cooked flavors and homogeneous texture, which may expand future food applications of whey proteins.

Key Words: cold gelation, whey proteins, calcium-fortified

W71 Use of caseinomacropeptide quantification by high performance liquid chromatography to estimate cheese whey addition in fermented milk beverages. E. H. P. Andrade, M. O. Leite, M. R. Souza, L. M. Fonseca*, M. M. O. P. Cerqueira, C. F. A. M. Penna, T. Roza, and N. M. A. Silva, *Federal University of Minas Gerais*, *Belo Horizonte, Brasil*.

The objective of this study was to evaluate quantification of caseinomacropeptide (CMP) as a method to estimate cheese whey addition in fermented milk beverages. Samples of fermented milk beverages were prepared in laboratory with 4 levels of whey (0, 10, 20 and 40%) and fermented with yogurt culture. After refrigerated storage (8–10°C) at different times (0, 7, 14, and 21 d) the samples were analyzed by high performance liquid chromatography (HPLC) according to official Brazilian method used to detect whey in milk and milk powder, based on caseinomacropeptide quantification. When the whey levels were analyzed along the storage time, there is no difference ($P > 0.05$) between fermented milk (0% of whey) and the fermented milk beverages added with 10 and 20% of whey for 0, 7, 14 and 21 d in refrigeration. However, for fermented milk beverage added with 40% of whey and stored by 21 d, the CMP concentration was higher than expected compared with the times before ($P < 0.05$). This increase in CMP quantity can be due to nonspecific proteolysis promoted for culture bacteria, especially *Lactobacillus*. Thus, it is possible to use CMP detection by HPLC according to official Brazilian method used to detect cheese whey in milk and milk powder as a method to quantify whey added to fermented milk beverages until 14 d of refrigerated storage.

Key Words: fermented milk beverages, whey, high performance liquid chromatography

W72 Comparison of solubility with methods for determining denaturation in whey protein. M. D. Allen* and P. S. Tong, *California Polytechnic State University*, *San Luis Obispo*.

Functional properties of whey proteins are very important for ingredient selection when incorporating in a food system. Solubility is one of the most important functional properties to consider when selecting a whey protein ingredient, especially for beverage systems. Processing parameters are known to have an effect on protein solubility and are often manipulated in efforts to improve solubility. Protein structures of whey proteins are considered to have an effect on solubility. Specifically, the degree of denaturation of whey proteins is thought to play a role in solubility. Previous studies concluded that bicinchoninic acid (BCA) assay and fluorescence spectroscopy are two relatively economical analytical methods that can be used to quantify denaturation of whey protein in liquid whey. The purpose of this current research is to compare these methods of quantifying denaturation to functional solubility of whey protein. A split plot experimental design was utilized with complete randomization. Raw bovine milk was skimmed and enzyme coagulated at natural pH to separate the whey. Liquid whey was then split into three plots and each received one of the following treatments: mild heat/ freeze dry, mild heat/spray dry and high heat/spray dry. Heat treatment was applied to liquid whey prior to a concentration step. Heat treated whey samples were then concentrated and dried accordingly. Powders were analyzed for denaturation using BCA and fluorescence spectroscopy and for solubility using an Insolubility Index. Statistical analysis of data indicates that there are differences among the three treatments for fluorescence spectroscopy, BCA and insolubility index, shown in Table 1. Peak intensity increases with denaturation in fluorescence spectroscopy, percent soluble at pH 4.6 decreases with denaturation in BCA analysis and mL soluble increases with denaturation by the insolubility index.

Table 1. Solubility and Measurements of Denaturation in Whey Powder

Treatment	Fluorescence Spectroscopy- Peak Intensity	BCA- %Soluble @ pH 4.6	Insolubility Index- mL Insoluble
Low Heat/Freeze Dry	173.85	93.24	0.587
Low Heat/Spray Dry	169.40	93.93	0.878
High Heat/Spray Dry	225.65	56.08	0.820

Key Words: whey protein, denaturation, solubility

W73 Whey protein fractionation with supercritical CO_2: Process optimization. L. M. Bonnaillie* and P. M. Tomasula, *USDA, Agricultural Research Services, Eastern Regional Research Center*, *Wyndmoor, PA*.

Supercritical CO_2 (SCO_2) fractionation of commercial whey protein isolates (WPI), containing 20% α-lactalbumin (ALA) and 55% β-lactoglobulin (BLG) protein (w/w), into 2 fractions enriched with either ALA or BLG, generates new whey protein ingredients with enhanced functional and nutritional properties. For example, ALA-rich protein products have improved nutritional properties for use in infant and geriatric foods, while BLG-rich products have enhanced gelling properties. Prefatory studies with HCl showed that ALA formed aggregates under acidic conditions at 50–70°C, while BLG remained mostly soluble. The separation of aggregated ALA was optimized around pH 4.2 and 60°C where the difference between the rates of aggregation of ALA and BLG was maximized. SCO_2 dissolved in concentrated WPI solutions in a high-pressure 1-L reactor generates carbonic acid that causes the selective precipitation of ALA, without tainting the 2 protein fractions with residual acid (pH 6) after depressurization. A turbine impeller ensured fast thermodynamic equilibrium. Solution pH was lowered with increased pressure, P, and reduced WPI concentration, C, according to extensive calibration performed with 1–28% (w/w) WPI solutions up to 14 MPa and extrapolated to 2–10% WPI solutions up to 34 MPa (pH 4.2–5). The kinetics of aggregation of ALA and BLG were followed for up to 4 h as a function of time, T, C and pH. A systematic kinetic study and modeling of the SCO2-induced precipitation of both proteins in the multi-parameter process enabled the optimization of processing conditions to both maximize ALA aggregation while keeping BLG precipitation low, and the optimization of protein recovery and purity in both fractions. In the 60–65°C range, up to 60%-pure ALA and 80%-pure BLG were obtained, with total protein recoveries of up to 98% and 90%, respectively. ALA purity is limited due to a noted increase in BLG precipitation at high SCO_2 pressure compared with HCl-treatment, caused by possible pressure and/or anti-solvent effects. Kinetic models will be useful to design scaled-up batch or continuous versions of the WPI/SCO_2 fractionation process.

Key Words: whey protein, fractionation, carbon dioxide

W74 Effect of applying power ultrasounds during the thermal denaturation of whey proteins in the presence of buttermilk. M. Saffon*[1], M. Britten[2], and Y. Pouliot[1], [1]*STELA Dairy Research Center, Institute of Nutraceuticals and Functional Food (INAF), Université Laval*, *Québec, QC, Canada*, [2]*Food Research and Development Center (FRDC), Agriculture and Agri-Food Canada*, *St-Hyacinthe, Québec, Canada*.

The use of ultrasound treatments in food processing has been considered as an emergent potential alternative to heat treatments. It was hypothesized that power ultrasounds could affect heat-induced denaturation by

favoring aggregates remodeling or rearrangement during the aggregation process. Cheese whey and buttermilk were concentrated by ultrafiltration up to 9.5% (w/v) protein content. Mixtures with various whey to buttermilk protein ratios were adjusted to pH 4.6 and heated to 90°C for 25 min (including come-up time). Power ultrasounds (20 kHz probe) were applied for the last 15 min of the thermal denaturation treatment. After cooling, mixtures were homogenized 5 times at 9500 psi. Aggregated material was separated by centrifugation at 15000g for 20 min. Protein aggregation, water holding capacity (WHC), consistency index (k) and flow behavior index (n) were performed on the homogenized mixtures. All the experiments were repeated 3 times, statistical analysis of the data was performed using ANOVA and the results were considered significantly when $P < 0.05$. The use of power ultrasounds significantly increased the protein aggregation and this effect depended on the proportion of buttermilk protein in the mixture. The highest protein aggregation was obtained with 25:75 whey-buttermilk fractions (78.5% ± 1.8 and 87.0% ± 1.2 with ultrasound). Ultrasound treatment had no significant impact on the WHC of the aggregates and only a slight decrease (0.12 g water/g protein) was associated with increasing the buttermilk protein ratio. The use of ultrasound treatment significantly increased the k and decreased the n of the homogenized aggregate mixtures. The highest k was obtained with aggregates from 25:75 whey-buttermilk ratio (0.94 Pa.s ± 0.10 and 1.12 Pa.s ± 0.10 with ultrasound), which also displayed the lowest n (0.36 ± 0.04 and 0.30 ± 0.05 with ultrasound). Our results suggest that heat-denaturation in the presence of power ultrasounds may have affected the shape and size distribution of protein aggregates.

Key Words: whey, buttermilk, aggregation

W75 Partitioning of minerals and protein using dialysis at different temperatures. N. On-Nom*, A. Grandison, and M. Lewis, *University of Reading*, *Reading, Berkshire, UK*.

Partitioning of minerals and protein in pasteurized milk has been measured at different temperatures, using dialysis with PVDF membrane (MWCO of 250 kdal). Dialysis conditions of 4, 20 and 40°C from 24 to 96 h and at 60 and 80°C from 1 to 5 h were used to prepare a suitable soluble phase for estimating pH, ionic calcium and protein partitioning. Dialysis bags were placed into baby cans which contained milk sample, which were then heated for the required temperature and time. Immediately after heating, dialysates were removed as quickly as possible and then cooled for 24 h before pH and ionic calcium were measured. The results showed that pH and ionic calcium decreased as temperature increased. It was also observed there are slight increases in pH and ionic calcium when the time of dialysis was increased at the same temperature. To measure protein partitioning, reducing SDS-PAGE was used. Results showed that at 4°C, β-casein and traces of α-casein and κ-casein, as well as whey proteins (α-lactalbumin and β-lactoglobulin) were detected while only whey protein was found at 20, 40 and 60°C. No soluble protein was observed at all conditions of 80°C. However, it was found that the intensity of the protein bands increased with increasing dialysis time. In contrast, no proteins were detected in dialysates produced using Visking tubing, which had a lower MWCO of 12 kdal.

Key Words: dialysis, minerals, proteins

W76 Measurement of pH and ionic calcium at high temperatures and their effect on the heat stability of milk supplemented with calcium chloride. N. On-Nom*, M. Lewis, and A. Grandison, *University of Reading*, *Reading, Berkshire, UK*.

Calcium chloride was added to milk in the range (0 - 20 m*M* Ca) with no pH adjustment. These milk samples where then subjected to in-container heating in the range 60 to 120°C for 1 h. Dialysis was performed on these samples during heating to estimate pH and ionic calcium at each heating temperature. Dialysis bags were removed as soon as possible after the heat treatment. The heat treated samples were inspected to assess their heat stability and those which had coagulated were centrifuged to produce a coagulum and supernatant. The results showed that calcium addition decreased pH and increased ionic calcium and that further reductions in both pH and ionic calcium occurred as temperature increased. Coagulation was observed to take place at lower calcium additions as the temperature increased. Furthermore, no coagulation took place if the pH was maintained above 6.30 and ionic calcium was below 0.46 m*M*, respectively, both measured at the heating temperature. However, when the milk samples cooled, pH and ionic calcium recovered, but not quite to their original value. Dialysis allows measurement of pH and ionic calcium at the heating temperature, which should improve understanding of their role in heat stability. Analysis of supernatants from coagulated milk samples heated at 115°C showed that over 90% of the milk protein coagulated, with only small amounts of whey protein and soluble casein remaining in the supernatant.

Key Words: heat stability, calcium, dialysis

W77 Production of single cell oil during growth of *Aspergillus* species on whey. A. Akpinar-Bayizit*, L. Yilmaz-Ersan, and T. Ozcan, *Uludag University, Department of Food Engineering*, *Bursa, Turkey*.

Oils and fats, lipids, form a class of natural compounds that serve as sources of energy and are considered an important component of our food. The demand for oils and fats, in general, is largely met from plant and animal sources. In view of this, utilization of industrial waste material into high value biological material is a cause of raw material limitation and increasing world population. Thus, conversion of food processing wastes into high-value and beneficiary products via microbial and enzymatic processes is gaining importance as they are ready-to-use substrates. Microbial lipids (SCO) with similar properties to vegetable or animal oils can be produced by microorganisms utilizing various carbon sources. Dairy industry wastes are good substrates for waste valuation as they contain appropriate ingredients that support microbial growth. Whey is the serum separated during the curding of milk for cheese production and contains 5% lactose. This research was planned in order to use cheese whey in production of high-value microbial lipids by five *Aspergillus* species, namely *A. niger*, *A. oryzae*, *A. ruber*, *A. versicolor*, *A. parasiticus*. The lipid accumulation in biomasses of examined fungi varied from 1.10 to 7.72 g/100 g. The amount of saturated fatty acids was found highest in *A. parasiticus* (65.70%), whilst the highest amount of unsaturated fatty acids was in *A. niger* (62.72%). The fatty acid profile of SCO obtained from *A. parasiticus* and *A. versicolor* revealed a high percentage of unsaturated 20-carbon fatty acids. It was observed that longer chain polyunsaturated fatty acids, which are not found in whey, have been detected in SCOs of *Aspergillus* species. This sheds light on the possibilities of exploring these fungi, having the ability to synthesize longer chain fatty acids from oleic (octadecenoic) or linoleic (octadecadienoic) acids through desaturase and elongase activity, to be used as supplement to edible fats and oils, and for other non-edible industrial purposes.

Key Words: whey, single cell oil, *Aspergillus*

W78 The effect of lysine and methionine on milk protein mRNA expression of bovine mammary epithelial cells in vitro. X. Y. Li, J. Q. Wang*, D. P. Bu, H. Y. Wei, H. Hu, and L. Y. Zhou, *State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China*.

The objective of this study was to examine the effect of lysine and methionine supplementation on milk protein of bovine mammary epithelial cells in vitro. The lysine was added to the DMEM/F12 culture medium containing 10% fetal bovine serum (FBS) at concentrations of 0, 0.05, 0.2, 0.4, 0.8, 1.6, 3.2, 6.4, 12.8, 25.6 mmol/L and the methionine was also added to culture medium at concentrations of 0, 0.025, 0.1, 0.2, 0.4, 0.8, 1.6, 3.2, 6.4, 12.8 mmol/L. The cell proliferation and milk protein mRNA expression were detected by MTT colorimetric assay and RT-qPCR. Experiment with 48 h. This experiment was repeated 2 times. Within each experiment were repeated 3 replicates for each treatment .The results showed that 0.8 to 1.6 mmol/L lysine and 0.4 to 0.8 mmol/L methionine at 48 h significantly improved the proliferation of bovine mammary epithelial cells ($P < 0.0001$), the mRNA expression level of α_{s1}-casein, β-casein were all significantly higher than other group at these concentrations. Thus, the lysine and methionine may improve milk protein synthesis.

Key Words: lysine, methionine, bovine mammary epithelial cells

W79 Identification of bovine casein phosphorylation using TiO_2 enrichment in combination with nano-ESI-MS/MS. S. S. Li, Y. X. Yang, J. Q. Wang*, D. P. Bu, H. Y. Wei, L. Y. Zhang, and L. Y. Zhou, *State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences*, *Beijing, China*.

Protein phosphorylation is an important post-translational modification that regulates milk protein structure and function. The objective of this study was to analyze the presence of phosphorylated casein. Bovine milk proteins were first separated by sodium dodecyl sulfate PAGE. After in gels digestion and extraction, phosphorylated peptide were enriched by titanium dioxide and identified by ultra performance liquid chromatography coupled with nano electrospray ionization tandem mass spectrometry. This method ensured the identification of 20 phosphorylated peptides, including 7 phosphorylated forms of α_{s1}-casein, 8 α_{s2}-casein, and 5 β-casein. Eight phosphorylated sites derived from 3 α_{s1}-caseins, 3 α_{s2}-caseins and 2 β-caseins were also identified. Phosphates group were localized on residues Ser^{61}, Ser^{63} and Ser^{130} in α_{s1}-casein; Thr^{145}, Ser^{146} and Ser^{158} in α_{s2}-casein; and Ser^{50} and Thr^{56} in β-casein. These findings provide valuable information for the investigating of the bovine milk casein phosphorylation.

Key Words: bovine milk casein, phosphorylation, mass spectrometry

W80 Developmental changes in the bovine whey proteome during the transition from colostrum to milk. L. Y. Zhang[1,2], J. Q. Wang*[1], Y. X. Yang[1], S. S. Li[1], D. P. Bu[1], and L. Y. Zhou[1], [1]*State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agriculture Science*, *Beijing, China*, [2]*Department of Animal Science, College of Agriculture, Hebei University of Engineering*, *Handan, China*.

Bovine milk whey proteins in colostrum are of more significance for newborn than whey proteins in milk, but no studies on the difference in whey protein patterns during the transition from colostrum to milk have been reported to date. This study separated whey proteins from d 1, day3, d 7 and d 21 after calving using 2-dimensional electrophoresis. Differentially expressed proteins in different collection time were identified using high-performance liquid chromatography tandem mass spectrometry (LC/MS/MS) and validated by enzyme linked immunosorbent assay (ELISA) to understand the developmental changes in the bovine whey proteome during the transition from colostrum to milk. Whey proteins from d 1 and d 3 were found to be the same except for immunoglobulin G. Seven proteins were found to be lower in d 7 and d 21 milk whey, including immunoglobulin G, immunoglobulin M, albumin, and lactotransferrin, which are involved in immunity and molecule transport. These proteins were detected using an advanced proteomic method, 2-dimensional electrophoresis coupled with LC/MS/MS, which confirmed that the changes in the differential expression proteins of bovine whey fraction did occur with increased concentrations of serum protein in colostral whey.

Key Words: bovine milk whey protein, colostrum, mass spectrometry

W81 Formation of nanofibers and hydrogels from a milk-derived peptide. M.-M. Guy[1], N. Voyer[2], S. F. Gauthier[1], and Y. Pouliot*[1], [1]*STELA Dairy Research Center, Institute of Nutraceuticals and Functional Foods (INAF), Université Laval*, *Québec, Canada*, [2]*Department of Chemistry and PROTEO Protein Structure, Function and Engineering Research Network, Université Laval*, *Québec, Canada*.

It has been previously shown that the N-terminal fragment of β-lactoglobulin, namely β-LG f1–8, isolated from a flocculated tryptic peptide mixture of whey protein isolate, undergoes self-assembly by a secondary structure transition to β-sheet conformation at basic pH. The objective of the present work was to investigate the physicochemical conditions that trigger self-assembly of peptide β-LG f1–8 and therefore lead to nanofibers and hydrogel formation. Nanostructures formed by self-assembly of peptide β-LG f1–8 in the pH range of 2.0 to 11.0 were studied by transmission electron microscopy (TEM). Hydrogel formation was studied as a function of pH and results evidence a link between hydrogel formation and charge distribution carried by the peptide structure. Finally, circular dichroism (CD) spectropolarimetry was used to characterize the effects of peptide concentration (0.4 to 2.0 mg/mL), temperature (20 to 80°C), and ionic strength (0 to 1 *M* NaCl) on the secondary structure of peptide β-LG f1–8. Hydrogels were obtained at peptide concentrations above 2.5 mg/mL. Peptide concentration and pH adjustment were shown to trigger self-assembly of β-LG f1–8 whereas temperature and ionic strength had only limited effects. Overall, results emphasize the role of particular molecular interactions in β-sheets self-assembly of peptide β-LG f1–8 and pH-dependent electrostatic interactions occurring between β-LG f1–8 units explain its propensity to self-assembly and flocculation in complex media such as whey protein tryptic hydrolysates.

Key Words: whey peptide, hydrogels, nanofibers

W82 Assessing learning outcomes: A comprehensive dairy cattle nutrition curriculum for practicing veterinarians. G. M. Schuenemann*, M. L. Eastridge, W. P. Weiss, J. D. Workman, S. Bas, and P. Rajala-Schultz, *The Ohio State University*, *Columbus*.

The purpose of the study was to assess the effectiveness of a team-based educational program designed to enhance the flow of applied, research-based, nutrition information to dairy veterinarians. A comprehensive dairy cattle nutrition curriculum was developed and participants from 11 veterinary practices located in 5 states (IN, NY, PA, NM, and OH), serving an estimated 186,150 dairy cattle in 469 herds, attended the 2 advanced nutrition modules (~2.5 d each and ~40 h of learning) in 2009. Nutrients, feeding transition cows, calves, and heifers (ration formulation/interpretation), dry mater intake, feed storage, metabolic diseases, evaluating cows (BCS, manure and lameness), metabolic blood profiles, record-keeping systems and feeding behavior were discussed. Educational materials were delivered through in-class lectures followed by case-based learning and group discussions. A farm visit and an out-of-class assignment were implemented. Attendees were assessed using pre- and post-tests of knowledge to determine the level of knowledge gained in both nutrition modules. Participants evaluated the program and provided feedback at the conclusion of each module. Veterinarians (100%) reported that the overall program, presentations and discussions were useful. Attendees found the presented information relevant for their work (agree = 60% and strongly agree = 40%) and of great immediate use to them (neutral = 6.5%, agree = 56% and strongly agree = 37.5%). The presented materials and the implemented educational delivery methods substantially increased the knowledge level of the attendees (16.9% points increase from pre-test to post-test scores; $P < 0.05$). Importance of feed particle size, ration evaluation, interpreting feed analysis, carbohydrate components, and metabolic profiling in fresh cows were listed as learned concepts that participants could apply in their practices. Results suggested that both nutrition modules were relevant and effective, offering new information with immediate field application. This program has important implications for dairy veterinarians since they are a vital source of information for dairy producers.

Key Words: dairy cattle nutrition, veterinary, CE

W83 A self-powered smart wireless identification and tracking sensor prototype for production agriculture applications. K. Dhakal*[1], J. F. Keown[1], and H. Sharif[2], [1]*Department of Animal Science*, *University of Nebraska-Lincoln,* [2]*Department of Computer and Electronics Engineering*, *University of Nebraska-Lincoln*.

There is a need for animal identification (ID) and disease traceability for proper livestock health and its management. An innovative solution, radio frequency identification (RFID) ear tag, has been developed to meet the United States Department of Agriculture (USDA) animal disease traceability requirement. The RFID ear tag supports animal identification, data management and real-time health monitoring within a reasonable distance. The prototype ear tag is a self–powered and capable of complete identification and tracking functions within a mile. It also possesses an integrated health sensor to monitor real time temperature and pulse rate. Information on animal health, breeding and vaccination records can also be retrieved from these small, economical and remotely accessible tags. Research is currently being conducted on the distance that animal ID can be transmitted under differing weather conditions, topographic features, interference from other radio transmissions and other electronic equipment. The research will show if a secondary transmission system will be needed to intercept the initial transmission to have the information downloaded at a central computer receiving station. With encrypted information for data privacy and its ability to harness energy from solar, thermal, and vibration energy the RFID ear tag would bring major impact in national economy as well as impact on the animal industry both in the United States and internationally.

Key Words: RFID, smart tag, tracking

W84 Impact of the 2009 economic crisis on Idaho dairies. M. Chahine*[1], G. E. Shewmaker[1], R. J. Norell[2], and C. W. Gray[1], [1]*University of Idaho*, *Twin Falls*, [2]*University of Idaho*, *Idaho Falls*.

A mail-in survey was conducted to evaluate the impact of the 2009 economic situation on Idaho dairies and to identify trends in forage use. The survey was mailed to every dairy producer registered in the state of Idaho (n = 518). The PROCSURVEYMEANS of SAS (SAS Inst. Inc., Cary, NC) was utilized to produce estimates of survey proportion in each category. Dairies were categorized as small ($n \leq 200$ cows; 48.8%), medium-sized (n = 201 to 1000 cows; 30.2%) or large ($n \geq 1000$ cows; 21.0%). Of the 518 surveys mailed, 98 surveys were returned for a response rate of 19%. The largest number of survey participants represented small (48.8%) dairies followed by medium-sized (30.2%) and large (21.0%) dairies. Small dairies averaged 87 cows, medium-sized dairies averaged 518 cows, and large dairies averaged 1697 cows. All respondents were dairy owners that used alfalfa hay in their lactating cow′s ration. Twenty-six percent of respondents indicated that cost and/or price limited the use of alfalfa hay on their dairies. A smaller percentage of respondents cited quality (14%), constraints from nutritionists (14%) and supply (9%) as important factors. During the crisis, 35% of respondents reduced the amount of alfalfa hay stored on their dairy. No significant reduction was encountered in the amount of alfalfa hay used in the ration while minerals, vitamins, additives, grains, and protein supplements were reduced. Dairies economized by culling heavily, eliminating new equipment purchases and capital expenditures that do not have short-term pay offs, lowering medication costs, purchasing cheaper semen, trimming labor, reducing employee benefits, purchasing cheaper teat dips and keeping low inventory of supplies. We conclude that during the crisis, dairy producers reduced the inventory of alfalfa hay stored on their facilities but did not decrease the amount included in the ration. Other components of the ration were, however, reduced. Dairy producers implemented a wide range of cost savings techniques. Most dairy producers are still worried about the future of the dairy industry.

Key Words: dairy, economic crisis, forages

W85 Nuisance fly production capacity of three types of manure handling systems. G. E. Higginbotham*[1], A. C. Gerry[2], C. C. Collar[3], and L. D. Reed[4], [1]*University of California Cooperative Extension*, *Fresno,* [2]*University of California*, *Riverside,* [3]*University of California Cooperative Extension*, *Hanford,* [4]*513 Fortuna Ave.*, *Modesto, CA*.

As dairy farms grow larger, producers struggle with handling large volumes of manure. Most manure handling systems include solids separators to remove fibrous particles from water used to flush alleys in cow housing areas. Inclined screens or settling basins are most common. Conventional settling basins have earthen or solid concrete sides and

a wood slatted weir at one end for particle separation. A novel settling basin design called a weeping wall has 214 cm high sides constructed with slotted steel hog flooring panels secured into reinforced concrete pillars. Slot spacing is 10 mm allowing effluent to weep from the slots while containing fibrous particles. Composting manure solids is an increasingly common practice on dairies. In this study, production of larval flies in manure compost piles (CP), conventional settling basins (SB), and weeping wall basins (WW) were compared at 6 dairies (3 SB and 3 WW) in the Central Valley of California. Two of the WW dairies used duplicate WW basins and one of the SB dairies used a duplicate SB. The other 3 dairies used a SB system. During the fly breeding season from June–August, manure samples (>20; 4 L total) from each system were collected weekly near inflow and outflow sections. Manure samples were washed thru a 16 mesh screen with larvae collected and identified. The most abundant fly species for all systems was the false stable fly (*Muscina stabulans*), however each system also produced house flies (*Musca domestica*) and stable flies (*Stomoxys calcitrans*). There was no difference ($P > 0.1$) in larval fly abundance of either SB or WW. Of the 3 systems, manure compost piles produced fewer total flies ($P < 0.0001$), as well as fewer house and stable flies ($P < 0.01$). For all dairies, neither overall fly production nor production of house and stable flies was different ($P < 0.05$) between SB with or without a WW. The use of a WW did not result in an increase in the production of nuisance or biting flies.

Key Words: house fly, manure, dairy

W86 Examining the dairy workforce in order to improve labor efficiency. L. A. Holden*, R. E. Bechtel, and G. A. Varga, *Penn State University*, *University Park*.

This research was part of a larger project examining the needs of the dairy workforce. The objective of this research was to determine the labor efficiency and key practices in a sample of Pennsylvania dairies to recommend strategies for improving workforce needs and labor efficiency. Data was gathered via a mail survey with a small monetary incentive for return and a series of survey mailings, postcard reminders, second survey mailings and final postcard reminders. Surveys were sent to 881 dairies representing approximately 15% of the largest dairies that were most likely to have hired labor in Pennsylvania. The response rate was 296 usable surveys plus 86 returned that indicated no longer in dairying for a usable response rate of 33.6%. All respondents had a herd size of at least 50 cows and average herd size was 259 ± 165.0 (n = 278). The average number of acres rented was 358 ± 277.1 (n = 251) and acres owned was 356 ± 210.3 (n = 264). Cows per worker was 41 ± 15.5 (n = 205) and pounds of milk sold per worker was 807,277 (n = 174). The average compensation for milkers was reported as $9.98/hr ± 1.69 (n = 188) and for managers was $13.23/hr ± 3.16 (n = 79). When asked about new milkers hired in the past 5 years only 13.13% of dairy owners were very satisfied with the quality of applicants and only 7.0% were very satisfied with the skill level of new milkers. Only 15.48% (n = 239) indicated that milkers had written job descriptions and only 21.67% (n = 96) indicated that workers received a monetary bonus. Survey results indicate opportunities exist for improving workforce practices such as written job descriptions, standard operating procedures and training for new workers as well as overall labor efficiency to increase cows per worker and milk sold per worker.

Key Words: dairy workforce, labor efficiency

W87 Effect of bedding material on flies, and behavior and innate immunity of calves reared in hutches. K. D. Gay*[1], S. D. Eicher[2], C. S. Wilcox[1,2], J. A. Bridges[1], M. H. Rostagno[2], S. E. Charley[1], M. J. Grott[1], R. E. Williams[1], and M. M. Schutz[1], [1]*Purdue University*, *West Lafayette, IN*, [2]*USDA-ARS Livestock Behavior Research Unit*, *West Lafayette, IN*.

Dairy calf hutches are often bedded with straw (STR), but sand (SND) and wood shavings (SHV) are becoming more common. The objective was to compare 3 beddings for presence of flies and measures of innate immunity and behavior of calves. Hutches were blocked by location and each of 3 hutches in a block was randomly assigned 1 of 3 treatments; SND, STR, or SHV. Twenty-eight heifer calves in the study were assigned sequentially by birth date to the next available hutch. The study was during a moderate summer (June to September 2008) at the Purdue Dairy Research and Education Center. Calves were observed twice weekly from birth until being weaned at approximately 8.5 wk of age. Blood samples were taken weekly and leukocytes analyzed for phagocytic function, CD14 (part of the LPS receptor) and CD18 (adhesion molecule) surface expression. Twice weekly, flies were counted manually on inside surfaces of hutches and counted on each leg of the calf after rising immediately before behavior observations. Bedding samples were collected to measure the presence of immature flies. Statistical models for fly counts and blood samples considered week and treatment. The percentage of cells that phagocytized beads, was least in wk 6 and 8 ($P < 0.05$). The percentage of cells expressing CD14 or CD18 increased over time ($P < 0.001$) and STR bedding resulted in more fluorescence of CD18 than did SHV ($P < 0.04$). Hutch fly counts were lowest ($P < 0.02$), but larvae counts were highest ($P < 0.02$) in hutches bedded with STR. It appears SND, STR, or SHV are acceptable bedding materials during moderate summer conditions in the Midwest, but fly larvae counts must be managed with STR.

Key Words: bedding, calf, immunology

W88 Management practices utilized by high-producing Kentucky dairy herds. C. O. Coombs and J. M. Bewley*, *University of Kentucky*, *Lexington*.

Dairy producers often make decisions based on what other producers in their region are doing. The objective of this research was to summarize management practices utilized by Kentucky Holstein herds with rolling herd average milk production greater than 10,000 kg per cow (n = 21) using records obtained from the Dairy Herd Improvement Association. Interviews were conducted on-farm and over the phone. Herd size ranged from 25 to 1590 lactating cows with a mean (±SD) of 186.54 ± 317.22. Daily milk production per cow ranged from 25.95 to 39.59 kg with a mean (±SD) of 32.56 ± 3.44. Test day somatic cell count ranged from 102,000 to 432,000 cells per ml with a mean (±SD) of 256,140 ± 56,170. Average days in milk ranged from 132 to 260 with a mean (±SD) of 212.38 ± 29.7. Days to first service ranged from 69 to 150 with a mean (±SD) of 103.04 ± 23.56. Pregnancy rate ranged from 9% to 20% with a mean (±SD) of 13.6% ± 2.80%. The most common management practices utilized by these producers were regular forage testing (100%), regular utilization of veterinary services for reproductive management (100%), fans or sprinklers (90%), artificial insemination for genetic improvement of lactating cows (86%), artificial insemination on heifers (86%), annual ration balancing (81%), annual hoof trimming (81%), sexed semen (71%), separate far-off and close-up dry cows (67%). The most common mastitis prevention methods utilized were drying teats before attaching milking units (100%), dry treating all quarters at dry-off (100%), pre-dipping (95%), post-dipping (95%), gloves worn by employees (81%), and automatic take offs (81%). When asked to identify the management practice that contributed the most to their milk production level, the most frequently cited reasons were (1) quality for-

ages (n = 4), (2) paying attention to detail (n = 4), (3) cow comfort (n = 3), and (4) balanced rations (n = 3). Generally, farmers in this study achieved high milk production levels by following recommended best management practices, paying attention to detail, and striving for optimal nutrition, milk quality, and cow comfort.

Key Words: best management practices, high milk yield, dairy survey

W89 Organic milk production in Maine: Attributes, costs, and returns. P. S. Heacock*, A. L. Cook, G. K. Criner, and L. A. Bragg, *University of Maine*, *Orono*.

Nearly one quarter of all commercial dairy farms in the state of Maine are certified organic producers. The objective of this study was to assess the current management and financial status of organic producers in the state. Management and financial information was collected from 30 organic dairy producers that completed the 2007 dairy cost of production survey implemented by the University of Maine and the Maine Milk Commission. Summary descriptive statistics were calculated by herd size. The farms were divided by herd size into 3 groups, small, medium and large with 9, 10, and 11 farms in each group respectively. The mean herd size was 30, 55, and 100 for the small, medium, and large farms with annual milk shipped of 130,780 kg, 341,755 kg, and 607,834 kg respectively. This equates to annual milk shipped per cow of 4,359 kg, 6,213 kg, and 6,087 kg for the small, medium and large farms. All farms relied primarily on family labor however the medium and large farms also had a substantial amount of hired labor. Full-time labor equivalents (FTE) for the farm size groups were 1.5, 3.0, and 3.2, with a mean cows per FTE of 20, 18, and 31 for the small, medium and large farms. Annual revenue per cow was $2,801, $4,269 and $4,565 for the 3 farm sizes. Purchased concentrate was the largest expense for all 3 farm sizes, however there was little difference between the 3 groups, ranging from 35 to 37% of total annual costs. Annual operating costs on a per cow basis were $1,963, $2,757, and $2,682 with annual overhead costs per cow of $824, $769, and $829 for the small, medium and large farms respectively. The return to family labor and ownership per cow was $13, $743, and $1,054 for the 3 farm sizes. Milk production per cow was highly correlated with profitability. Results showed that the larger organic dairy farms in Maine are benefiting from economies of size while the smaller operations rely on on-farm diversification and off-farm income to remain viable.

Key Words: organic, finances, herd size

W90 Effectiveness of genetic evaluations in predicting daughter performance in individual herds. H. D. Norman[1], J. R. Wright*[1], C. D. Dechow[2], and R. C. Goodling Jr.[2], [1]*Animal Improvement Programs Laboratory, ARS, USDA*, *Beltsville, MD*, [2]*Pennsylvania State University*, *University Park*.

Response to genetic selection has been demonstrated nationally for US dairy cattle, but producers are more likely to appreciate the value of genetic selection if trends within their own herds can be shown. Responses from 2004 through 2008 in individual herds by Holstein and Jersey cows were documented for yield (milk, fat, and protein), somatic cell score, productive life, and daughter pregnancy rate. Sire and dam predicted transmitting abilities (PTA) or parent average (PA) from evaluations before first calvings were the independent variables, and phenotypic performance (standardized first-parity yields, somatic cell score, lifetime days milked, and days open) was the dependent variable. Minimum number of cows with usable records per herd was 50. Mean coefficients for regression of standardized yield on PA for the same trait was 0.73 for milk, 0.79 for fat, and 0.69 for protein for 8,257 Holstein herds and 0.79, 0.72, and 0.73 for 441 Jersey herds. The majority of individual herd regression coefficients for yield traits were between 0.3 and 1.0; their standard deviations were between 0.38 and 0.47. Regression coefficients may have been < 1.0 because PA was based on all-parity yield whereas phenotypic yield was only from first parity or because the heritability assumed for calculating PTA was too high. Mean regression coefficients for somatic cell score, productive life, and daughter pregnancy rate were 0.82, 0.65, and 0.81, respectively, for Holsteins and 0.65, 0.56, and 0.85 for Jerseys; their corresponding standard deviations were 0.66, 0.75, and 1.07 for Holsteins and 0.77, 0.80, and 1.14 for Jerseys. Mean coefficients for regression of sire PTA on phenotypic performance ranged from 0.53 to 0.80; mean regression coefficients for dam PTA ranged from 0.43 to 0.86. Although standard errors were large, response to genetic selection on a within-herd basis could be demonstrated, which should help increase confidence in national genetic evaluations.

Key Words: herd prediction, yield, fertility

W91 Winter feeding strategies for lactating organic dairy cows. P. S. Heacock*, D. P. Marcinkowski, G. W. Anderson, M. R. Stokes, and R. Kersbergen, *University of Maine*, *Orono*.

In northern climates, the highest feed costs for organic dairies are seen during the non-grazing season. The objective of this project was to examine the effects of different forage and concentrate systems on the nutrition, production and economics of winter-fed, organic dairy cows. Two organic forage systems were compared, the first consisting entirely of grass haylage (GH) and the second consisting of grass haylage and corn silage with other summer annuals (CS). Two concentrate supplementation methods were also compared, the first consisting of a commercially available pellet (P) and the second a mixture of homegrown grains and commodities (C). Four rations were developed to support 31.75 kg of milk/day. Each ration consisted of one forage and one concentrate option. Twenty-eight Holstein cows were divided into 4 groups and fed the 4 rations in a 4 × 4 Latin square design. All of the feeds fed were organically certified and the cows were managed organically for the duration of the project. Few production differences were found between the treatments. Daily energy-corrected milk (ECM) was similar, averaging 28.25 kg for the GH-C, 28.04 kg for CS-C, 27.31 kg for GH-P and 26.80 kg for the CS-P ($P > 0.05$). Milk fat was lower with the CS-C ration and there was a difference in milk urea nitrogen (MUN) between all 4 treatments with 17.27 mg/dL for the GH-P, 14.80 mg/dL for the GH-C, 12.52 mg/dL for the CS-C and 11.20 mg/dL for the CS-P ration. Feed costs and income over feed costs (IOFC) varied greatly between the treatments. Daily feed costs averaged $9.18, $9.03, $7.87 and $7.25 for the CS-P, CS-C, GH-P and GH-C respectively. IOFC was $7.47, $8.47, 9.08 and 10.27 for the CS-P, CS-C, GH-P and GH-C respectively. Organic dairy producers have fewer feeding options so they must rely on high quality forages and homegrown grains for the majority of their nutrient needs. Results showed a financial advantage to haylage diets when compared with corn silage diets due to the high cost of organic protein sources.

Key Words: organic, nutrition, feed cost

W92 A milker's school for international refugees resettled in Idaho. J. C. Dalton*[1], K. S. Jensen[2], R. Manzo[3], and L. Whiteford[3], [1]*University of Idaho*, *Caldwell*, [2]*University of Idaho*, *Owyhee County*, [3]*International Rescue Committee*, *Boise, ID*.

Each year approximately 1,000 documented, work-authorized refugees are resettled in Idaho. These refugees originate from over 20 different countries, and speak more than 27 different languages. At the request of the International Rescue Committee in Boise, Idaho, University of Idaho Extension developed an introductory-level milker's school for international refugees resettled in Idaho. The program consisted of 4 h of classroom teaching, and was held in Caldwell, Idaho. Topics included udder anatomy, cow preparation and sanitation, milk letdown, milk removal and milking unit handling, mastitis, prevention of antibiotic residues in bulk tank milk, milking systems, and the role of the dairy industry in Idaho's economy. All material was presented in English and translated for refugees from Burma, Somalia, Eritrea, Uzbekistan, Nepal, Iraq, Afghanistan, Togo, and Bhutan. In 2009, 4 milker's schools were conducted, with 128 refugees attending. A certificate of completion was awarded to all participants at the conclusion of the program. Sixteen refugees are currently working at a dairy in Oregon. In anticipation of emergence from the economic recession and stabilization of the dairy economy, further educational opportunities are planned, including calving management and artificial insemination schools, to provide refugees with additional marketable skills necessary to secure employment on dairies. The delivery of this program provided: 1) an educational opportunity for international refugees resettled in Idaho, 2) participants the knowledge and skills necessary to succeed as dairy employees, and 3) increased the diversity in University of Idaho Extension programs.

Key Words: milker, refugee, dairy

W93 Limitations and opportunities of beef and dairy operations for the use of ethanol co-products. J. I. Navarro*[1], L. J. Snyder[1], R. P. Lemenager[1], and S. L. Lake[2], [1]*Purdue University*, *West Lafayette, IN*, [2]*University of Wyoming*, *Laramie*.

A survey instrument was developed to assess the attitudes and the potential for bio-fuel co-products use among beef and dairy producers. The main objective was to inventory resources that currently offer challenges and opportunities for the utilization of bio-fuel by-products by small and medium-sized beef and dairy producers. The survey was distributed at 10 of the Regional Beef meetings during the winter of 2006–2007 and at 5 of the Regional Dairy meetings during the spring of 2007 organized by Purdue University Extension. Participants represented 414 different operations. The instrument contained 22 questions related to demographic characteristics, resources available, average production characterization, production goals, management practices, soil quality and environmental concerns. Some of the most evident limitations identified by the survey participants were size of the operation, storage facilities and equipment required. An additional analysis of the 13 ethanol plants across Indiana and the location of the participants operation were performed to identify possible links between the availability of distiller's grains and the willingness use these as alternative feeds. The survey results indicated that the majority of the participants, 75% of the beef and 84% of the dairy operations, have considered using bio-fuel co-products as a source for livestock feed. This data suggests that there is an opportunity for the use of co-products to lower feed cost and improve profitability in the beef and dairy industries if viable methods were implemented for small and medium-sized producers to utilize ethanol co-products.

Key Words: cattle producers, ethanol co-products, feed alternatives

W94 Farm animal welfare: Assessing public concern and attitudes. D. R. Deemer[1], J. A. Pempek*[1], L. M. Lobao[1], G. J. Coleman[2], and M. L. Eastridge[1], [1]*The Ohio State University*, *Columbus,* [2]*Monash University*, *Clayton, Victoria, Australia*.

Farm animal welfare has long concerned animal scientists, social scientists, and the food animal industry. However, relatively little is known about the US population's recent views regarding farm animal welfare. Much of our knowledge is based on case-studies or other research with limited generalized inferences. Among the questions consistently raised by analysts is the relationship between the public's knowledge of farm animals and their attitudes and food consumption behavior. Our research addresses the gap in the literature by examining the public's knowledge of farm animals, as well as other key covariates and their relationship to attitudes and food consumption behavior. Data are from a large, random sample of the Ohio population (N=1,000) and a comparative smaller nationwide sample taken during 2007. Along with variables measuring knowledge about farm animal production, we evaluated the relevance of key demographic variables, such as rural-urban residence, gender, income, and ethnicity. Multiple regression models using different dependent variables of animal welfare attitudes and behavior were employed. These models explained about 20% of the variance in attitudes, similar to studies of general attitudes. Across these models, the most consistent correlates of greater concern with farm animal welfare were gender (women) and urban residence, with standardized betas values ranging from (−0.130 to −0.207) for gender and from (−0.003 to −0.146 for urban residence). Based on these and other control variables of income and ethnicity, knowledge of farm animal production had little impact on attitudes and behavior. These results suggest that educational outreach to improve knowledge of farm animal production may have limited impact on attitudes and behavior relating to farm animal welfare.

Key Words: farm animal welfare, attitudes, behaviors

W95 Reproductive indicators in dairy cattle enterprises with different technological level. A. Pacheco Cervantes, D. V. Mariscal Aguayo*, H. Estrella Quintero, M. Huerta Bravo, R. Rangel Santos, and R. Núñez Domínguez, *Universidad Autónoma Chapingo*, *Jalisco, México*.

The objective of the study was to assess the reproductive behavior of family dairy enterprises that used Chapingo-Agropec Star, the technological development model for advice and consulting. The farms were stratified in 2 technological levels, transition and business, based on the following components: education, bovine equivalent, equivalent irrigation area, and production technology. The information used for the study was obtained from the general report generated by Agropec Star software which was captured by advisors of the farms. The database was made up of 17 enterprises with a total of 2,041 Holstein cows from 1996 to 2008. Age at first parturition (EPP), interval from calving to first estrus (IPC), interval from calving to first service (IPS), services per conception (SPC), days open (DA), and calving interval (IEP) were the evaluated variables. Effects in the statistical model included technological level (NT), number (NP), year (AP), and season (EP) of calving, and significant interactions ($P < 0.05$). The technological level affected ($P < 0.05$) IPS and IPC. Furthermore, the technological level interaction by year of calving not only affected these 2 variables (IPC and IPS) but also influenced EPP. Intervals at first estrous and first service interval presented at the technological business level (63.8 ± 6.2, 75.7 ± 5.5) were lower than the transitional technological level (90.8 ± 2.7, 91.1 ± 2.3). No significant differences ($P > 0.05$) were found for DA; however there was a tendency ($P > 0.08$) for an improvement in the reproductive behavior of the family business system.

Key Words: farms, Holstein, stratification

W96 Case study: Characterization of lying behavior in dairy cows transitioning from a freestall barn to a compost bedded pack barn. C. Gravatte*, C. Coombs, and J. Bewley, *University of Kentucky*, *Lexington*.

Cows devoid of ample lying time exhibit both physiological and behavioral signs of stress. Some dairy producers have begun using a new housing system, called a compost bedded pack barn. The key component of a compost bedded pack barn is an open resting area generally bedded with sawdust, dry fine wood shavings, or other organic materials. Compared with freestalls, cows have more room for movement and are able to lie down in a more natural manner. Our hypothesis states lying times would increase in a herd transitioning from a freestall barn to a compost bedded pack barn. The lying times of 11 lactating Holstein-Friesian cows were measured using an activity monitor in a commercial dairy herd. Cows were divided among 3 milk production categories (high, medium, and low). An IceTag animal activity monitoring sensor (IceRobotics Ltd., Edinburgh, Scotland, UK), which measures posture (lying versus standing) and steps, was attached to a hind leg of each cow above the fetlock. The MIXED procedure of SAS was used to fit a model describing the differences in hours lying between the 2 housing systems. Because of a delay in barn construction, more days were recorded (n = 872) for the freestall barn than the compost bedded pack barn (n = 212). LSMeans for hours lying were 9.7 ± 0.4 h/d and 13.5 ± 0.5 h/d for cows housed in the freestall barn and compost bedded pack barns, respectively ($P < 0.0001$). Older cows (Parity 2) spent significantly more ($P < 0.01$) time lying (12.7 0.6 h/d) than younger cows (parity 1) cows (10.5 0.4 h/d). Additionally, lying times were significantly shorter for cows with a locomotion score of 3 (10.5 0.5 h/d) than for cows with a locomotion score of 1 (12.2 0.7 h/d, $P < 0.05$) or 2 (12.2 0.0.7 h/d, $P < 0.05$). Although other factors may have affected lying behavior as the cows progressed through lactation and environmental conditions varied, lying times were significantly longer after the cows were housed in the compost barn. These results are representative of one dairy operation, though the significant increase in lying time demonstrates a need for further research.

Key Words: precision dairy farming, compost bedded pack barn, lying time

W97 Composting school: An educational tool to bring together dairy producers and other community members. M. E. de Haro Martí*[1] and J. A. Robbins[2], [1]*University of Idaho*, *Gooding*, [2]*University of Idaho*, *Jerome*.

Composting organic waste is an environmentally sound technique used around the world. Several studies have demonstrated the benefits of compost as soil amendment, sustainable waste treatment, and sound agricultural practice. In fall 2008 a unique "Composting School" program was held at the Gooding County Extension Office in response to stakeholder's questions and to teach them composting techniques and use. The program included 2 sessions that were conducted at the Gooding County Extension Office in late summer and early fall 2008. Two novelties made this program different from others offered in Idaho. First, the targeted audience was very heterogeneous including dairy producers, home owners, small farmers, and owners of horses, llamas, hogs, and sheep. The second idea included a hands-on section addressing composting techniques. After receiving theoretical training about composting, participants had the opportunity to build different systems for on-farm, home, and worm composting on site. During the second session, participants received a deeper overview of on-farm composting including mortality composting and compost use. Participants continued with the hands-on section by turning the piles and analyzing the performance of the different composting techniques built during the first session. The performance analysis detected a significant difference ($P < 0.01$) in temperature between the on-farm composting techniques and the home techniques. None of the 6 home composting units reached temperatures required by the Processes to Further Reduce Pathogens (PFRP). All 3 on-farm composting units reached PFRP. Forty-two participants attended the program. The program evaluations demonstrated that 50% of the respondents learned "a great deal," and 88% indicated they would adopt 2 or more techniques not used before attending the school. A permanent composting facility display remains at the Gooding Extension Office and is used with new programs.

Key Words: composting, waste management, extension

Food Safety 2

W98 Efficacy of ultraviolet light systems for control of microorganisms in poultry and beef brine and marinade solutions. K. L. Beers*, P. E. Cook, C. W. Coleman, and A. L. Waldroup, *MCA Services*, *Rogers, AR*.

Brine and marinade solutions injected into raw beef and poultry products have increasingly become a food safety concern due to continuous injection and recycling of the solution, allowing for a significant microbial increase. This results in several food safety issues including transfer of microorganisms into the sterile muscle of the products and deterioration of the injection solution as microorganisms increase to unacceptable levels. Safe Foods Corporation conducted a series of 8 individual trials, either in a laboratory setting (MCA Services, Rogers, AR) or at USDA-inspected processing facilities, to investigate the effects of using commercially available UV light (UVL) systems, specifically, Fresh*Light* models 210 and 220, for control of naturally occurring and inoculated pathogens in these solutions. The laboratory testing included inoculation of solutions with pathogenic bacteria including *Salmonella typhimirium*, *E. coli* O157:H7 and *Listeria innocua*. Processing plant trials involved evaluating solutions for naturally occurring organisms. The flow rate in the UVL systems ranged from 30 to 150 L/minute depending on the UVL model and application. In all 8 trials, regardless of the bacteria evaluated (naturally occurring organisms or inoculated pathogens), location of testing (laboratory or processing facility) or the UVL system utilized, the original level of microorganisms in the solutions was significantly reduced by >2 logs/mL (99%) to as much as 6 logs/mL (99.9999%) at standard plant operating conditions. In some trials, the UVL system eliminated all microorganisms from the solutions. In conclusion, the commercially available Fresh*Light* 210 or 220 is fully capable of consistently controlling, and/or eliminating, microorganisms from poultry and beef brine and marinade solutions while providing the processor with an affordable means of significantly improving the safety and quality of their injected products.

Key Words: Fresh*Light*, ultraviolet light, brines and marinades

W99 Antimicrobial susceptibility profile of enterotoxigenic *Staphylococcus* sp. recovered from foodborne outbreaks in Minas Gerais state, Brazil, from 1998 to 2002. J. F. Veras, C. F. A. M. Penna, M. R. Souza, M. O. Leite, L. M. Fonseca, L. S. Carmo, and M. M. O. P. Cerqueira*, *Federal University of Minas Gerais state*, *Belo Horizonte, Minas Gerais, Brazil*.

The aim of the present study was to evaluate the antimicrobial susceptibility profile of the *Staphylococcus* sp recovered from 16 outbreaks involving milk and dairy products that took place from 1998 to 2002 in the State of Minas Gerais, Brazil. These outbreaks were investigated by Fundação Ezequiel Dias (FUNED), Brazil and in 16 food poisoning outbreaks, 14 (87.5%) were due to cheese consumption and 2 (12.5%) were due to raw milk intake. For the isolated food, the main agents were enterotoxigenic *Staphylococcus* sp and *Salmonella* sp, *Shigella* sp. and fecal coliforms. The average of *Staphylococcus* sp strains was 8.6×10^7 CFU/g or mL (7.93 log CFU/g or mL). The enterotoxins detected isolately were SEB and SEC, and in association were SEA + SEB. For antimicrobial susceptibility profile of 152 samples recovered, at least 48 samples (31.57%) were resistant to one or more antimicrobial. It was observed that 18.42% (28) of these samples were resistant to penicillin G, 12.5% (19) to erythromycin, 7.9% (12) to tetracycline, 6.5% (10) to oxacillin, 5.92% (9) to cephalosporin, 3.28% to gentamycin, and same percentage to chloramphenicol. *S. aureus* showed the highest percentage to antibiotic resistance.

Key Words: antimicrobial, susceptibility, enterotoxigenic *Staphylococcus* sp.

W100 Occurrence and antimicrobial resistance of *Campylobacter jejuni* isolated from poultry carcasses commercialized at the Federal District area, in Brazil. A. P. Santana*, D. C. Ruy, H. M. Moura, and S. Perecmanis, *Universidade de Brasília*, *Brasilia, DF, Brasil*,

Worldwide, campylobacteriosis is a disease that causes diarrhea in humans and poultry have been identified as a significant source of the *Campylobacter jejuni*. Frequently this disease is associated with the consumption of contaminated poultry meat or cross-contaminated with other foods. In Brazil, there are few researchers studying the occurrence of this microorganism and analyzing antimicrobial resistance in this type of food, however, not at the Federal District area. The aim of this work was to verify the occurrence of *C. jejuni* in cooled carcasses of poultry commercialized in the Federal District, as well as to analyze the antimicrobial resistance. From a total 101 samples of cooled carcasses were analyzed, 9 of them were acquired in popular markets without previous sanitary inspection and 92 samples with. Considering the 101 samples, *C. jejuni* was detected in 17.82% of samples (18 carcasses), all from markets with previous sanitary inspection. However, *C. jejuni* was not detected in any of the 9 samples from popular markets without sanitary inspection. In this study, a total of of 18 strains were isolated from the carcasses but only 16 were successfully not cultivated in plates. The 16 strains of *C. jejuni* were submitted to the antimicrobial analysis to 8 drugs (nalidixic acid, streptomycin, gentamycin, erythromycin, amoxicillin, chloramphenicol, ciprofloxacin and tetracycline). All 16 (100%) strains of *C. jejuni* were resistant to ciprofloxacin, 15 (93.75%) were resistant simultaneously to nalidixic acid, streptomycin, tetracycline and gentamycin, 14 (87.5%) of strains were resistant to amoxicillin, 11 (68.75%) were resistant to erythromycin and the minor resistance observed was to chloramphenicol 6 (37.5%). Considering the presence of antimicrobials resistance, these results were similar to other countries, however superior in percentage of resistance, except for ciprofloxacin and nalidixic acid. These results suggest imperfections in many phases of processing of poultry carcasses and a possible problem of public health due the high resistance observed.

Key Words: resistance, *Campylobacter jejuni*, chicken meat

W101 Antibacterial activity of trans-cinnamaldehyde, eugenol, carvacrol, and thymol on *Salmonella* Enteritidis and *Campylobacter jejuni* in chicken cecal contents *in vitro*. A. Kollanoor Johny*[1], M. J. Darre[1], M. I. Khan[2], A. M. Donoghue[3], D. J. Donoghue[4], and K. Venkitanarayanan[1], [1]*Department of Animal Science, University of Connecticut*, *Storrs,* [2]*Department of Pathobiology and Veterinary Science, University of Connecticut*, *Storrs,* [3]*Poultry Production and Product Safety Research Unit, ARS, USDA*, *Fayetteville, AR,* [4]*Center for Excellence in Poultry Science, University of Arkansas*, *Fayetteville*.

Salmonella Enteritidis and *Campylobacter jejuni* are 2 major food-borne pathogens that are transmitted through poultry products. These pathogens colonize the chicken cecum leading to contamination of carcasses during slaughter and subsequent processing operations. We investigated the antimicrobial efficacy of 4 GRAS-status, plant-derived molecules

namely, trans-cinnamaldehyde (TC), eugenol (EUG), carvacrol (CAR) and thymol (THY) against *Salmonella* Enteritidis and *Campylobacter jejuni* in chicken cecal contents in vitro. The plant molecules were added at different concentrations (ranging from 10 to 75 m*M* for *S.* Enteritidis and 10 to 30 m*M* for *C. jejuni*) to autoclaved chicken cecal contents inoculated with ~7.0 $\log_{10}$ CFU/mL of *S.* Enteritidis or *C. jejuni*. The pathogen populations in the cecal contents after 15 s, 8 h and 24 h of incubation at 39°C were determined. Duplicate samples of treatments and control were included, and the study was replicated 3 times. *C. jejuni* was more sensitive to all the molecules than *S.* Enteritidis ($P < 0.05$). All molecules were highly bactericidal, with the lowest concentration of TC (10 m*M*) significantly reducing ($P < 0.05$) *S.* Enteritidis populations by > 6.0 $\log_{10}$ CFU/mL after 8 h and > 8.0 $\log_{10}$ CFU/mL after 24 h of incubation. TC at 25 m*M* completely inactivated ($P < 0.05$) *S.* Enteritidis by 8 h of incubation. On the other hand, TC at all tested concentrations (10, 20, and 30 m*M*) completely killed *C. jejuni* ($P < 0.05$) after 8 and 24 h of incubation. CAR and EUG completely inactivated *S.* Enteritidis and *C. jejuni* at 50 and 75 m*M* and 20 and 30 m*M*, respectively. THY was also equally effective in killing both pathogens. The results indicate that these aforementioned molecules could potentially be used to reduce *S.* Enteritidis and *C. jejuni* in chicken ceca, however follow up in vivo studies are necessary.

Key Words: *Salmonella*, *Campylobacter*, antimicrobial, plant-derived molecules

W102 Effects of dietary antimicrobials on fecal shedding of *Campylobacter, Salmonella*, and Shiga-toxin producing *Escherichia coli* in production swine. J. E. Wells*, N. Kalchayanand, E. D. Berry, and W. T. Oliver, *USDA, ARS, US Meat Animal Research Center*, *Clay Center, NE*.

Antimicrobials are used in swine diet to improve growth and reduce disease. Increasing pressure to remove antimicrobials from swine diets could alter efficiency, but little information is reported on the impact of feeding antimicrobials on zoonotic pathogen shedding. Barrows (n = 160) were sorted by weight into 2 treatments, and fed growing, grow-finishing, and finishing diets from age 10 to 14 wk, 14 to 18 wk, and 18 to 22 wk, respectively. For each feeding phase, diets were prepared without (A-) and with (A+) dietary antimicrobials (chlortetracycline, 10 to 18 wk; bacitracin, 18 to 22 wk). At wk 10, 14, 18, 19, 20, and 22, fecal swabs were collected from each animal for *Campylobacter* and *Salmonella* spp. and fecal grabs were collected from one-quarter of the piglets for Shiga-toxigenic *Escherichia coli* and Shiga-toxin gene analyses. *Salmonella* was only observed early in the study at low prevalence and was not affected by treatment. *Campylobacter* was not found in piglets at wk 10, but prevalence increased over the study for both treatments. In the growing and grow-finishing phases (wk 14 and 18), *Campylobacter* was present in 23 and 7% ($P = 0.04$) and *stx* genes were present in 25 and 17% ($P = 0.05$) of samples from A- and A+ groups, respectively. In the finishing phase, time was an interaction with treatments. *Campylobacter* did not differ between treatments for pooled wk 19 and 20 (15 vs. 9.4%, A- and A+; $P = 0.09$) but was different for wk 22 (19 vs. 38%, A- and A+; $P = 0.007$). The prevalence of *stx* genes was not different between treatments for wk 19 (39 vs 26%, A- and A+; $P = 0.06$), but by wk 20 and 22 *stx* gene prevalence was different (49 vs. 68%, A- and A+; $P = 0.01$). Shiga-toxin producing *E. coli* serogroups O26, O103, and O145 were isolated from 7.2% of the samples with fewer positives found at end of trial ($P > 0.1$). Diets with chlortetracycline reduced pathogen shedding, but switching to bacitracin at 18 wk of age increased pathogen shedding with time compared with the A- group.

Key Words: antibiotics, food safety, pathogens

W103 Persistent effect of thymol and diphenyliodonium chloride against *Campylobacter coli* in vitro. N. A. Krueger*, R. C. Anderson, T. R. Callaway, T. S. Edrington, and D. J. Nisbet, *USDA-ARS Southern Plains Agriculture Research Center, Food and Feed Safety Research Unit*, *College Station, TX*.

Campylobacter are important foodborne pathogens that may colonize the gut of food producing animals. The objective of this experiment was to determine if a single administration of the purported deaminase inhibitors, thymol and diphenyliodonium chloride (DIC), each may effectively reduce *Campylobacter coli* concentrations during consecutive batch culture of mixed populations of swine gut bacteria. Gut bacteria present in freshly collected fecal material (0.3 g) were mixed with 150 mL anaerobic (100% N_2) Bolton broth and inoculated with approximately 10^6 colony-forming units (CFU) of an overnight grown (in Bolton broth) *C. coli* culture. Ten-milliliter volumes were distributed in triplicate to crimp top tubes preloaded with 0.1 mL volumes of water, thymol or DIC to achieve a single initial treatment of either 0, 1.0 m*M* thymol or 0.01 m*M* DIC and were incubated at 39°C. After 8 h incubation, 1 mL was withdrawn from each tube and inoculated into a second series of tubes containing 9 mL fresh anaerobic Bolton broth but without treatment additions. The second tube series was then incubated for 8 h after which time the process was repeated to achieve the completion of 5 consecutive batch cultures. Log_{10}transformations of *C. coli* CFU determined at the beginning and end of each culture series were subjected to a general ANOVA. Results revealed a treatment × time × series interaction ($P < 0.0001$). Counts measured upon initiation of the first incubation series averaged 5.73 ± 0.05 (SD) $\log_{10}$ CFU mL^{-1} but declined ($P < 0.05$) more than 3.4 $\log_{10}$ CFU mL^{-1} from this value by the end of the first culture series for thymol and DIC-treated cultures and never recovered thereafter; being below our detection limit (1.3 $\log_{10}$ CFU mL^{-1}) by the end of the third transfer series. Conversely, *C. coli* counts in nontreated cultures were not reduced from initial values until the end of the third cultures series, at which time C. coli counts were 2.7 $\log_{10}$ CFU mL^{-1} lower ($P < 0.05$) but always above our level of detection. Results demonstrate that a single initial treatment of thymol or DIC effectively and persistently reduced *C. coli* during anaerobic culture in vitro.

Key Words: *Campylobacter*, food safety, swine

W104 Evaluating different gas delivery methods that create a microaerophilic environment for culturing *Campylobacter jejuni*. M. D. Haines*, K. N. Eberle, C. D. McDaniel, and A. S. Kiess, *Mississippi State University*, *Mississippi State*.

Most techniques used for culturing *Campylobacter* species require a microaerophilic gas atmosphere. Currently there are several different methods available to deliver the appropriate microaerophilic gas environment. The objective of this experiment was to evaluate *Campylobacter jejuni* growth using 3 different gas delivery methods (Anoxamat, Campy EZ Gas-Pak, and Zip-Lock bags). Approximately 50 to 100 *Campylobacter* cells were suspended in brucella broth and spread plated onto Campy-Cefex agar plates. Plates were placed into either Mart anaerobic canisters or zip-lock bags for culturing. The microaerophilic gas was delivered to the plates in the Mart anaerobic canisters by either the Anoxomat AN2CTS Mark II System or through the activation of 3 Campy EZ Gas-Paks. For plates being incubated in zip-lock bags, the microaerophilic gas was delivered by directly flushing the bag with a pre-mixed gas; once the bag was full it was sealed. The canisters and zip-lock bags were then placed into a low temperature incubator for 24 h, at 42°C. After the 24 h incubation period, plates were counted. The entire experiment was then repeated. The results indicated that no difference in colony counts existed between the methods evalu-

ated. Colonies on plates which had the gas delivered by the Campy EZ Gas Pak method were much smaller in size than colonies on plates that had the gas delivered by the other 2 methods. In conclusion, all 3 gas delivery methods were able to produce similar *Campylobacter* results between experimental runs. Additionally, the smaller colonies from the EZ Gas-Pak method could be a result of our media choice or the anaerobic chamber used. It is important to consider these issues when deciding on the appropriate microaerophilic gas delivery method to use for culturing *Campylobacter*.

Key Words: *Campylobacter*, microaerophilic, gas delivery

W105 Aflatoxicosis in Haiti: Detection and detoxification strategies. M. E. Filbert* and D. L. Brown, *Cornell University*, *Ithaca, NY*.

Aflatoxins are carcinogenic, immunosuppressive agents produced by *Aspergillus* mold in crops. Haiti's climate facilitates fungal growth, threatening staple foods such as peanuts and maize, which are highly susceptible to aflatoxin contamination. The danger of aflatoxin poisoning is of concern in Haiti where food is scarce and consumption of the toxin is inevitable. Because of serious health risks, the maximum allowable level of aflatoxin in agricultural commodities (except milk) intended for human consumption is 20 μg aflatoxin/kg product. The overall objective of this research project was to determine the nature and extent of aflatoxicosis in a malnourished population. There are no food safety standards or regulations on any level of food production in Haiti. Our laboratory has not yet found Haitian peanuts from any source that did not exceed allowable aflatoxin limits. Initial peanut samples taken in northern Haiti in 2005 and analyzed using ELISA-aided fluorometry, averaged 797.5 ± 218.5 μg/kg and ranged from 380 to 1567 μg/kg. In 2006, sampled peanuts from a public market found to average 412.5 ± 32.1 μg/kg; peanuts from a farmer's stored supply averaged 125 ± 7.1 μg/kg. A visibly unspoiled sample from a local farm was tested, averaging 26.8 ± 7.0 μg/kg. Another post-sorting sample taken in early 2007 averaged 0.20 ± 0.10 μg/kg, revealing the effectiveness of selection and sorting methods in the elimination of aflatoxin. Peanut butter samples collected in 2009 averaged 236.4 ± 196.7 μg/kg and ranged in levels from 7.3 to 720 μg/kg, validating the need for implementation of sorting methods at every level of food production. An ongoing study using urine will assess aflatoxin catabolism in a malnourished population. Health risks can be reduced by determining contamination levels and understanding aflatoxin metabolism. The results of this study will provide the information needed to meet the long-term goals of implementing food preparation procedures to remove aflatoxin as a barrier to the nutritional support and recovery of malnourished individuals.

Key Words: aflatoxin, peanuts, Haiti

W106 Conjugated linoleic acid does not modify liver histology and hepatic triglyceride content in young pigs. I. Fernandez-Figares*[1], A. Martin[2], M. Lachica[1], R. M. Nieto[1], and J. F. Aguilera[1], [1]*CSIC, Spanish Research Council*, *Granada, Spain*, [2]*Servicio de Anatomia Patologica, HU Virgen de las Nieves*, *Granada, Spain*.

Interest in feeding CLA to pigs has increased in the last decade as a result of its potential to improve growth parameters as well as to reduce body fat (J Anim Sci. 79:1821–8). Interestingly, in mice, adipose tissue reduction was accompanied by liver enlargement and esteatosis (Diabetes. 49:1534–42). In pigs, however, there is no evidence of enhanced liver weight after CLA administration (J Anim Sci. 86:102–11). Therefore, the aim of the present work was to evaluate possible adverse effect of feeding CLA supplemented diets to pigs on liver fat content and histology. Twenty gilts (20 kg BW) were individually penned and fed at 95% ad libitum barley-soybean meal based diets (12% CP, 0.81% lysine and 14.8 MJ ME / kg DM) containing 1% CLA (60% CLA isomers, half *cis*-9, *trans*-11 and half *trans*-10, *cis*-12 in FFA form, BASF) or linoleic acid. At 50 kg, pigs were slaughtered and liver samples immediately frozen in liquid nitrogen and preserved at −80°C until analysis. Thawed liver samples were homogenized and TG extracted with 2:1 chloroform/methanol using the Folch method and dissolved in isopropanol. TG content was determined quantifying the glycerol content, using an enzymatic colorimetric assay. For histology, the livers were thawed and fixed in 10% buffered formaline. After routine processing, livers were embedded in paraffin, sectioned at 5 μm and stained with hematoxylin-eosin and reticulin stain. Triglycerides data were analyzed as one-way ANOVA in a completely randomized design with treatment as the fixed effect. Significance was set at $P < 0.05$ and differences among means were determined using a Tukey's *t*-test. Overall, no differences in triglyceride content was encountered when CLA fed pigs were compared to control pigs (2.1 and 1.6 mg/g, respectively; $P > 0.10$). In the histological study, all livers showed normal histology, without evidence of inflammatory changes, fibrosis or esteatosis.

Key Words: CLA, pig liver, triglycerides

W107 Use of *Pleurotus oestreatus* to change the nutritional quality of maize stover. O. D. Montañez-Valdez*[1], J. M., Tapía-Gonzalez[1], G. Rocha-Chavez[1], J. A. Martínez-Ibarra[1], C. E. Guerra-Medina[2], E. O. Flores-García[2], and J. H. Avellaneda-Cevallos[3], [1]*Centro Universitario del Sur de la Universidad de Guadalajara*, *Ciudad Guzmán, Jalisco, México*, [2]*Universitario de la Costa Sur de la Universidad de Guadalajara*, *Autlán, Jalisco, México*, [3]*Universidad Técnica Estatal de Quevedo*, *Santo Domingo. Quevedo, Los Ríos, Ecuador*.

A study was conducted to evaluate the effect of *Pleurotus oestreatus* on chemical composition of maize stover. Maize stover treated and untreated with *Pleurotus oestreatus*, were obtained from a commercial facility. Ten samples of maize stover used previously as substrate to culture edible fungus were collected randomly. The negative control group consisted of the pasteurized maize stover untreated with *Pleurotus oestreatus*. All samples were analyzed to determinate dry matter (DM), organic matter (OM), crude protein (CP), neutral detergent fiber (NDF), acid detergent fiber (ADF), cellulose (C), hemicellulose (HC) and lignin (L). Data were analyzed by mean comparison using a Student's *t*-test. No differences ($P \geq 0.05$) between treatments were found for DM, CP, C and HC; however, treated maize stover ($P \leq 0.02$) showed higher percentages of OM (89.07 vs. 84.83), NDF (69.65 vs. 63.74), and ADF (48.18 vs. 43.68) as well as a lower L value (9.20 vs. 12.22). The growth of *Pleurotus oestreatus* on maize stover changes its chemical composition by increasing organic matter content and modifying cell wall components, this may improve the nutritional quality of agricultural byproducts. This process may allow using *Pleurotus oestreatus*-treated maize stover for ruminant feeding

Key Words: agricultural byproducts, white rot fungi, chemical composition

W108 Effect of the fermented apple pomace (manzarina) on the rumen epithelia growth with lamb feedlot diets. C. Rodríguez-Muela*[1], H. E. Rodríguez-Ramírez[1], A. Grado[1], A. Corral[1], O. Ruiz-Barrera[1], A. Arzola[1], and R. Bocourt[2], [1]*Universidad Autónoma de Chihuahua*, *Chihuahua, México*, [2]*Instituto de Ciencia Animal*, *La Habana, Cuba*.

The objective of this research was to evaluate the effect of manzarina (mzn) in the development of the ruminal epithelia, antioxidant activity and blood chemistry profiles of sheep plasma. Four treatments (Tr) were designed (n = 24, 12 males and 12 females): Tr1, males with 10.9% mzn diet (DM basis); Tr2, females with mzn diet; Tr3, males with basal diet; Tr4, females with basal diet. Basal diet contained (DM basis) 38.5% alfalfa hay, 12.4% soybean meal, 42.5% steam rolling corn, 2.0% animal fat, 3.1% molasses, 0.7% salt and 0.8% vitamin and mineral premix. Lambs remained in individual cages (0.5 × 1.0m), with water and food ad libitum by 58d. Two samples of blood were taken every 30 d (beginning, intermediate and at the end of the experiment), to determinate antioxidant activity (AA by Ferric Reductive Ability of Plasma) and the blood chemistry profiles (BC). Animals were slaughtered and 4 samples were taken of rumen wall to measure the long and wide of papillae on ruminal epithelia. Data of AA and BC was analyzed with a mixed model (fixed effects: Tr, sampling, sex and their interactions). An experimental unit nested in Tr as random effect was used. A hierarchical model was used to analyze long and wide of papillae. Effects of Tr, sex and their interaction were nested in the sampling rumen area. Results showed that AA of Tr1 was greater ($P < 0.06$) than AA of Tr2 animals on sampling 3 (24.34 vs. 21.79 mM Fe_2). There was an increment over time ($P < 0.05$) of leucocytes in all animals (7.52×10^3 uL^{-1} to 9.14×10^3 uL^{-1}). Leucocytes began to increase at 30th day of feeding period, with values inside the normal rank of these animal species without treatment effect ($P > 0.05$) for the remaining BC indicators. Animals of Tr1 had greater ($P < 0.05$) long of papillae (3.04 ± 0.07 mm) than Tr3 animals (2.43 ± 0.05 mm). Wide of papillae was greater ($P < 0.05$) in the animals consuming mzn diet (1.99 ± 0.02 mm) versus animals consuming diet without mzn (1.90 ± 0.02 mm). We conclude that the use of the manzarina in lamb feedlot diets improved the AA in plasma and stimulated the growth of the Rumen Epithelia.

Key Words: antioxidant, leucocytes, papillae

W109 Effects of ensiling king grass with *Albizia lebbeck* on fermentation and nitrogenous compounds of silage mixtures. T. Clavero* and R. Razz, *Centro de Transferencia de Tecnologia en Pastos y Forrajes, Universidad del Zulia*, *Maracaibo, Estado Zulia, Venezuela*.

King grass (*Pennisetum purpureum* × *Pennisetum typhoides*) silage is low quality with low nitrogen concentration. This study determined whether addition of albizia (*Albizia lebbeck*) would improve the quality or nitrogen status of the silage in a tropical dry forest in northwest Venezuela. The treatments for silage making were: 100% king grass (KG), 30% albizia (A):70% KG, 50% A:50% KG, 70% A:30% KG, 100% A. Chopped fresh plant materials of at least 1 cm length were ensiled into a laboratory silos and stored at 25°C for 45 d. After opening silos, dry matter (DM), pH, total nitrogen content (TN), protein nitrogen (PN), soluble nitrogen (SN), PN/TN, ammonia nitrogen (AN), neutral detergent fiber nitrogen of total nitrogen (NNDF/TN), and acid detergent fiber nitrogen of total nitrogen (NADF/TN) were determined. The experiment was a completely randomized design with 3 replications. Significant means were separated with Tukey test. Silage DM increased ($P \leq 0.01$) with increasing proportion of albizia in the mixtures, and was greatest (25.21%) with 70%. All levels of albizia showed decreases in pH values ($P \leq 0.01$), showing the lowest value (3.41) with 100% albizia. Values of NADF/TN and NNDF/TN were not affected by treatments ($P \geq 0.05$). The TN, PN, SN and PN/TN contents increased linearly ($P \leq 0.01$) as the percentage of albizia increased in the mixtures. A small amount of AN was detected in silage, however, throughout there were not significant differences ($P \geq 0.05$) between 50 and 100% mixing levels of albizia. These results indicated that mixing albizia with king grass in the silage making was shown to be successful in the improvement of fermentation quality and nitrogen levels in silages.

Key Words: silage mixtures, *Albizia lebbeck*, nitrogenous compounds

W110 Detection of mycophenolic acid and roquefortine C mycotoxins in Canadian corn silage. H. V. L. N. Swamy*[1] and N. A. Karrow[2], [1]*Alltech Canada*, *Guelph, ON, Canada*, [2]*University of Guelph*, *Guelph, ON, Canada*.

Academic research to date has been focused on 5 silage *Penicllium* mycotoxins that are implicated in animal disorders—mycophenolic acid (MPA), patulin (PAT), penicillic acid (PA), PR toxin (PR), and Roquefortine C (RFC). It is critical that this academic research is complemented by the analysis of these mycotoxins in silage collected from commercial dairy farms. Nine corn silage samples (year 2008 crop) were collected

from Ontario dairy farms and each sample was divided into 2 equal parts. One part was submitted to TLR International Laboratories (the Netherlands) for MPA, PAT and RFC analyses while the other part to Trilogy Analytical Laboratories Inc. (USA) for PR analysis. Among these 9 samples, 3 each were collected from well, moderate and poorly managed silage bunks/silos. The bunks were classified as well, moderate or poor based on the silage density and face management. Following Penn State procedure, silage samples were collected from 12 different points of silage face and then were mixed thoroughly before taking one representative sample for analysis. The detection limits for MPA, PAT, PR and RFC were 25, 50, 500 and 10 ppb, respectively. MPA, PAT and RFC were analyzed by liquid chromatography with double in-line mass spectrometers (LC-MS/MS) and PR was analyzed by thin layer chromatography (TLC). None of the samples indicated any detectable levels of PR toxin. The detection limit for PR, however, was high (500 ppb) and future efforts should be made to analyze this mycotoxin with LC-MS/MS so that detection limit of at least 50 ppb is achieved. Two of the silages obtained from poorly managed bunks/silos indicated detectable levels of *Penicillium* mycotoxins. One sample was contaminated with 70.8 ppb MPA and the other with 27.1 ppb RFC. The levels of MPA, PAT and RFC were below the detection limits for the remaining silage samples. To the best of our knowledge, these are the first reported *Penicillium* mycotoxins in commercial corn silage produced in Canada. Silages, therefore, should be tested for *Penicillium* mycotoxins along with vomitoxin (DON) to assess the total animal toxicity.

Key Words: silage, *Penicillium*, mycotoxins

W111 Fermentation profile over nine months of storage of brown midrib and non-brown midrib hybrid corn silage. K. E. Nestor Jr.*, P. Krueger, J. Anderson, J. Brouillette, and K. Emery, *Mycogen Seeds, Inc.*, *Indianapolis, IN*.

The objective of this study was to examine the difference in fermentation patterns and changes in nutrient content in silages made from brown midrib hybrids (bmr) or non brown midrib hybrids over time of storage. A total of 19 bmr corn hybrids and 24 non bmr corn hybrids were collected from 15 plot locations in the Midwest and Northeast regions of the United States. At each plot location at least one bmr and one non-bmr were collected together. Ten samples of each hybrid were chopped and collected into vacuum sealed bags and then stored in an environmentally controlled room until analysis. Samples were sent to Cumberland Valley Analytical Services on a monthly basis for analysis. Each sample was analyzed for dry matter (DM), crude protein (CP), soluble protein (SolP), net energy of lactation (NEL), acid detergent fiber (ADF), neutral detergent fiber (NDF), lignin, starch, sugar, 7 h in vitro starch degradability (DegStarch), pH, titratable acid, lactic acid, acetic acid, total volatile fatty acids (TotVFA), ammonia, and 30 h NDF digestibility (DNDF). Data by month was analyzed by paired *t*-test and pooled hybrid data was analyzed by ANOVA. When the data was pooled across all time points the bmr hybrids were higher ($P < 0.001$) in CP, NEL, DNDF and higher ($P < 0.01$) in acetic acid and TotVFA and higher ($P < 0.05$) in lactic acid. The bmr hybrids were lower ($P < 0.001$) in ADF, NDF, lignin and lower ($P < 0.01$) in ammonia and lower ($P < 0.05$) in DegStarch. Within month of fermentation, there were several, but inconsistent differences between the hybrids in several of the parameters measured. The fermentation patterns of each hybrid class were similar. Other than the differences in nutrient content, the results of this study suggest that bmr hybrids are not different than non-bmr hybrids in fermentation patterns over time of storage.

Key Words: silage, bmr, fermentation

W112 Herbage mass, botanical and chemical composition of forage sorghum and annual legumes in monoculture and intercropped. R. W. Colbert, E. Valencia*, and J. Beaver, *University of Puerto Rico, Mayaguez*, *Mayaguez, Puerto Rico*.

Forge sorghums (*Sorghum bicolor* cv. Brown midrib) and the legumes lablab (*Lablab purpureus* cv. Rongai) and velvet bean (*Mucuna pruriens* cv. Vine 90d) are excellent forages for the dairy industry in Puerto Rico. Brown midrib (BMR) is low in crude protein (CP; 6%) at 90 d harvest, limiting its use in the industry. There is potential to increase CP by intercropping legumes with BMR, but this has not been documented. This study was conducted to assess the effect of monoculture or intercropping BMR, Rongai and Vine 90d on herbage mass (HM), botanical and chemical composition. Treatments were BMR, Rongai and Vine 90d, and BMR-Rongai and BMR-Vine 90d intercropped. Experimental plots (25 m^2) were planted in May and August, 2008 in a randomized complete block with 5 replicates. Herbage mass was estimated in a 2 m^2 area 90 d after planting. Dried sub-samples (500 g) were ground in a Willey mill and used for CP and neutral detergent fiber (NDF) and acid detergent fiber (ADF) analysis. Data were analyzed using PROC Mixed in SAS and mean separation when significant was conducted with Fisher LSD. There were no differences ($P > 0.05$) for HM between BMR intercropped with legumes and BMR in monoculture. Herbage mass was 8.9, 8.8, and 8.4 Mg ha^{-1}, for BMR-Rongai, BMR-Vine 90d, and BMR, respectively. Botanical composition for Rongai did not vary ($P > 0.05$) in HM between May and August, with means values of 2.7 and 3.9 Mg ha^{-1} in intercropping and monoculture, respectively. Vine 90d presented the lowest ($P < 0.05$) HM, 2.8 and 1.3 Mg ha^{-1} for May and August, respectively. Both NDF and ADF ($P > 0.05$) were not different with values of 60.1 and 63.9% and 40.1 and 46.5%, for BMR-Rongai and BMR-Vine 90d, respectively. However, there were differences ($P < 0.05$) in CP for monoculture and intercrops. The CP for Rongai, Vine 90 d, and BMR in monoculture were 14.1, 11.1, and 6.0%, respectively. When intercropped, CP for BMR-Rongai and BMR-Vine 90d were 9.8 and 9.1, 3 percentage units greater ($P < 0.05$) than BMR. In conclusion, BMR intercropped with Rongai and Vine 90d improved its nutritive value from a ruminant nutrition perspective.

Key Words: brown midrib, Rongai, Vine 90 d

W113 Comparisons among predictive equations and NIR for determination of in vitro indigestible NDF of hay crop silages. R. Ward*[1], S. Weaver[1], and R. A. Patton[2], [1]*Cumberland Valley Analytical Services*, *Maugansville, MD*, [2]*Nittany Dairy Nutrition*, *Mifflinburg, PA*.

There may be advantages to using indigestible NDF (INDF) values in ration balancing programs if they could be derived in a time efficient and economical fashion. NIR holds promise as a means of generating this information. To investigate the accuracy of NIR compared with predictive equations, a data set of 130 hay crop silages with indigestible NDF determined at 120 h of incubation by the Tilley and Terry method was developed. Types of silages were 19 grass, 27 legume, 20 mixed mainly grass (MMG), 26 mixed mainly legume (MML) and 38 small grain silages. Using this data, chemically determined INDF was compared against equations developed using analyzed nutrients from a smaller data set for all hay crop silages and for individual forage types, as well as calculation of INDF as lignin*2.4. The mean square predicted error statistic of Bibby and Toutenburg was used to compare predictions with observed values. The overall determined equation was INDF = 1.409 + (2.838 * lignin %DM), $R^2 = 0.82$. For grass silage, the equation was INDF = (1.720 * ADF %DM) - 40.101, $R^2 = 0.96$, while legume was INDF = 8.803 + (2.045 * lignin), $R^2 = 0.97$, for MMG INDF = 6.336 + (3.052 * starch %DM) + (0.337 * Ash %DM), $R^2 = 0.99$, for MML INDF

= (1.267 *ADF %DM)-23.971, R^2 = 0.97, and for small grain, INDF = 15.987 + (0.528 * NDICP %DM), R^2 = 0.99. Using an equation of lignin*2.4 (R^2 = 0.77) considerably under predicts the amount of INDF in hay crop silages whether determined at 120 or 240 h of incubation. We conclude that there is a strong relationship of lignin to INDF for hay crop silages. Further these results suggest that NIR is a better predictor of INDF than equations and that feed specific equations are better than general equations using only lignin as a predictor.

Table 1.

						Error Due To	
Model	Mean	Std Dev	RMSPE	% Mean	Bias	Regression	Random
Observed	18.11	4.87	-	-	-	-	-
NIR	17.96	4.32	2.01	11.2	0.5	0.3	99.2
Feed Specific	18.41	4.27	4.87	27.2	0.4	19.3	80.3
Overall	16.96	4.53	3.61	20.2	10.2	6.9	82.9
Lignin*2.4	13.15	3.83	5.96	33.3	69.3	0.2	30.5

Key Words: hay crop silage, NIR, INDF

W114 Relating dry matter density to dry matter loss within corn silage bunker silos. K. E. Griswold*[1], P. H. Craig[2], J. S. Graybill[1], and S. K. Dinh[1], [1]*Penn State Cooperative Extension*, *Lancaster,* [2]*Penn State Cooperative Extension*, *Dauphin*.

The objective was to refine the relationship between dry matter (DM) density and DM loss within corn silage bunker silos. Poly-weave nylon bags (36 per silo) containing chopped brown mid-rib (BMR) corn were buried in 3 bunker silos during filling on the same farm. Bags were blocked by depth from the end of the bunk, 10.6 m (front), 27.8 m (center), and 44.9 m (back), level from the silo floor, 0.6 m (bottom), 1.5 m (middle), and 2.15 m (top), and within level, location from the east wall, 0.9 m (I), 4.7 m (II), 8.4 m (III), and 12.2 m (IV). Upon feed-out, all bags at a specific depth were retrieved and silage cores for DM density were obtained at each bag position. Cores were collected using a 5.08 cm diameter stainless-steel coring tube driven by a gas-powered drill. Corn and silage DM was determined using a Koster moisture tester. Data were analyzed using PROC MIXED and RSREG within SAS. The model included the fixed effects of depth, level, location, all interactions, and the random effect of bunk. Significance was set at $P < 0.05$, and trends at $0.05 < P < 0.10$. There were no significant interactions. Density was affected ($P < 0.0001$) by depth, level, and location. Density was 201, 253, and 255 kg DM/m^3 for the front, center, and back, respectively. Density was 284, 268, and 224 kg DM/m^3 for the bottom, middle and top, respectively. Density was 219 and 211 kg DM/m^3 for I and IV compared with 260 and 254 kg DM/m^3 for II and III, respectively. DM loss % was affected ($P < 0.001$) by depth and level but not location. Loss was 9.2, 6.5, and 7.3% for the front, center, and back, and 6.5, 5.0 and 8.4% for the bottom, middle and top, respectively. There was a linear inverse relationship (R^2 = 0.18) between loss and density. Response surface regression of DM density and DM% versus DM loss also showed an inverse relationship (R^2 = 0.28). These results suggest a large degree of variation in DM loss is not associated with the DM density and DM% of the corn silage within a bunker silo.

Key Words: corn silage, density, loss

W115 Silo-King improves dry matter (DM) recovery and lowers the yeast, mold, and clostridia populations in high quality alfalfa balage. D. H. Kleinschmit*, D. P. Casper, D. J. Schauff, G. P. Gengelbach, K. E. Lanka, D. F. Jones, G. Ayangbile, and D. A. Spangler, *Agri-King, Inc.*, *Fulton, IL.*

High quality alfalfa balage is an excellent forage source for dairy cattle, however it may be susceptible to microbial deterioration and DM loss during ensiling. Silo-King is a silage fermentation aid designed to both improve the initial fermentation process via enhanced production of lactic acid and inhibit the growth of spoilage organisms so it may be an appropriate additive to aid in the production of high quality balage. On May 20, 2008 a total of 12 bales of alfalfa balage were made, with 6 bales (541 ± 9.43 kg) untreated (UNT) and 6 bales (524 ± 9.30 kg) treated with Silo-King via baler mounted applicator at a rate of 0.033% of fresh forage weight (SK) and wrapped with 8 mils of plastic. The nutrient content of both treatments before ensiling were similar. After 65 d of ensiling, final weights for determination of DM recovery and core samples for nutrient analysis and microbial counts were obtained from each bale. The experiment was analyzed as a completely randomized design with ANOVA being conducted with the MIXED procedure of SAS. The model was y = treatment + rep with rep being the random variable and least squares differences used for means separation. Even though nutrient content and 30-h in vitro DM digestibility were not altered by treatment in this study, UNT succumbed to more ($P < 0.01$) DM loss compared with SK (0.56 vs. 0.05% for UNT and SK, respectively). This was likely due to a tendency for SK to have a lower ($P < 0.10$) pH compared with UNT (5.35 vs. 5.25 for UNT and SK, respectively). Balage treated with SK had lower ($P < 0.02$) populations of clostridia (2067 vs. 97 colony forming units (cfu)/g of forage for UNT vs. SK, respectively) and yeasts (3317 vs. 25 cfu/g for UNT vs. SK, respectively) and a tendency for less ($P < 0.06$) molds (1203 vs. 7 cfu/g for UNT vs. SK, respectively). Based on the results in this study, the use of Silo-King as a forage enhancer is a viable tool to preserve the valuable DM in high quality balage and to enhance its feeding value by almost eliminating the presence of undesirable organisms, such as yeasts, molds, and clostridia.

Key Words: alfalfa, inoculants, yeasts

W116 Nutritional value of corn silage associated with additives. R. H. de Tonissi e Buschinelli Goes*[1], E. S. Myagi[2], K. A. de Souza[1], K. A. G. Nogueira[1], R. A. Patussi[1], M. G. de Menezes Gressler[1], C. E. Dambros[2], and E. R. de Oliveira[1], [1]*Universidade Federal da Grande Dourados*, *Dourados, MS, Brasil*, [2]*Universidade Federal de Goiás*, *Goiânia, GO, Brasil*.

Corn plant, cut at 90 d, was ensiled in 72 experimental silos in randomized design, in factorial 4 × 6 square (4 treatments and 6 d-opening) with 3 replicates, and the averages compared by Tukey's test at 5% probability, for evaluate the nutritional value of corn silage associated with additives. The corn silage was associated with additives at 5% in natural matter, and the treatments were: soybean hulls (CS+5%SH), rice meal (CS+5%RM) and crushed sunflower (CS+5%SC). The control was 100% of the corn plant (CS). The silos were opened at 0, 28, 56, 84, 112 and 140 d of fermentation. The pH reduced from 28 d of fermentation, with lowest value (3.39) at 112 d. All additives reach a pH favorable to preservation of forages. There was effect ($P < 0.05$) for additive and time of opening for dry matter (DM), crude protein (CP), ether extract (EE), NDF and total carbohydrates (TC). Crushed sunflower increased DM of silage on day zero, independent of the additive DM decreased to 140 d of fermentation. The CP increased with additive addiction. Crushed sunflower increased the CP, in 71% (average 13.3%), CS had a mean of 7.7% and CS+5%SH and CS+5%RM (9.1 and 9.6%). Crude protein was higher for the 112 and 140 d after ensiling. The addition of soybean hulls reduced the concentration of EE (1.5%) and crushed

sunflower and rice meal increased EE (24.8 and 10.9%); because chemical composition of the additive. The NDF decreased according ensilage time. The lower values of NDF occurred at 112 d (63.02, 65.46, 57.83 and 60.98% for CS, CS+5%SH, CS+5%RM and CS+5%SC, respectively). The levels of total carbohydrates remained stable over the days of fermentation for addition of soybean hulls, rice meal and CS (averages 85.5, 75.2 and 86.5%). CS+5%SC had the lowest values of TC for all opening days (mean 58.4%). Ash content was increased for addition of soybean hulls and rice meal (4.2 and 3.9%), while the CS+5%SC and corn silage presents average of 3.5 and 3.4%. Ash decreased after 56 d of fermentation. The addition of 5% soybean hulls, rice meal and crushed sunflower improve the nutritional value of corn silage

Key Words: crude protein, ether extract, chemical composition

W117 Nutritive value and fermentation parameters of warm-season grass silage. J. M. B. Vendramini*[1], A. T. Adesogan[2], M. L. A. Silveira[1], L. E. Sollenberger[2], O. C. M. Queiroz[2], and W. F. Anderson[3], [1]*University of Florida*, *Ona,* [2]*University of Florida*, *Gainesville,* [3]*USDA ARS*, *Tifton, GA*.

The objective of this study was to investigate the nutritive value and fermentation characteristics of different species of warm-season grass silages treated with or without inoculants in Florida. Nine forage species and cultivars, elephantgrass (*Pennisetum purpureum*), Mulato (*Brachiaria* sp.), bahiagrass (*Paspalum notatum*), stargrass (*Cynodon nlemfuensis*), Tifton 85 bermudagrass (*Cynodon* sp.), Jiggs bermudagrass (*Cynodon dactylon*), Coastcross 2 bermudagrass, Florakirk bermudagrass, and Floralta limpograss (*Hemarthria altissima*) were treated with or without (control) a microbial inoculant solution (Si-All) in a split-plot arrangement with 3 replicates. Plots were harvested on July 17 and October 9 2008. Forage was packed into mini-silos at a density of approximately 450 kg fresh forage/m^3 and ensiled for 84 d. The data were analyzed using PROC MIXED of SAS with forage species (main plot) and inoculant treatment (sub-plot) as fixed effects. Replicate and its interactions were considered random effects. The means were compared using the PDIFF statement of SAS. In the summer, NDF concentration was greater for the bermudagrasses than the average of other species (68 vs. 65%, $P < 0.01$, SE = 1). Mulato had the lowest NDF concentration (57%, $P < 0.03$, SE = 0.8) and the greatest IVTD concentration (63%, $P < 0.05$, SE = 1) compared with other treatments. Limpograss silage had the lowest pH (6.5, $P < 0.07$, SE = 0.3) and the greatest lactic acid concentrations (2.6%, $P < 0.01$, SE = 0.1). Elephantgrass silage had decreased lactic acid concentration (0.1%, $P < 0.001$, SE = 0.01) with greater pH (8.3, $P < 0.01$, SE = 0.3) than the other species. Inoculated silages had a lesser lactic acid concentration than control (0.62 vs. 1.84%, $P < 0.001$, SE = 0.2). In the fall, elephantgrass silage pH was less (7.2 vs. 8.8, $P < 0.06$, SE = 0.6) and the concentrations of total volatile fatty acids (4.6 vs. 0.4%, $P < 0.01$, SE = 0.2), lactic acid (1.5 vs. 0.2%, $P < 0.05$, SE = 0.5) and acetic acid (2.1 vs. 0.2%, $P < 0.001$, SE = 0.3) greater than in the bermudagrasses. There was no effect ($P > 0.10$) of the inoculant on the nutritive value and silage fermentation parameters in the fall.

Key Words: warm-season grass, silage, nutritive value

W118 Chemical composition and nutritive value of some cowpea (*Vigna unguiculata* L. Walp) haulm varieties. U. Y. Anele*, J. Hummel, O. M. Arigbede, C. Böttger, and K.-H. Südekum, *University of Bonn*, *Bonn, Germany*.

A study was carried out to evaluate the chemical composition, in vitro gas production, in vitro apparent and true substrate degradability, efficiency of microbial crude protein (CP) production, CP flow to the duodenum, methane production, protozoa population, and short chain fatty acids production of the haulms of 6 cowpea varieties. The study was arranged in a 2 × 2 × 2 factorial design, with 3 replicates. Three improved (ITA2, ITA6 and ITA8) and 3 commercial (Oloyin, Peu and Sokoto) cowpea varieties harvested in Nigeria during the wet and dry seasons were used for the study. After an initial gas test to evaluate 96 h gas production profiles of haulms with and without polyethylene glycol (PEG), the time to half maximal gas production was calculated and a second incubation conducted with fermentation stopped at substrate specific half time and 24 h for each substrate. True substrate degradability was measured from incubated residues and combined with gas volume to estimate the partitioning factor. Crude protein flow to the duodenum was estimated by combining gas volume with the measured ammonia nitrogen in the incubated fluid. Addition of PEG did not have any effect ($P > 0.05$) on all the variables determined. Interaction between group (improved vs commercial) and season was observed for the CP ($P = 0.002$), lignin ($P = 0.003$) and hemicellulose ($P = 0.030$) contents of the haulms. A group × season interaction was observed for some of the variables at both substrate specific half time and 24 h. On the average, the commercial cowpea haulms had greater microbial mass and produced less methane than the improved cowpea haulms. The improved cowpea haulms were less degraded in the rumen and as a result ensured greater amount of CP flow to the duodenum. The results validated that cowpea haulm is an important agro-based by-product that is adequate in protein and energy to sustain ruminant animal production in Nigeria and other Sub-Saharan African countries during the extended dry season.

Key Words: in vitro gas production, legume, protein value

W119 Silage characteristics, and nutritive value of sugar beet tops and crown harvested by two different methods. M. Raisianzadeh*[1], M. Danesh[2], H. Fazaeli[3], and M. Nourozi[1], [1]*Khorasan Agriculture and Natural Resources Research Center*, *Iran*, [2]*Ferdosi University of Mashhad*, *Iran*, [3]*Animal Science Research Institute*, *Karaj, Iran*.

Two areas of 500 m^2 in each of 3 sugar beet farms, that were different according to plant covers were selected. In one area, sugar beet tops and crowns (SBTC) before harvesting (method 1) but in another one SBTC were cut after harvesting of tuber (method 2).Costs and quality of obtained SBTC compared. The SBTC collected in method 1, had better quality than that of the method 2 but because of more labor used for method 1, it was more costly when compared with method 2. In a completely randomized block experiment, with 2 treatments (2 methods of SBTC collectives) and 4 replications the SBTC was ensiled with addition of 10%molasses and 2% urea to study its silage characteristics. In the last stage, digestibilities of silages obtained from each harvesting methods were compared. Result showed that SBTC silage collected by method 1 had better quality with higher organic matter and crud protein but lower pH ($P < 0.05$).The protein fractions including true protein and non protein nitrogen were significantly ($P < 0.05$) different between the treatments. Silages from method one, had higher quality compared with silages from method 2 and hence they had different pH and organic matter ($P < 0.05$). Silage made from TC cut before harvesting had higher ($P < 0.05$) crude protein, true protein and NPN contents, may be due to the lower percentage of SB crowns produced in the first method. Also highest levels of DM, OM, d.value digestibility percentage were observed in the first method.

Key Words: sugar beet tops and crowns, harvesting methods, silage characteristics

W120 Dry matter of corn at harvest alters whole plant chemical composition and predicted milk yields. P. M. Walker[1], J. M. Carmack*[1], L. H. Brown[2], and F. N. Owens[2], [1]*Department of Agriculture, Illinois State University*, *Normal,* [2]*Pioneer Hi-Bred International, A DuPont Business*, *Johnston, IA*.

Objectives of this trial were to determine effects of plant maturity (DM) on nutrient composition, projected milk per acre and milk per ton. Six commercial Pioneer corn hybrids (105 to 116 d CRM) with 24 rows per hybrid to minimize cross pollination effects were planted on May 12, 2009 near Normal, IL. Plants (replicate sets of 5 plants per harvest date) from each hybrid were randomly harvested in the 4 middle rows and cut 7 inches above ground level twice each week starting August 10 until DM content reached 50% (October 12). Sets of harvested plants were chopped, sampled, dried, and assayed via calibrated NIR analysis. By regression analysis from 25 to 45% DM, effect of plant DM on nutrient composition averaged across hybrids was examined. Using linear, quadratic, and cubic regression analysis, effects of harvest DM on milk yield per ton and per acre were calculated (based on Milk 2006 equations) for each hybrid and date. Finally, stepwise regression was used to determine the relative importance of specific nutrients and measurements on milk per ton and milk per acre. For each 1% increase in harvest DM, the percentage of starch in DM increased by 2% ($P < 0.01$) while decreases ($P < 0.01$) were detected for NDF (1.1%), sugars (0.7%), and ash (0.1%). Because hybrids differed in nutrient composition on various harvest dates, milk per acre and milk per ton were altered by harvest DM, and ranking of hybrids changed with harvest date. Compared with harvest at 30% DM, harvest at the optimum DM content (between 33 and 36% for these hybrids) increased projected milk yield by 5 to 13% per ton. Harvest between 33 and 40% DM increased milk yield per acre by 7 to 25% above harvest at 30% DM. Hybrid ranking at 35% DM differed from that at 30% DM ($R^2 = 0.62$; NS). Across hybrids and harvest dates, milk per ton depended primarily (($P < 0.01$) on starch content and NDFD (partial $R^2 = 0.82$ and 0.06) while milk per ton varied with starch and protein yields (partial $R^2 = 0.86$ and 0.07). Results from this trial suggest that milk per ton and acre will vary with harvest dry matter, and starch content and yield will affect projected milk yields.

Key Words: NDF, corn silage, maturity

W121 Effect of bunker silo sidewall plastic on fermentation, nutrient content and digestibility of corn silage. K. E. Griswold*[1], E. E. McDonell[2], L. Kung Jr.[2], and P. H. Craig[3], [1]*Penn State Cooperative Extension*, *Lancaster,* [2]*University of Delaware*, *Newark,* [3]*Penn State Cooperative Extension*, *Dauphin*.

The effect of sidewall plastic (SP) on fermentation, nutrient content and digestibility of corn silage was investigated in 20 dairy farm bunker silos, 10 without and 10 with SP. Samples were collected at 5 sites in each silo. Approximately 0.65 m from an outside wall at 3 levels, bottom ≈0.65 m from floor, top ≈0.65 m from top, and middle ≈equidistant to bottom and top. The fourth site was ≈1.3 m from the outside wall and ≈0.65 m from the floor. The fifth site, serving as an internal control, was collected equidistant to the walls and 2.0 m from the floor. At each site, 3 samples were collected in a triangular pattern using a stainless-steel coring tube. Samples were stored on ice until analysis. Data were analyzed using PROC MIXED within SAS. The model included fixed effects of plastic, location, interaction of plastic by location, and random effect of farm. Significance was set at $P < 0.05$, and trends at $0.05 < P < 0.15$. There were no interactions. Silage was wetter ($P < 0.0001$) at the wall bottom compared with all other sites, and was drier ($P < 0.0001$) in the center compared with all other sites. Silage tended ($P = 0.10$) to be drier in SP silos (31.8% DM) compared with silos without SP (29.5% DM). Data were then sorted by presence or absence of SP and analyzed with a model including fixed effect of location, random effect of farm, and single DF contrast of center versus wall samples. Silos without SP tended to have less acetic acid ($P = 0.08$) and less ethanol ($P = 0.01$) in wall samples versus the center while there were no differences between wall and center samples in SP silos. Silos with SP had less lactic acid ($P < 0.02$) in wall samples versus the center while silos without SP showed no difference between wall and center samples. The 30-h NDF digestibility was not different between wall and center samples in SP silos, but was less ($P < 0.04$) in wall samples versus the center for silos without SP. These results suggest that use of sidewall plastic in bunker silos alters fermentation, and may produce drier corn silage with greater digestibility.

Key Words: corn silage, sidewall plastic, digestibility

W122 Quality traits of the stem from corn hybrids for silage production according to the maturity stage. M. Zopollatto*[1], L. G. Nussio[1], J. O. Sarturi[2], C. M. M. Bittar[1], P. Schmidt[3], and G. B. Mourao[1], [1]*University of Sao Paulo*, *Piracicaba, Brazil*, [2]*University of Nebraska*, *Lincoln*, [3]*Federal University of Parana*, *Curitiba, Brazil*.

The objective of this study was to evaluate the stem quality traits from corn hybrids for silage production harvested across maturity stages. A randomized block design, with an 8x6x2 factorial scheme based on 8 harvesting times, 6 corn hybrids and 2 harvesting years (2001/02 and 2002/03) was performed. The hybrids CO 32, semi-hard endosperm; AG 5011, soft endosperm; P 3041, hard endosperm; DKB 333B, semi-hard endosperm; AG 1051, soft endosperm and Z 8550, semi-soft endosperm were harvested when they reached 50% tasseling, 15 d later and weekly, totaling 8 harvesting times. Plant was fractionated in leaf, stem, cob, grain and husk. Stem portion was analyzed for CP, NDF, digestible NDF (dNDF) and IVTDDM using the NIRSystems 5000 spectrophotometer. Variables were analyzed using the PROC MIXED procedure (SAS), and the averages compared by the Student *t*-test, with 5% level of significance. Maturity advance resulted in decreases ($P < 0.05$) in stem dNDF (55.2 to 39.6%), CP (7.0 to 4.23%) and in IVTDDM (66 to 53.7%). For the NDF content and digestible DM production (DDMP), the hybrids showed different responses along the maturity stage. At the ensiling stage (30–35% DM – between 5th and 6th harvesting time, from 94 to 112 d after seeding), stem NDF, dNDF, CP, IVTDDM and DDMP were 71.1 to 78.5% DM, 40.9 to 48.5% DM, 3.81 to 4.97% DM, 55.8 to 64.1% and 2.333 to 4.529 kg/ha, respectively. At the ensiling stage, Z8550 showed the most desirable stem quality characteristics for silage production, the lowest ($P < 0.05$) NDF (71.1% DM, SEM = 0.86) content and the highest ($P < 0.05$) stem dNDF (48.5% DM, SEM = 0.74), IVTDDM (64.1% DM, SEM = 0.96) and DDMP (3.651 kg/ha, SEM = 237). Hybrids P 3041, DKB 333B and AG 1051 also presented the highest ($P < 0.05$) stem DDMP at the ensiling stage, 4.107 (SEM = 285), 4.257 (SEM = 237) and 4.529 (SEM = 237), respectively. Monitoring the stem quality traits of corn hybrids for silage is an important tool for selecting corn hybrids based on the influence on the nutritive value of the whole plant.

Key Words: digestibility, fiber, harvesting time

W123 Butyric acid in commercially analyzed legume silage samples. L. R. Jones*[1] and R. T. Ward[2], [1]*American Farm Products, Inc.*, *Ypsilanti, MI,* [2]*Cumberland Valley Analytical Services, Inc.*, *Maugansville, MD*.

Butyric acid production by clostridia bacteria in hay crop silages has been associated with fermentation failure, significant dry matter losses, and reduced dry matter intake. A data set of 563 forage samples submitted for commercial analysis was evaluated for fermentation and descriptive statistics. Samples coded as either legume or legume grass mixes and having a dry matter level of 25–45% were included in the data set. Forage samples were analyzed for dry matter (DM), crude protein (CP), ammonia as a percent of CP (ammCP), lignin as a percent of NDF (ligninNDF) Ash, pH, lactic acid (LA), and butyric acid(BA) content. In the data set, 26% of samples had BA levels > 0.1% DM (BA1), 14% had BA levels > 0.5% DM (BA5) and 10% had BA levels > 1.0% DM (BA10). The incidence of BA was evaluated for 3 DM contents: < 32.5% (L), 32.5% 37.5% (M), and >37.5% (H), as well as pH levels of < 4.25 (LL), 4.25–4.75 (L), 4.75–5.25 (M) and >5.25 (H). For the L DM level, incidence of each butyric acid level (BA1, BA5, and BA10) increased as pH increased (17%, 0%, 0% for LL; 37%, 16%, 6% for L; 68%, 45%, 35% for M and 71%, 71%, 65% for H, respectively). For the M DM level, incidence of each BA level increased as pH increased (9%, 0%, 0% for LL; 13%, 3%, 1% for L; 42%, 22%, 17% for M and 56%, 44%, 38% for H). BA levels are highly correlated ($P < 0.0001$) with pH (r = 0.43), LA (r = −0.39), ammCP (r = 0.76), ADF (r = 0.38), NFC (r = −0.33). Samples with higher BA levels have higher pH, ammCP, and ADF levels and lower LA and NFC levels. Terminal pH was highly correlated ($P < 0.0001$) with LA (r = −0.62), ammCP (r = 0.50), ligninNDF (r = 0.40), ash (r = 0.35). LA accounts for 38% of the variation of pH. LA levels were highly correlated ($P < 0.0001$) with ammCP (r = −0.37), ADF (r = 0.38) and NFC (r = 0.34). Ammonia (ammCP) is correlated with all factors associated with BA possibly due to the proteolytic activity of clostridia organisms responsible for BA production. Across all DM levels, BA is prevalent when pH is not reduced; however, there is an interaction of DM level and pH level necessary to inhibit BA production.

Key Words: silage, butyric acid

W124 Environmental factors affecting changes in dry matter content of corn planted for summer or fall silage harvest in a subtropical climate. J. K. Bernard*[1], B. T. Scully[2], and J. S. Barlow[1], [1]*University of Georgia*, *Tifton,* [2]*USDA-ARS*, *Tifton, GA*.

A 3-yr trial was conducted to determine the environmental factors related to changes in the dry matter (DM) content of temperate corn (*Zea mays*) planted for summer or fall harvest as silage in a subtropical climate. Corn was planted in late March or early April (Pioneer 31Y42 and Masters Choice 590) for July harvest followed by a second crop planted in July (AgraTech 760 and Pioneer 33M52) for harvest in late October. When corn reached half-milk line stage of maturity, 3 replicate plots of corn plants were hand harvested every hour from 0600 through 1800 h. The corn plants were chopped using a field chopper to 1.9 cm theoretical chop length. A subsample of the chopped material was dried in a forced air oven for 60 h at 55°C to determine the DM content. Environmental temperature and relative humidity (RH) were continuously measured inside (IN) and outside (OUT) of the corn canopy. During the summer, the DM content increased 1.7% after 0900 and increased linearly throughout the remainder of the day. In the fall, the DM content increased 1.5% after 1000 and 1.7% after 1200 before peaking at 1500 and then declining. Temperature-humidity index (THI), THI^2, and RH^2 were computed for use in the statistical analysis. The RH ($P = 0.02$) and RH^2 ($P < 0.01$) measured IN were negatively correlated with DM content across both seasons. During the summer, the DM content was negatively correlated ($P < 0.02$) with RH and RH^2 measured IN and OUT and positively correlated ($P < 0.01$) with temperature, THI, and THI^2 IN and OUT. However, only RH and RH^2 measured IN were negatively correlated ($P < 0.05$) with DM content in the fall. Stepwise regression analysis of data was conducted across seasons as well as within season. Across seasons, the final equation was $\%DM = 32.49 - 0.001RH^2(IN) + 4.884THI(IN) - 0.026THI^2(IN) + 0.107RH(OUT) - 4.859THI(OUT) + 0.026THI^2(OUT)$ ($R^2 = 0.50$, $P < 0.0001$). Results of this trial indicate that the DM content of the whole corn plant changes differently in the summer compared with fall, primarily in response to changes in the RH inside the canopy.

Key Words: corn silage, DM content, drying rate

W125 Relationship of vomitoxin levels in corn silage to in vitro dry matter digestibility. R. Ward[1] and R. A. Patton*[2], [1]*Cumberland Valley Analytical*, *Maugansville, MD*, [2]*Nittany Dairy Nutrition*, *Mifflinburg, PA*.

There is increasing awareness of the damage that can be caused by Fusarium mycotoxin ingestion by dairy cattle. One reason for detected mycotoxins may be greater usage of BMR corn silage varieties. It is hypothesized higher digestibility may result in greater susceptibility to corn plant molds. Vomitoxin (DON) has often been used as a marker for contamination by Fusarium mold species. To investigate this, a data set composed of all corn silages submitted to Cumberland Valley Analytical Services for DON analyses was prepared. There were 1948 silages in the data set with 185 being identified as BMR varieties; 1068 were confirmed positive to DON. DON was measured using HPLC at 220 nm UV detection. Limit of detection was 0.5 ppm. Assessment of differences for levels of DON between silage types was by Proc Mixed of SAS. Incidence of infection was investigated using logistic regression. Samples identified as BMR had 1.135 ppm of DON and normal contained 1.295 ppm ($P = 0.24$). When non-positive samples were excluded, BMR contained 2.386 ppm (n = 155) and normal silage 2.303 ppm DON (n = 913;$P = 0.72$). Of BMR samples submitted, 83.8% were positive, but only 51.8% for normal silage. Logistic regression found that BMR was 1.419 times more likely to be infected than normal corn silage ($P < 0.004$). Caution should be applied to these statistics as these samples were screened as having problems and are not random. To further investigate the influence of NDF digestibility (NDFd) on DON levels, groups were constructed based on the following scheme: (1) >65% NDFd; (2) 60–64.99%; (3) 55–59.99%; (4) 50–54.99%; (5) 45–49.99; (6) <45%. Mean DON levels for the groups are (1) 1.177 ppm, (2) 1.140 ppm, (3) 1.215 ppm, (4) 1.470 ppm, (5) 2.022 ppm, and (6) 0.982 ppm. Only group 5 was significantly different from the others ($P < 0.05$), although group 2 tended to be lower than groups 3 and 4 also ($P < 0.10$). We conclude that although BMR corn silage may have a higher incidence of DON than normal corn silage, levels of infection are not different, and it would not be due to differences in NDFd. Further work will be needed on a random basis to verify the infective rate of BMR corn.

Key Words: DON, mycotoxins, corn silage

W126 Fermentation and ruminal degradability of corn silage inoculated with *Lactobacillus buchneri*. F. C. Basso[1], R. A. Reis*[1], D. M. Figueiredo[1], D. A. Mota[2], K. A. Magalhães[1], T. F. Bernardes[3], and J. F. H. Rodrigues[1], [1]*UNESP/FCAV*, *Jaboticabal, São Paulo, Brazil*, [2]*UFAM*, *Parintins, Amazonas, Brazil*, [3]*UFRA*, *Pará, Belém, Brazil*.

The aim of this trial was to evaluate the effect of *L. buchneri* doses on fermentation and ruminal degradability of corn silage. *L. buchneri* (NCIMB 40788) was applied to corn hybrid Maximus at: SLB - control (not inoculated); LB1 – 5×10^4, LB2 - 1×10^5, LB3 - 5×10^5, LB4 - $1 \times$

10^6 CFU/g of forage. Four plastic buckets (7 L) per treatment were filled with 4 kg of treated corn, sealed and stored at room temperature. After 130 d of fermentation, buckets were opened, spoiled forage discarded and the remainder was homogenized and placed in plastic buckets, and maintained in a closed room at room temperature. For determination of aerobic stability (AS) the silage temperature was measured every half hour by a data logger during the aerobic exposition (288 h) and room temperature was measured by data logger distributed near the buckets. Samples were collected to evaluate dry matter content (DM), pH values, acetic acid concentration (%DM), lactic acid (%DM), counting of yeasts and molds (Log CFU/g) in potato dextrose agar and ruminal degradability (measured by in situ procedure by 48 h). Nylon bags (9 x14 cm) with a pore size of 40μm were filled with 5 g of DM of silage samples. The statistical analysis included one-way ANOVA and Tukey's test ($P < 0.05$). The DM content was higher in the SLB and LB1 treatments ($P < 0.05$). The pH value, lactic acid (%DM) and molds did not differ significantly among silages. Acetic acid concentrations were higher in treated silages ($P < 0.05$). The number of yeast was lower in the silages with *L. buchneri* ($P < 0.05$). Aerobic stability of corn silage increased with *L. buchneri* ($P < 0.05$). The inoculant did not affect the ruminal degradability (%DM) of corn silages ($P < 0.05$). All doses reduced yeasts and improved aerobic stability.

Table 1. Fermentation, microbial dynamic and ruminal degradability of corn silage with *L. buchneri*

Treatments	DM	pH	Acetic Acid	Lactic Acid	Yeasts	Molds	AS	Degradability
SLB	32.04a	3.9a	0.80b	6.62a	4.71a	3.71a	46.3b	59.23a
LB1	32.03a	4.0a	1.06ab	6.7a	1.71b	2.97a	154.9a	58.45a
LB2	29.03b	3.95a	1.24a	6.5a	1.7b	2.45a	151.7a	55.83a
LB3	29.08b	4.0a	1.18a	6.88a	1.25b	2.97a	223.9a	55.92a
LB4	29.62b	4.0a	1.34a	6.47a	2.31b	2.69a	165.2a	57.5a
CV (%)	2.67	1.45	16.73	20.33	32.78	32.43	8.81	4.91

Means followed by equal letters are not different by Tukey test ($P>0.05$).

Key Words: heterofermentative bacteria, microbial dynamics, yeasts

W127 Dispersion of an inert marker in water on freshly chopped whole plant corn by two methods to simulate addition of an inoculant. J. M. Lim*, M. C. Santos, J. P. Rigueira, M. C. Der Bedrosian, and L. Kung Jr., *University of Delaware*, *Newark*.

Silage inoculants are often added in a liquid form to the forage mass at harvest. A common method of application is to add the inoculant with a sprayer system at the chopper in the field. Applying the inoculant via a "shower" method to the top of a forage mass in a forage truck or wagon is also practiced. Even distribution of an inoculant using the shower method has been questioned. Thus, the objective of this study was study the distribution of an inert marker applied to harvested whole plant corn using 2 methods. Forage was either 1) untreated (C) or treated with water containing dysprosium chloride (DY) via a 2) shower method (SHO), or 3) a spray (SPR) method. Dysprosium was applied to achieve a target of 2 ppm/kg of forage DM for treatments 2 and 3. Treatment via SHO was by manually pouring water with DY on the top surface of a forage in truck (7.25 t of wet forage) with a surface dimension of 5 × 2.7 m (length × width). For SPR, water was applied via a conventional sprayer system at the chopper. Application of water in both methods was set to achieve 2.2 L of water/t of wet forage. For all treatments forage was unloaded at the silo and spread and packed over a surface of about 13 × 6 m (length × width) in the bunker silo. Treatments were replicated twice with 9 samples randomly collected after packing. Control samples were collected from forage loads that were untreated. The concentration of DY in forage samples was determined using inductively coupled plasma spectrometry. Recovery of elemental DY in a spiked forage sample was 97 ± 2%. The concentrations of DY differed among treatments and were 0.09 ± 0.21, 0.47 ± 0.50 and 2.1 ± 0.66 ppm/kg of forage DM for C, SHO, and SPR respectively ($P < 0.0001$). The average concentration of DY for SPR was closer to the theoretical target (2 ppm/kg) and was less variable (CV of 31 vs. 106%) than for SHO. The results of this study suggest that distribution of an inoculant in water has the potential for better distribution if it is applied at the chopper compared with a shower method on the forage truck.

Key Words: silage, inoculant

W128 Treating first-cutting alfalfa in Michigan with Silo-King reduces heating during the ensiling process. D. P. Casper, G. P. Gengelbach*, M. E. Donaldson, D. F. Jones, D. H. Kleinschmit, K. E. Lanka, and D. J. Schauff, *Agri-King, Inc.*, *Fulton, IL*.

The generation of heat through the oxidation of carbohydrates during the ensiling process can dramatically affect forage quality. A field survey evaluated the post-ensiling temperature rise of 1st cutting alfalfa ensiled in bunker silos during 4 crop years (2005, 2006, 2008, and 2009) in Michigan. Bunker temperatures were measured once weekly for 4 weeks following ensiling using a 51-cm compost thermometer. Treatments were untreated Control (CON), competitor inoculant currently used by producer (COMP) or Silo-King (SK). The number of bunkers sampled, by treatment, for each year was: 2005 (9, 0, 11), 2006 (7, 7, 16), 2008 (21, 11, 11), and 2009 (27, 29, 18) for CON, COMP, and SK, respectively. The highest temperature recorded in the weeks post-ensiling was considered the peak temperature (PT). Data on PT were analyzed using a completely randomized design having a factorial arrangement of treatments using the PROC MIXED procedure of SAS. The interaction of Treatment by Year was non-significant ($P > 0.10$), so data were pooled and analyzed for the main effects of Treatment and Year. The lowest PT ($P < 0.01$) were for alfalfa bunkers treated with SK (42.4, 40.6, and 32.5°C, for CON, COMP, and SK, respectively) compared with CON and COMP treated bunkers, which were similar. The PT for bunkers varied across Year with 2005 and 2009 being similar ($P > 0.10$) and the highest, 2006 intermediate and 2008 being the lowest ($P < 0.06$) (40.4, 37.6, 36.8, and 39.2°C for 2005, 2006, 2008, and 2009, respectively). The rise in PT that normally occurs during the ensiling of 1st cutting alfalfa in bunkers can be prevented by treating the forage with Silo-King. Over the years, Silo-King performance was consistent and repeatable in reducing the PT of bunkers through inhibiting heat generation by preventing the oxidation of carbohydrates by plant respiration and spoilage organisms during the ensiling process.

Key Words: alfalfa silage, silage inoculant, silo heating

W129 Effect of harvest moisture, bale wrapping, and an organic acid on forage quality in grass. E. Allen*, K. Martinson, and C. Sheaffer, *University of Minnesota-Twin Cities*, *St. Paul*.

The relationship between forage moisture at baling and chemical composition has not been evaluated in grass hay intended for equine feed. Mold in hay is a serious risk and is known to cause respiratory problems in horses. The objective was to determine the relationship between moisture at time of baling, wrapping, and the application of an organic acid preservative on forage quality and mold growth in grass hay. Thirty-six 1.2 × 1.5 m first cutting orchardgrass round bales were randomized in a complete block design using 4 replicates of 3 target moistures: < 150

g/kg (LM), 200–250 g/kg (MM), and 300–350 g/kg (HM) (wet basis). In field bale moisture was estimated with a bale moisture probe. At baling, a commercially available organic acid hay preservative (Fresh CUT Plus) was applied at 4.5 kg/ton to bales containing MM and HM. After baling, bales were cored and samples were analyzed for chemical composition. Four LM (without preservative), 8 MM (4 with and 4 without preservative) and 4 HM (without preservative) moisture bales were individually wrapped with 6 mils of plastic. After 10 weeks, cores were taken on each bale to determine forage quality and mold counts. Data was analyzed using Proc Mix in SAS and mold counts were log-transformed. Actual moistures for hay baled at the targets of LM, MM, and HM averaged 120, 200, and 260 g/kg respectively. After 10 weeks, moisture content of MM and HM wrapped bales were maintained, while moisture of unwrapped bales decreased to 130 and 180 g/kg, respectively ($P = 0.01$). For all treatments, no changes over time were observed for CP (90 g/kg), ADF (390 g/kg), NDF (590 g/kg), and DE (2.04 Mcal/kg). For MM and HM, wrapping reduced ($P < 0.001$) mold growth (1,700 and 5,700 cfu/g, respectively) compared with no wrapping (4 million and 3 million cfu/g, respectively). The preservative did not reduce or inhibit mold growth at any moisture. Reducing mold growth and maintaining forage quality was achieved by baling dry hay (<150 g/kg moisture) and wrapping wet hay (200–350 g/kg moisture).

Key Words: harvest moisture, bale wrapping, organic acid

W130 Effects of sulfite-based preservatives on preservation and aerobic stability of alfalfa haylage and corn silage. C. J. Fu*, T. W. Clark, and D. V. Dhuyvetter, *Ridley Nutrition Solutions, Ridley Inc.*, *Mankato, MN*.

Experiments were conducted to determine the effects of forage preservatives on alfalfa (*Medicago* L.) haylage and corn (*Zea mays* L.) silage preservation and aerobic stability. Preservatives included sulfite-based commercialized and experimental products in liquid and dry forms. Experiments included laboratory and field trials of varying size that included 18-L pail and 20-ton bag testing. All experiments were completely randomized experimental design with 2 to 4 replications. Products were applied according to the label instruction and the same rates were applied for experimental products. For laboratory trials, whole plant corn at 40% DM with about 19 mm cut and first cutting alfalfa at 50%DM with 13 mm cut were harvested with a convention pull-type harvester. The packing density was 0.2 Kg DM per liter. For the field trial, first cutting alfalfa at 30% DM with 13 mm cut was harvested with the same type harvester and packed in 2.74 m wide Ag-Bag(Ag-Bag International Ltd.). Treatments included control (CONT) carrier only, liquid preservative (LIQP), bunk stabilizer dry form (STAD), experimental liquid preservative (EXPL), and experimental bunk stabilizer dry form (EXSTA). The mini-silo haylage test showed that EXPL significantly increased the lactic acid percentage of total VFA compared with CONT and LIQP, and showed a 5 to 10 times reduction in yeast and mold count ($P < 0.05$). The 82 d bag haylage test indicated that EXPL increased DM recovery from 93% to 98% ($P < 0.05$) compared with CONT. Laboratory aerobic stability tests of corn silage showed EXSTA held temperature lower by 11 to 16°C compared with CONT and STAD ($P < 0.05$) either at ambient (21°C) or warmer (27 to 35°C) temperatures. Furthermore, EXSTA reduced yeast and mold counts by 100 to 1000 times compared with those of STAD and CONT, respectively ($P < 0.01$). From these experiments, it can be concluded that EXPL and EXSTA have potential to improve alfalfa haylage and corn silage preservation in addition to bunk stability.

Key Words: alfalfa haylage, corn silage, preservatives

W131 Effect of alfalfa entries selected to tolerate agricultural machinery traffic on forage yield and regrowth. J. Santillano-Cázares*[1] and J. L. Caddel[2], [1]*Universidad Autónoma de Baja California*, *Mexicali, Baja California, México*, [2]*Oklahoma State University*, *Stillwater*.

It has been suggested that wheel traffic reduces alfalfa (*Medicago sativa* L.) yields and stand persistence. Thus, efforts have been made to select alfalfa cultivars to tolerate wheel traffic. The objective of this research was to determine if selected alfalfa entries out produced forage yields and regrowth rate non traffic-selected entries. The experiment was conducted on one of Oklahoma State University's experimental stations, in Stillwater, OK. Soil textures in the station were sandy-loam and loam. Twenty alfalfa entries were planted at 20 kg ha-1 on March 2002. The alfalfa entries tested included commercial varieties and experimental lines. Alfalfa entries included alfalfas selected for wheel traffic tolerance and not selected for wheel traffic tolerance. Entries were subjected to either traffic or no traffic. Traffic treatment was applied by driving the front and rear tires with a 100 horse power tractor over the plots during 3 years, 5 d after each harvest. The treatment structure was a 2 × 20 factorial and treatments were assigned by using a RCBD in a split-plot design structure, with 6 replications. Main plots were the traffic treatments and subplots were the alfalfa varieties. Plot size was 1 × 5 m (5 m^2) and the size of the sampling area was 0.6 × 5 m (3 m^2). Forage yields were measured in 2002, 2003, and 2004 from 1 × 5 m (5 m^2) plots. Regrowth was estimated only in the first harvest year of the study (2002) by measuring stem height from soil level to the tips of the stems, 5 d after harvest. The alfalfa entry × wheel traffic interaction was not significant ($P > 0.05$) for forage yields or regrowth rate. No interaction indicates that the selected entries were injured about the same as the normal entries (without selection) when driven on 5 d after harvests. It was concluded that under the actual environmental and management conditions of this study, alfalfa selection for traffic tolerance was ineffective. However, it clearly demonstrated that wheel traffic reduced alfalfa yields and should be avoided when possible.

Key Words: wheel traffic, alfalfa selection, yield

W132 Influence of maturity on leaf fiber and protein fractions of different alfalfa varieties. A. Palmonari*, M. Fustini, G. Canestrari, G. Biagi, and A. Formigoni, *Università di Bologna*, *Bologna, Italy*.

Impact of leaves on the hole plant fibrous and protein fractions in alfalfa is usually affected by harvesting systems and the preference for forage quantitative production.
Leaves are very rich in nitrogen and protein, being active in photosynthesis. On the other hand, leaves are more subject to the co-association between lignification and decreased amount of protein and soluble carbohydrates. Aim of this study was to determine how plant maturity influences fibrous and protein fraction in alfalfa leaves. Four alfalfa varieties (P, M, L, BC) were collected at three different stages of maturity (10, 20, and 30 d of age). All samples were collected using scissors, trying to preserve the integrity of the hole plant. After drying at 65°C, leaves were separated from stalks, ground, and analyzed chemically for NDF, ADF, ADL, CP, SolP, NPN, and NDIP. Data were analyzed using two-way ANOVA with alfalfa variety and time as the main effects. From Day 10 to Day 30, NDF decreased from 24.1 to 23.1%, while ADF and ADL increased from 16.2 to 18.0% and from 5.7 to 7.8%, respectively ($P < 0.01$). Among tested varieties, P contained ($P < 0.01$) less ADL (5.2 vs. 6.8, 6.9, and 7.7% for M, L, and BC, respectively) and ADF (15.7 vs. 17.6, 17.1, and 18.1% for M, L, and BC, respectively) and more NDF (24.4 vs. 23.5, 22.8, and 23.3% for M, L, and BC, respectively).

Average values of CP, SolP, NPN, and NDIP in alfalfa leaves were 28.8, 10.4, 9.7, and 28.3%, respectively. As expected, from Day 10 to Day 30, CP (−29%), SolP (−38%), NPN (−42%), and NDIP (−21%) decreased ($P < 0.01$). Variety of alfalfa had no significant effect on leaf protein content. These data suggest that maturity strongly influences the composition of alfalfa leaves. In conclusion, this study produces evidence that maturity increases ADL and reduces protein in leaves, thus reducing their nutritional value. Interestingly, maturity had no effect on ADF content of P leaves, suggesting a higher nutritional value of this variety.

Key Words: alfalfa leaves, maturity, chemical composition

W133 Effect of a bacterial inoculant on the quality of and nutrient losses from corn silage produced in farm-scale silos. O. C. M. Queiroz*[1], A. T. Adesogan[1], K. G. Arriola[1], and M. F. Queiroz[2], [1]*Department of Animal Sciences, University of Florida*, *Gainesville,* [2]*Department of Animal Sciences, UNESP*, *Jaboticabal, SP, Brazil*.

This project aimed to determine effects of applying an inoculant containing homofermentative and heterofermentative bacteria on the fermentation and aerobic stability of and nutrient losses from corn silage produced in farm-scale silos. Corn forage was harvested at 34% DM, treated without (Control) or with 1 × 106 cfu/g of *Lactobacillus buchneri* and *Pediococcus pentosaceus*, packed (45 tons) in quadruplicate into 3.7-m-wide Ag bags, and ensiled for 166 d. Silage removed from the bags (500 kg/d) was separated into spoiled (visibly darker, heating or moldy) and good portions and weighed for 35 d. Weekly composites were analyzed for chemical composition, aerobic stability (time to 2°C above ambient temperature) and fungal counts. The experiment had a completely randomized design. Data were analyzed with a model including treatment, time, and the interaction. Inoculation did not affect the chemical composition of the spoiled or good silage but decreased the quantity (5.7 vs. 12.9 kg/d; $P = 0.002$) and percentage (3.4 vs. 7.8; $P = 0.004$) of spoiled silage by over 50%. Losses of CP (0.23 vs. 0.92 kg/d; $P = 0.03$), gross energy (433 vs. 1842 kcal/d; $P = 0.02$), and NDF (1.34 vs. 4.12 kg/d; $P = 0.04$) in spoiled silage were less in inoculated versus Control silages. Inoculated silages had a lower pH (3.91 vs. 3.99; $P = 0.01$), lactate concentration (0.69 vs. 0.86%; $P = 0.04$), lactate: acetate ratio (0.61 vs. 1.41%; $P = 0.04$) and a greater acetate (1.15 vs. 0.73%; $P = 0.04$) concentration than the Control silage. Inoculated silages tended to have fewer yeasts (2.59 vs. 4.62, log cfu/g; $P = 0.07$) than Control silages, but aerobic stability did not differ (14.7 vs. 9.5 h; $P = 0.71$). The inoculant inhibited the growth of yeasts and substantially reduced the amount of spoilage and the associated energy and nutrient losses.

Key Words: *Lactobacillus buchneri*, *Pediococcus pentosaceus*, inoculant

W134 Changes in cell wall fractions and in vitro dry matter digestibility, of corn silage associated with additives. R. H. de Tonissi e Buschinelli Goes*, K. A. de Souza, K. A. G. Nogueira, D. de Faria Pereira, T. da Cunha Cornélio, M. G. de Menezes Gressler, E. R. de Oliveira, and K. C. da Silva Brabes, *Universidade Federal da Grande Dourados*, *Dourados, MS, Brasil*.

Corn plant, cut at 90 d after planting, was ensiled in 72 experimental silos in a completely randomized design, in a factorial square 4 × 6 (4 treatments and 6 d opening) with 3 replicates; and the averages compared by Tukey test at 5% probability, for evaluate the changes in cell wall fractions and in vitro dry matter digestibility (DMD) of corn silage associated with additives. The corn silage was associated with additive at 5% in natural matter, and the treatments were: soybean hulls (CS+5%SH), rice meal (CP+5%RM) and sunflower crushed (CS+5%SC). The control was composed of 100% of the corn plant (CS). The silos were opened 0, 28, 56, 84, 112 and 140 d. The pH showed ($P < 0.05$) reduction from 28 d of fermentation, with 112 d to the lowest value (3.39). All additives were able to reach a pH favorable to preservation of forages. There was a significant effect ($P < 0.05$) for inclusion of additives and time of opening, where the NDF decreased in their levels. The lower values of NDF occurred at 112 d (63.02, 65.46, 57.83 and 60.98% for CS, CS+5%SH, CS+5%RM and CS+5%SC, respectively). Reduction of NDF indicates the solubilization of the wall cell. There was effect ($P < 0.05$) of time of ensiling for hemicellulose (HCEL), and ADF. The HCEL reduced when increases the time of silage, no difference between the opening d 0 to 112; with average of 29.36%. ADF reduced to the extent until at 140 d, with value of 34.9%. Lignin and cellulose had effect for addition of additive ($P < 0.05$), where the addition of soybean hulls, rice meal and sunflower crushed reduced the lignin content of corn silage, averaging 10.6, 8.7 and 11.0%, respectively. The lignin content of corn silage was 12.2%. The addition of soybean hulls increased the cellulose content of silage, while the levels for CS, CS+5%RM and CS+5%SC, were 26.4, 24.3, 24.8%. DMD ($P < 0.05$), improved after 84 d of ensiling, with values of 69.3%. The DMD for day zero was 62.9%. The addition of 5% of additives changes the composition of the cell wall of corn silage. The in vitro digestibility of dry matter increased according to the time of ensiling.

Key Words: sunflower crushed, rice meal, soybean hulls

W135 Effect of oxygen barrier film on the storage temperature and top losses of corn silage in stack silo. F. C. Basso[1], R. A. Reis*[1], T. F. Bernardes[2], E. C. Lara[1], F. B. Assis[1], M. Nogueira[1], and A. P. T. P. Roth[1], [1]*UNESP/FCAV*, *Jaboticabal, São Paulo, Brazil*, [2]*UFRA*, *Bélem, Pára, Brazil*.

The aim this trial was to study the effect of the oxygen barrier film on the storage temperature and top losses of corn silage in stack silo. One trial was carried out on 1 commercial farm in Jaboticabal, Brazil, in 2009. Whole-corn crops were harvested at around the 50% milk-line stage and ensiled in stack silo. The covering treatments were: a sheet of 200-µm-thick black-on-white polyethylene film (ST) and a sheet of 45-µm-thick transparent oxygen barrier film (OB) plus a sheet of ST over the OB film. The stack silo was divided in 2 parts along the length: half was covered with ST film and half with OB plus ST film. Both films were secured with soil around the silo. During silo filling, 20 bags (10 for each treatment) containing 3.5 kg of herbage and one data logger were buried at the peripheral zone (15 cm of depth) of the silo to determine storage temperature and top losses of silage during the conservation period. After 45 d of fermentation, the bags were removed during feedout. The bags were weighed to determine dry matter (DM) losses. The DM content, number of yeasts and molds and pH value were measured. The storage temperature of corn silage under OB film always was lower than under ST film after 13 d of fermentation. The storage temperature was lower in corn silage under OB film until 5.1°C. The DM content was 25.86% in corn silage covered with ST film and 27.31% in corn silage under OB film ($P < 0.05$). The corn silage under the OB film had fewer molds compared with the silage under the ST film (3.93 vs. 4.61 Log_{10} CFU/g, respectively - $P < 0.05$). The number of yeasts (5.27 Log_{10} CFU/g under OB film vs. 5.93 Log_{10} CFU/g under ST film) and pH value (4.09 under OB film vs. 4.07 under ST film) did not differ ($P > 0.05$) between silages. The DM losses were 7.39% in silage covered with OB film, while in corn silage under ST film the DM losses were 10.18%, but this difference was not significant ($P >$

0.05). Oxygen barrier film plus polyethylene film reduced the storage temperature and the number of molds.

Key Words: polyethylene film, polyamide film, aerobic stability

W136 Effects of microbial inoculant on fermentation, microbial dynamics and aerobic stability of corn silage. F. C. Basso[1], R. A. Reis*[1], E. C. Lara[1], F. B. Assis[1], M. Nogueira[1], A. P. T. P. Roth[1], and T. F. Bernardes[2], [1]*UNESP/FCAV*, *Jaboticabal, São Paulo, Brazil*, [2]*UFRA*, *Bélem, Pára, Brazil*.

The aim of this trial was to evaluate the effects of microbial inoculant on fermentation, microbial dynamics and aerobic stability of corn silage. Whole-plant corn (350 g/kg) was ensiled in quadruplicate laboratory silos (7L) after the following treatments: untreated (control), *Lactobacillus buchneri* NCIMB 40788 (LB - 1×10^5 CFU/g of fresh forage), *Bacillus subtilis* (BS - 1×10^5 CFU/g of fresh forage), *Propionibacterium acidicipropionici* MA26/4U (PA - 1×10^5 CFU/g of fresh forage), *Lactobacillus plantarum* MA18/5U (LP - 1×10^5 CFU/g of fresh forage), *L. buchneri* plus *L. plantarum* (LBLP), *B. subtilis* plus *L. plantarum* (BSLP) and *P. acidicipropionici* plus *L. plantarum* (PALP). After 96 d of ensilage, silos were opened, spolied forage discarded and the remainder was homogenized and placed in plastic buckets and maintained in a closed place at room temperature. To determine aerobic stability (AS), silage temperature was measured every half hour by a data logger inserted in the center of mass during the aerobic exposure and room temperature (average 24°C) was measured by data logger placed near the experimental silos. Dry matter content (DM), pH value, ammonia nitrogen (NH3/TN) content and yeasts and molds counts (Log CFU/g) in potato dextrose agar were measured. The statistical analysis included one-way ANOVA and Tukey's test ($P < 0.05$). The DM, NH3/TN and molds counts were not different among treatments. The pH value was lower in silages without inoculant and with *P. acidicipropionici* ($P < 0.05$). The corn silage with *L. buchneri*, *L. buchneri* plus *L. plantarum*, *B. subtilis* and *P. acidicipropionici* had lower number yeasts and improved aerobic stability ($P < 0.05$). The microbial inoculant with heterofermentative bacteria and the association between *L. buchneri* plus *L. plantarum* is effective in decreasing the numbers of yeasts and improves the aerobic stability of corn silage.

Table 1. Fermentation, microbial dynamic and aerobic stability of corn silage with microbial inoculant.

Treatments	DM	pH	NH3/NT	Yeasts	Molds	AS
Control	34.92	3.81b	5.17	3.99a	3.80	23.33d
LB	34.11	3.87ab	5.02	1.25b	3.85	100.42a
BS	34.32	3.86ab	4.85	1.0b	4.0	78.42abc
PA	33.91	3.81b	4.9	2.39ab	3.55	70.25bc
LP	34.05	3.87ab	5.56	3.86a	3.8	54.75c
LBLP	34.46	3.89a	5.52	2.58ab	3.65	87.08ab
BSLP	35.06	3.83ab	5.03	3.34a	4.37	52.67c
PALP	35.58	3.85ab	4.64	3.89a	3.57	58.75c

Means followed by equal letters do not differ by Tukey test ($P>0.05$).

Key Words: heterofermentative bacteria, homofermentative bacteria, *Lactobacillus buchneri*

W137 In vitro gas production and microbial protein synthesis in alfalfa-timothy mixtures. F. Hassanat*[1], G. Tremblay[2], G. Allard[3], G. Bélanger[2], A. Bertrand[2], Y. Castonguay[2], R. Michaud[2], and R. Berthiaume[1], [1]*Agriculture and Agri-Food Canada*, *Sherbrooke, Qc, Canada*, [2]*Agriculture and Agri-Food Canada*, *Quebec, Qc, Canada*, [3]*Faculté des sciences de l'agriculture et de l'alimentation, Université Laval*, *Quebec, Qc, Canada*.

Forage diets containing an optimal balance between crude protein (CP) and nonstructural carbohydrates (NSC) sources maximize microbial protein (MP) yield and minimize NH_3 output, which would improve metabolizable protein availability to animals. Impact of increasing the ratio of NSC:CP on in vitro gas production (IVGP) and MP yield was investigated by increasing the proportion of grass in legume:grass mixtures. In a completely randomized block design, triplicates of alfalfa:timothy mixtures of 100:0, 75:25, 50:50, and 25:75 (DM basis) were incubated for 24h using ANKOM^{RF} gas production monitoring system in separate days. Gas production data were fitted to a Michaelis-Menten model to estimate gas production parameters. Incubation residues were refluxed with neutral detergent fiber (NDF) solution to isolate MP from undegradable residues. Linear ($P_{lin.}$) and quadratic ($P_{quad.}$) components of the effects of treatments were determined. Increasing timothy proportion linearly increased NSC and NDF but reduced CP concentration; maximum changes with highest timothy proportion compared with alfalfa alone were +44% for NSC, +49% for NDF, and −48% for CP. These changes increased IVGP from 308 to 352 mL gas g^{-1} OM ($P_{lin.} < 0.01$), increased time to ferment 50, 75 and 90% of the substrate ($P_{quad.} < 0.05$) and reduced maximal degradation rate from 0.18 to 0.16% h^{-1} ($P_{lin.} < 0.01$). In vitro true dry matter degradability was highest for alfalfa alone and decreased ($P_{lin.} < 0.01$) as timothy proportion increased. The amount of substrate available to rumen microbes was therefore reduced when the proportion of timothy increased which in turn reduced MP yield ($P_{lin.} < 0.05$). However, when expressed on a CP basis, MP yield increased ($P_{quad.} < 0.05$) with increasing timothy proportion. The reduction of NH_3 concentration ($P_{lin.} < 0.01$) with increasing timothy proportion suggests that the dietary protein was utilized more efficiently for MP synthesis. Although MP yield per g dry matter was highest for alfalfa alone, the 25:75 alfalfa:timothy mixture supplied the best NSC:CP ratio for efficient in vitro MP synthesis.

Key Words: in vitro gas production, forage mixture, microbial protein

W138 Prediction of Tanzânia grass dry mass production using agrometereological parameters. L. C. Araujo*[1], P. M. Santos[2], J. R. Pezzopane[2], and P. G. da Cruz[1], [1]*"Luiz de Queiroz" College of Agriculture/USP*, *Piracicaba, São Paulo, Brazil*, [2]*Embrapa Southeast Cattle*, *São Carlos, São Paulo, Brazil*.

Mathematical models that predict the effect of climatic variables over forage production may be used as a decision support toll on farms. The objective of this study was to determine the effect of climatic events on *Panicum maximum* cv. Tanzânia (Tanzânia grass) production and parameterize models to predict forage accumulation rate. Tanzânia grass was cultivated in São Carlos, SP, Brazil (21°57′42″ S, 47°50′28″ W, altitude 860 m). Pastures were fertilized during the raining season and rotationally grazed all around the year. Data from 53 periods of pasture growth, between 1999 and 2005, were used to verify its relation with climatic variables. Daily temperature (maximum, minimum and mean), rain and solar radiation were monitored. Growing degrees days was calculated considering 17°C as lower basal temperature. Potential evapotranspiration (Eto) and actual evapotranspiration (Eta) were calculated based on water balance for every 5 d. Growth index (GI) was calculated using minimum temperature, solar radiation and the relationship between Eta/Eto. To estimate the effect of water availability on forage production, the relationship between Eta and Eto was used as a factor to penalize the accumulation of energy, measured as growing degree days or solar radia-

tion. Linear and exponential regression analysis was done to determine the relationship between forage accumulation rate (dependent variable) and climatic parameters (independent variable). Results confirm that herbage accumulation rate depends on climatic variables. The coefficient of determination was higher when both energy and water availability was considered on the model: Eta (R^2 = 0.85), growing degree days corrected by Eta/Eto (R^2 = 0.83) and GI (R^2 = 0.81). It was concluded that Eta, growing degree days corrected by Eta/Eto and GI may be used to predict Tanzânia grass herbage accumulation rate when climate is the major limitation factor for forage production.
Supported by FAPESP.

Key Words: mathematical models, tropical grass, weather

W139 Effects of chemical additives on the ensilage of sugarcane. A. F. Pedroso*, W. Barioni Jr., G. B. Souza, and V. R. Del Santo, *Brazilian Agricultural Research Corporation - Embrapa*, *São Carlos, SP, Brazil*.

The objective was to evaluate efficacy of chemical additives at controlling alcoholic fermentation and DM losses and increasing aerobic stability (AE) of sugarcane silages. Mechanically harvested sugarcane (12 mo old; 22° Brix; DM: 330 g/kg) was ensiled in 15 × 30 cm PVC tubes (4 replicates/treatment). Nine treatments were applied to the forage at ensiling (fresh basis): untreated - Control; urea (5 g/kg) + sodium benzoate (0.5 g/kg) - UB1; urea (7.5 g/kg) + benzoate (0.5 g/kg) - UB2; urea (5 g/kg) + benzoate (0.75 g/kg) - UB3; urea (7.5 g/kg) + benzoate (0.75 g/kg) - UB4; sodium propionate at rates of 1, 2 and 4 g/kg - PROP1, PROP2 and PROP3, respectively; calcium hydroxide (10 g/kg) - CA. Additives were applied in aqueous solutions. Minisilos were weighed and sampled on d 0 and 78 d after ensiling. Dry matter loss (DML) was calculated and aerobic stability was defined as the time (h) that elapsed before the temperature of aerated silages exceeded room temperature by 2°C. Data were analyzed as a completely randomized design and differences among means were tested using *t*-test. Control silage presented characteristic high ethanol content, high DML and poor AE (Table 1). Silage treated with CA had 90% less ethanol and 69% lower DML relative to control ($P < 0.05$). Ethanol content and DML did not differ ($P > 0.05$) between the lowest doses of urea + benzoate (UB1) and CA and higher doses of urea and benzoate (UB2, UB3, UB4) were not more effective than UB1. Among propionate treatments, only PROP3 reduced ($P < 0.05$) simultaneously ethanol content and DML in the silage compared with control (64% and 76% less, respectively). Only CA improved ($P < 0.05$) silage AE compared with control. pH values differed among treatments but all values indicated adequate conservation.

Table 1. Fermentation parameters and aerobic stability of experimental silages

Treatment[1]	pH	Ethanol (g/kg DM)	DM loss (g/kg DM)	Aerobic stability (h)
Control	3.50^{e}	76.2^{ab}	188^{a}	40^{bc}
UB1	3.64^{cd}	26.5^{cd}	88^{cd}	41^{bc}
UB2	3.73^{b}	34.7^{c}	77de	34^{c}
UB3	3.69^{bc}	29.6^{c}	115^{bc}	48^{ab}
UB4	3.70^{b}	28.7^{c}	65de	42^{bc}
PROP1	3.54^{e}	58.2^{b}	129^{b}	45^{bc}
PROP2	3.63^{d}	79.1^{a}	164^{a}	46^{bc}
PROP3	3.67^{bcd}	27.2^{c}	46^{e}	52^{ab}
CA	3.94^{a}	7.4^{d}	58de	60^{a}
SE	0.04	11.5	19	7

[1]Refer to the text; [abc] Means in columns with unlike superscript differ ($P < 0.05$) by the *t*-test.

Key Words: aerobic stability, alcoholic fermentation, silage

W140 Effect of cutting management (PM vs. AM) and maceration on forage total nonstructural carbohydrates concentration and cattle preference. G. Raggio*[1], A. L. Tucker[1], M. Mongeon[2], R. Bergeron[1], and R. Berthiaume[3], [1]*Campus Alfred Université de Guelph*, *Alfred, Ontario, Canada*, [2]*Ministry of Agriculture, Food and Rural Affairs*, *Alfred, Ontario, Canada*, [3]*Dairy and Swine Research & Development Centre, Agriculture and Agri-Food Canada*, *Lennoxville, Canada*.

The aim of this study was to assess the effect of hay made from forage cut at sundown (PM) or sunup (AM) and macerated or not (control) on forage nonstructural carbohydrates (NSC) and cattle preference. Half of a timothy-alfalfa field at the late bud stage was cut at 18:00 whereas the second half was cut at 0600 h the next morning. Half of both the PM and AM cut were then macerated at 0900 h on d 2 with the remaining quarters being left to wilt without maceration (control). Hay was field dried, baled, and chopped before usage. A preference trial was conducted over 6 consecutive days with 6 Holstein heifers. During adaptation, hay from each treatment was offered alone as meals. Four treatments were used: AM control, AM macerated, PM control and PM macerated. Each possible pair of the 4 treatments (n = 6) was randomly assigned to the animals (one pair d-1), over 6 consecutive days. Two heifers at a time were moved to an adjacent pen separated in 2, offered 2 kg of each type of hay in adjacent tubs, and allowed 30 min to eat. Intake was calculated as the difference between hay offered and leftover. Hay samples were collected during the 6 experimental days and pooled by treatment. Heifer positions in the pen, treatments and treatment positions (left or right) were randomized daily. Data were analyzed as a multidimensional scaling and also by ANOVA with a model including animal effects and hay. Orthogonal contrasts were used to test for cutting time, maceration and cutting time × maceration effects. Feed composition (DM basis) was not affected by treatments (DM 88 ± 0.7%, CP 10 ± 0.7%, ADF 39 ± 1.0%, NDF 64 ± 1.8%). However, cutting time (AM vs. PM) tended to affect NSC concentration (24 vs. 25 ± 0.4%, $P = 0.09$). Overall, cutting in PM vs. AM (1359 vs. 754 ± 112 g DMI, $P = 0.01$) and macerating vs. control (1521 vs. 592 ± 112 g DMI, $P < 0.01$) increased hay consumption. There was no interaction between cutting time and maceration. These results suggest that both mowing in the PM and maceration were effective at increasing short-term dry matter intake.

Key Words: preference, cattle, conditioning

W141 Effect of leukemia inhibitory factor on feed intake and body temperature in sheep. J. L. Sartin*[1], D. L. Marks[2], B. K. Whitlock[3], J. A. Daniel[4], and B. P. Steele[1], [1]*Auburn University*, *Auburn, AL,*[2]*Oregon Health Sciences University*, *Portland,* [3]*University of Tennessee*, *Knoxville,* [4]*Berry College*, *Mt Bery, GA*.

Leukemia inhibitory factor (LIF) has been suggested to function as a potent inhibitor of feed intake in rodents. These studies were designed to determine whether LIF was found in the ovine hypothalamus and whether LIF inhibited feed intake in sheep. Sheep hypothalami were used to clone LIF to indicate presence of the gene in the hypothalamus. The sequence was similar to published data. Another group of sheep were provided intracerebroventricular (ICV) cannulas and injected with doses of LIF at 250, 500, 1000 and 2500 ng per sheep, ICV. Feed intake was inhibited by the 1000 and 2500 ng dose (trt, $P < 0.0001$; time × trt, $P < 0.02$). All doses of LIF elevated temperature above 40 C, indicating a fever. In a second experiment, the sheep were injected ICV with 2500 ng LIF, and blood samples collected at 10 min intervals for 6 h for assay of luteinizing hormone (LH), growth hormone (GH) and 30 min interval samples assayed for glucose and free fatty acids. There was no effect of LIF on GH. There was no effect of trt for LH, but there was a time × trt interaction indicating reduced LH ($P < 0.0001$). There was an effect of trt and a time × trt interaction indicating elevated plasma free fatty acids ($P < 0.03$; 0.001) and glucose ($P < 0.006$; 0.0001), opposite to the effects of LIF in rodent models. The effects of LIF on feed intake and other parameters is similar to the effects of LPS and leads to a hypothesis that LIF expression in response to LPS may be a component of the mechanism for feed intake inhibition in disease.

Key Words: appetite, free fatty acids, luteinizing hormone

W142 Effects of late gestation metabolizable protein (MP) supplementation on ewe organ and blood parameters. T. J. Swanson*[1], L. A. Lekatz[1], T. L. Neville[1], M. L. Van Enom[2], C. S. Schauer[2], K. R. Maddock Carlin[1], C. J. Hammer[1], and K. A. Vonnahme[1], [1]*North Dakota State University*, *Fargo*, [2]*Hettinger Research Extension Center*, *Hettinger, ND*.

To examine the effects of maternal MP supplementation in late gestation on blood and organ parameters multiparous ewes (n = 45) were allotted randomly to one of 3 treatments, 75% (LOW), 100% (CON), or 125% (HIGH) of MP requirements fed from d 100 to d 130 of gestation. Blood samples were drawn before initiation of diets and before slaughter for chemistry panel analysis. Body measurements including loin eye area, back fat, and body wall thickness where taken using ultrasound before treatment initiation and before slaughter to examine changes in body condition. At d 130 ewes were slaughtered and dissected. Ewes carried singletons and twins therefore fetal number was included as a main effect. There was no effect of treatment or fetal number on final BW, loin eye area, back fat, body wall thickness, eviscerated body weight (EBW), or weights of blood, perirenal fat, thyroid, and adrenals ($P \geq 0.06$). There was a treatment effect on heart weight with CON being heavier than LOW and HIGH which were not different ($P \leq 0.01$). Kidney weight was also affected by treatment with LOW being lighter compared with HIGH and CON which were not different ($P \leq 0.01$). Ewes carrying twins had increased liver, mammary, and gravid uterus weights ($P \leq 0.03$). Ewes with singletons had increased lung weights compared with ewes carrying twins ($P \leq 0.03$). When organ weight was examined as a proportion of EBW (g/kg) there was no difference in heart, perirenal fat, kidney, lung, or thyroid masses ($P \geq 0.06$). Ewes carrying twins had increased blood, liver, mammary, and gravid uterus weights as a proportion of EBW ($P \leq 0.02$). Initial chemistry panel results showed no differences in parameters of interest. Treatment decreased aspartate aminotransferase and blood urea nitrogen ($P \leq 0.01$) in LOW ewes compared with HIGH and CON ewes which did not differ. Change in gamma-glutamyl transpeptidase was greater in ewes carrying twins ($P \leq 0.01$). Results indicate that litter size and dietary MP supplementation during late gestation alters ewe organ weights.

Key Words: gestation, metabolizable protein, organ weights

W143 Effect of to PFKM and TFDP2 gene expression on muscle growth in sheep. J. W. Buchanan*[1], M. L. Thonney[2], and R. G. Mateescu[1], [1]*Oklahoma State University*, *Stillwater*, [2]*Cornell University*, *Ithaca, New York*.

Muscle growth rate in response to testosterone is an important characteristic of meat producing species utilized in production agriculture. The onset of puberty and subsequent testosterone release in males causes differential gene expression within sexually dimorphic muscles, resulting in measurable hypertrophy. Phosphofructokinase muscle type (PFKM) and transcription factor Dp-2 (TFDP2) are 2 genes recently shown to have significantly higher transcript levels in callipyge lambs. PFKM is a kinase directly involved in glycolysis, and TFDP2 is a transcription factor that has been implicated in the initiation of the cell cycle as well as DNA replication. The objective of this project was to compare the expression of these 2 genes in 2 different skeletal muscles in sheep. Muscle samples were collected from 18 sets of twins, with one individual from each set castrated at birth. Each set of twins was randomly assigned to 4 groups corresponding to 77, 105, 133, and 161 d of age at slaughter. Total RNA was extracted from semitendinosus (non-sexually dimorphic) and splenius (sexually dimorphic) muscle samples collected from each individual. Two-step reverse transcription polymerase chain reaction (RT-PCR) utilizing oligo(dT) primers was used to synthesize complimentary DNA. A quantitative polymerase chain reaction (q-PCR) was then performed to quantify the amount of PFKM and TFDP2 mRNA transcript in the muscle samples. The difference in gene expression between the SP and ST muscles was analyzed using the General Linear Model procedure of SAS to determine the effect of sex, age class and their interaction. No statistically significant difference was found in PFKM or TFDP2 mRNA level between the 2 muscles in rams and wethers at any age. Identifying genes that control muscle hypertrophy has the potential to create increased gains and efficiency in populations utilizing a marker assisted selection program. Further expression analysis is needed to determine the response of other candidate genes controlling hypertrophy in sexually dimorphic muscles.

Key Words: gene expression, muscle growth, sheep

W144 Excessive maternal selenium intake induces inflammatory response in the ovine fetal gut. H. Wang*[1], J. Zhao[1], Y. Huang[1], X. Yan[1], A. Meyer[2], M. Du[1], K. Vonnahme[2], L. Reynolds[2], J. Caton[2], and M. J. Zhu[1], [1]*Department of Animal Science, University of Wyoming*, *Laramie,* [2]*Department of Animal Science, North Dakota State University*, *Fargo*.

Selenium (Se) is a coenzyme for glutathione peroxidase and thioredoxin reductase, and its dietary supplementation has anti-inflammatory effects.

Many areas of North Dakota and other states have soils enriched in Se, rendering sheep and cattle grazing in these areas ingesting excessive Se. The objective was to evaluate the effects of higher energy diets and elevated Se intake on inflammatory response in lamb ileal tissues, a major immune organ. Rambouillet ewes (age = 240 ± 17 d; initial BW = 52.1 ± 6.2 kg) were fed either a control diet (adequate Se: 11.5μg Se.kg $BW^{-1}.d^{-1}$) or a high Se diet (77.0 μg Se.kg $BW^{-1}.d^{-1}$) with Se provide as Se-enriched wheat millrun. On 40 d of gestation (dG) ewes in each Se group were assigned randomly to 100%, or 140% of dietary requirements except for Se. At parturition, offspring were removed before nursing and raised independent of the dams until necropsy at 20 d of age. Offspring ileal tissues were sampled for immunoblotting and qRT-PCR analyses. Control, high energy (COB) and control, high Se (SEC) had no major difference in inflammatory signaling compared with control, normal Se (CC). However, high inflammatory signaling was detected in high energy, high Se (SEOB) group, as shown by increased ($P < 0.05$) mRNA expression of tumor necrosis factor (TNF)α and chemotaxis interleukin (IL)8. Consistent with this, phosphorylation of c-Jun N-terminal kinase (JNK), a primary inflammatory signaling, was greater ($P < 0.05$) in ileal tissue from offspring of SEOB treated dams. Both mRNA and protein content of transforming growth factor (TGF) β was also greater ($P < 0.05$) in SEOB lambs. No difference in mRNA expression of IL6, CD14, IL1α and β, and toll-like receptor (TLR) 2 and 4 were observed. In conclusion, high Se or maternal gestational high energy diet had no major effects on inflammatory signaling, but combining high energy diet with excessive Se induced inflammatory response in offspring intestine.
INBRE P20RR016474; USDA-NRI 2008–35203–19084.

Key Words: selenium, ovine, inflammation

W145 Serum concentrations of ghrelin, IGF-I, and prolactin in Rambouillet lambs during the preweaning period. C. D. Felker*, M. J. Hendricks, K. A. Jurado, A. D. Stapp, L. E. Camacho, and D. M. Hallford, *New Mexico State University*, *Las Cruces*.

During a 60-d preweaning period in each of 2 yr, Rambouillet lambs (n = 75 and 52 for yr 1 and 2, respectively) were used to examine effects of sex (77 females, 50 males) and type of birth (TOB; 46 single, 81 multiple lambs) on serum concentrations of ghrelin (total), IGF-I, and prolactin (PRL). Lambs were born in mid-March of each year and were weighed on the day of birth (d 0; 5.1 ± 0.1 kg) and at weaning (60 d, 20.1 ± 0.4 kg). Serum was harvested by centrifugation from blood collected (jugular venipuncture) on d 1, 14, 28, 42, and at weaning. Data were examined by ANOVA for a randomized complete block design with a 2 (sex) x 2 (TOB) factorial arrangement, sampling day as a repeated measure, and year as the block. Males were heavier at birth than females ($P < 0.001$), but weaning weight and ADG were similar ($P > 0.35$). Single lambs were heavier ($P < 0.001$) at birth and weaning and had greater ADG ($P < 0.001$) than multiple lambs. Serum ghrelin was similar ($P > 0.24$) in male and female and in single and multiple lambs. However, ghrelin declined during the preweaning period with values of 557, 373, and 358 (±9) pg/mL (quadratic, $P < 0.001$) on d 1, 28, and 60, respectively. Serum PRL and IGF-I were influenced ($P < 0.05$) by sex × day and TOB × day interactions. Males and females had similar ($P = 0.23$) IGF-I on d 1; but on d 14, 28, 42, and at weaning, males had greater ($P < 0.05$) IGF-I than did females. Serum IGF-I was greater ($P < 0.02$) in single than in multiple lambs on all sampling days. Serum PRL was similar ($P > 0.10$) in male and female lambs throughout preweaning. However, single lambs had greater ($P < 0.001$) serum PRL concentrations than did multiple lambs on d 42 and at weaning. In general, PRL and IGF-I tended to increase in a quadratic ($P < 0.01$) fashion across the preweaning period. Correlation coefficients determined on d 60 between serum IGF-I, PRL, and ghrelin concentrations and preweaning ADG were 0.65, 0.44, and −0.26 ($P < 0.005$), respectively. Sex of lamb, type of birth, and age should be considered when evaluating serum hormone profiles in rapidly growing lambs.

Key Words: sheep, growth, hormones

W146 Patterns of fat growth in the primal cuts of beef composites. L. A. Goonewardene*[1], Z. Wang[2], R. W. Seneviratne[1], J. A. Basarab[1], J. Stewart-Smith[3], J. L. Aalhus[4], M. A. Price[2], and E. K. Okine[2], [1]*Alberta Agriculture and Rural Development*, *Edmonton, AB, Canada*, [2]*University of Alberta*, *Edmonton, AB, Canada*, [3]*Beefbooster Inc.*, *Calgary, AB, Canada*, [4]*Agriculture and Agri-Food Canada*, *Lacombe, AB, Canada*.

Beef composites (C) have combined favorable traits of pure breeds. The objective was to compare the growth rates (GR) and partitioning patterns of total fat (F), inter muscular (IM), body cavity (BC) and subcutaneous (SC) fat in 5 primal cuts of serially harvested Beefbooster composites (SM = C of small breeds n = 37, AH = C of Angus and Hereford n = 69 and GLC = C with Gelbvieh, Limousin or Charolais terminal sires n = 71) from 274 to 456 d (d) of age in relation to composite type and primal cut. Analysis of covariance obtained the slopes (GR/d) for total F, IM, BC and SC fat within each cut and C type. The GR of total fat deposition in AH was 24.7% higher ($P < 0.10$) than SM and 23.6% higher than GLC. The GR of total fat in the chuck was over 3 times higher than the loin and short loin and over twice the GR of the rib and round in each composite. The GR of IM fat in the chuck and rib was higher ($P < 0.10$) than BC and SC fat, but the GR of SC fat was higher than IM in the round and loin in each composite. The round and rib had similar GR for IM fat in SM and GLC but in the AH a 40.5% difference in GR for IM fat was observed. Pronounced differences were observed in the GR of SC fat between composites in the round and loin, and AH had higher ($P < 0.10$) GR compared with SM and GLC was in between. The difference in the fattening patterns in the 3 composites was most pronounced in the SC depot followed by the IM with little change in the BC depot. Selective breeding and the development of beef composites have primarily resulted in changes in SC fat partitioning in the 5 primal cuts and IM fat in the chuck. More fat trim at retail may be needed in the AH compared with SM and GLC.

Key Words: fat, growth, beef

W147 Prepartum supplementation in primiparous beef cows affected hepatic IGF-I mRNA expression in female calves. J. Laporta*[1], A. L. Astessiano[1], A. Scarsi[1], R. Pérez-Clariget[1], G. Quintans[2], and M. Carriquiry[1], [1]*School of Agronomy, UdelaR*, *Uruguay*, [2]*Instituto Nacional de Investigación Agropecuaria*, *Treinta y Tres, Uruguay*.

We examined the effect of supplementation during the last month of gestation of primiparous cows, on hepatic gene expression of growth hormone receptor (GHR), insulin–like growth factor–I (IGF–I) and IGF binding protein–3 (BP3) of their calves. The experiment was conducted in INIA Treinta y Tres (33°15′S 54°28′W) using 20 crossbred (Angus/Hereford) calves (n = 5 per treatment and sex). Cows, ranked by body weight (BW) and body condition score, were blocked by calving day and assigned randomly to control or supplement treatments. Supplemented cows were offered (1 kg/100 kg BW, 4.5 kg/d) a mix (67:33% as–fed basis; 16% CP, 11% ADF) of sorghum grain and protein concentrated from 33 ± 1.4 d prepartum until calving. Before, during and after the supplementation period, cows grazed together a native

pasture paddock (60 ha) with an average forage mass available of 1345 kg DM/ha (10.4% CP, 45.2% ADF). Calf BW, and liver samples were collected at weaning. Total RNA was extracted and mRNA abundance determined by SYBR Green RT–PCR in real time and normalized to hypoxanthine phosphoribosyl transferase (HPRT) expression. Means from a mixed model analysis were considered to differ when $P < 0.05$. Prepartum supplementation, calf sex, or their interaction did not afect BW at weaning (155 ± 11 kg at 180 ± 1.4 d). The expression of HPRT mRNA was not affected by supplementation, calf sex or their interaction. Although GHR, BP3 and IGF–I mRNA did not vary with supplementation, GHR expression tended ($P = 0.08$) to be greater and IGF–I mRNA was greater ($P = 0.04$) in female than male calves. There was an interaction ($P < 0.05$) between treatment and calf sex for IGF–I and BP3 mRNA, supplementation increased their expression only in females. Results suggest that prepartum supplementation during periods of limited forage availability of native pastures, through its effect in the fetal stage or the suckling period, could affect potential growth of female beef calves at weaning.

Key Words: liver, prepartum nutrition, RTP–CR

W148 Glucagon-like peptide 2 may mediate growth and development of the bovine gastrointestinal tract. E. E. Connor*[1], R. L. Baldwin[1], A. V. Capuco[1], C. M. Evock-Clover[1], S. E. Ellis[2], and K. S. Sciabica[3], [1]*USDA-ARS, BARC*, *Beltsville, MD*, [2]*Clemson University*, *Clemson, SC*, [3]*Beckman Coulter, Inc.*, *Brea, CA*.

Glucagon-like peptide 2 (GLP-2), secreted by enteroendocrine cells, promotes growth, reduces apoptosis, and enhances blood flow, nutrient absorption, and barrier function in intestinal epithelium of monogastric species. Regulatory functions of GLP-2 in the ruminant gastrointestinal tract (GIT) are unknown. Our objectives were to characterize expression of GLP-2 pathway members throughout bovine GIT including proglucagon (GCG) mRNA, the parent peptide from which GLP-2 is derived through cleavage by prohormone convertase (PCK1), PCK1 mRNA, GLP-2 receptor (GLP2R) mRNA, and mRNA for dipeptidyl peptidase IV (DPP4), the enzyme that inactivates GLP-2. Gene expression was evaluated in rumen, reticulum, omasum, abomasum, duodenum, jejunum, ileum, cecum, and rectum collected at slaughter from prepubertal heifers, mature cows in early, mid, and late lactation, and non-lactating cows (n = 3/stage) by a multiplex gene expression profiling assay based on traditional RT-PCR that uses a universal priming strategy. Further, mRNA expression of 14 genes involved in nutrient transport, enzyme activity, blood flow, apoptosis, and proliferation were evaluated in the 9 GIT tissues for association with GCG and GLP2R mRNA. Results indicated that mRNA expression of GCG, PCK1, GLP2R, and DPP4 varies across the 9 GIT tissues ($P < 0.001$), with greatest expression in intestines, and generally non-detectable levels in forestomachs. Expression of DPP4 and GLP2R mRNA varied by developmental stage or lactational state ($P < 0.05$) in intestinal tissues. Expression of GCG or GLP2R mRNA was correlated with markers of proliferation, apoptosis, blood flow, enzyme activity, and urea transport, depending on tissue type, supporting involvement of GLP-2 in these processes in ruminants. Lastly, GLP2R protein was localized to cells lining the intestinal crypts by immunohistochemistry, consistent with distribution in monogastric species. Our findings support a functional role of GLP-2 in bovine GIT and its potential use to improve intestinal function and nutrient absorption in ruminants.

Key Words: cattle, gene expression, GLP-2

W149 Effects of maternal metabolizable protein supply on fetal organ weights. T. L. Neville*[1], L. A. Lekatz[1], T. J. Swanson[1], M. L. Van Emon[2], C. S. Schauer[2], K. R. Maddock Carlin[1], C. J. Hammer[1], and K. A. Vonnahme[1], [1]*Center for Nutrition and Pregnancy, Department of Animal Sciences, North Dakota State University*, *Fargo,* [2]*Hettinger Research Extension Center, North Dakota State University*, *Hettinger*.

Objectives were to investigate the effects of maternal MP supply during gestation on fetal target organ weights. Multiparous ewes (n = 45; 15/treatment) were fed an isocaloric and isonitrogenous diet that contained either 75% (LOW), 100% (MOD), or 125% (HIGH) of MP requirements from d 100 to 130 of gestation. At d 130 ewes were harvested and fetuses dissected. Ewes carried singletons and twins, therefore fetal number was included in the model. Fetal weight, curved crown rump, heart girth, eviscerated BW, brain, and several target tissues were not affected by maternal MP supply during gestation ($P \leq 0.06$). Fetal right ventricles (mm) from LOW ewes were thicker ($P = 0.05$) than MOD ewes with those from HIGH ewes being intermediate. Fetuses from HIGH and LOW ewes had thicker ($P = 0.01$) right ventricles than MOD ewes (0.095, 0.098, and 0.082 ± 0.004 mm/g brain weight for HIGH, LOW and MOD respectively). Fetuses from LOW ewes had lighter ($P = 0.01$) ovaries (g/g brain weight) than MOD and HIGH ewes. Singleton lambs from LOW ewes had lighter ($P = 0.02$) adrenal glands than singleton lambs from MOD ewes and twins from LOW ewes with all other lambs being intermediate. Total gastrointestinal tract was heavier ($P \leq 0.03$) in twin lambs from LOW ewes compared with singleton lambs from LOW and twins from HIGH ewes with all other lambs being intermediate. These data indicate maternal dietary MP during the last trimester impacts fetal organ growth near term.

Key Words: fetal lambs, metabolizable protein, organ weights

W150 Nutrient restriction from early to mid-gestation in the cow increases offspring adipocyte size at slaughter. C. B. Tousley[1], N. M. Long*[1,2], S. P. Ford[1,2], W. J. Means[2], B. W. Hess[2], and M. Du[2], [1]*Center for the Study of Fetal Programming*, *University of Wyoming, Laramie,* [2]*Depertment of Animal Science, University of Wyoming*, *Laramie*.

Multiparous Angus × Gelbvieh cows were used to evaluate effects of nutrient restriction on adipose tissue morphology of beef steers and heifers at standard production endpoints. At 45 d after AI from a single sire, pregnancy was confirmed, and cows (n = 8 per treatment) were allotted randomly to be individually fed a control diet (C,100% of NRC recommendations), nutrient restricted (NR,70% of C NEm), or NR + protein supplement (NRP,NR + protein to equal C metabolizable AA). At 185 d of gestation (dG), all cows were comingled and fed the C diet. Bull calves were castrated at birth and all calves weaned at 210 d of age, backgrounded for 28 d, and then placed in the feedlot. Steers and heifers were harvested on separate days at an average 12th rib fat thickness of 7.6 mm. Selected organ weights and carcass characteristics were determined. Adipose tissue from selected depots was collected and fixed in paraffin and adipocyte diameters determined by image analysis. There was no difference ($P < 0.23$) in BW or BCS between C, NRP, and NR cows at 45 dG, which averaged 489.74 ± 17.7 kg and 5.35 ± 0.13, respectively. At 185 dG, C and NRP cows had similar BW (566.1 ± 14.8 and 550.2 ± 14.8) and BCS (6.34 ± 0.27 and 5.59 ± 0.27), but BW (517.9 ± 14.8) and BCS (4.81 ± 0.27) of NR cows were less ($P < 0.05$). There were no treatment differences ($P < 0.26$) in live BW, carcass characteristics or organ weights of steers and heifers at slaughter. In contrast, average adipocyte diameters of NR offspring increased or tended to increase (Table 1) in finished steers and heifers, which could contribute to altered adiposity and metabolism in later life.

Table 1. Average adipocyte diameter (um) from selected depots of offspring (4 steers and 4 heifers per treatment) at slaughter

	Control	NRP	NR
Subcutaneous	74.5 ± 2.6[a,]	81.6 ± 2.5[ab]	86.9 ± 2.7[b]
Perirenal	113.5 ± 3.5[c]	115.6 ± 3.5[c]	124.69 ± 3.8[d]
Mesenteric	113.03 ± 3.8C[a]	121.37 ± 3.5[ab]	129.28± 3.5[b]
Omental	117.2 ± 4.5[a]	114.4 ± 4.2[a]	129.6 ± 4.3[b]

[a,b]Means differ $P \leq 0.05$; [c,d]Means differ $P < 0.10$.

Key Words: prenatal programming, adipocyte size, cows

W151 Two messenger RNA targets, Programmed Cell Death Protein 4 and Phosphatase and Tensin Homolog, of microRNA-21 are expressed in cultured bovine adipocytes. S. L. Pratt*, T. A. Burns, and S. K. Duckett, *Clemson University*, *Clemson, SC*.

Adipogenesis is regulated in part by post-transcriptional gene regulation through small non-coding inhibitory RNA, microRNA (miRNA), via translational repression or RNA interference. We have shown miR-21 expression to increase in adipocytes compared with preadipocytes as differentiation progresses, and this miRNA is known to promote cell survival and hypertrophic growth, in part, by the translational inhibition of Programmed Cell Death Protein 4 (PDCD4) and Phosphatase and Tensin Homolog (PTEN). Neither the protein nor message for PDCD4 or PTEN has been reported to be expressed in, or involved in adipogenesis/adipocyte function. Our objective was to detect and quantify the mRNA for bovine PDCD4 and PTEN in primary bovine cell cultures. Bovine preadipocyte cell lines generated from subcutaneous adipose tissue obtained from 18 mo old Angus steers were cultured to confluence and held 2 d in Dulbecco's modified eagles medium (DMEM) containing 10% fetal calf serum (FCS), and 2X antibiotiotic/antimycotic (AB/AM). Cells were differentiated using a 2- step process by culture for 2-d in DMEM containing 5% FCS, 2X AB/AM, insulin at 2.5 ug/ml, 0.25 uM dexamethasone, 5 uM troglitasone and 0.5 mM isobutylmethylxanthine (IBMX) for 2-d followed by a 4-d or 10-d incubation in DMEM containing 5% FCS, 2X AB/AM, insulin, and troglitasone. tcRNA was isolated for each cell line at 2-d confluence (Control), and after 2-d (D2), 4-d (D6) and 10-d (D12) of differentiation. tcRNA was used in real time qRT-PCR to determine expression levels for the respective message for bovine PTEN and PDCD4. Expression levels for PTEN and PDCD4 across all days ranged from −0.8- to 1.0-fold compared with Control ($P > 0.05$). In contrast, miR-21 was previously shown to be upregulated during the same stages of adipogenesis. We hypothesize that miR-21 downregulates the proteins PDCD4 and PTEN by translational inhibition during adipogenesis allowing cells to survive and undergo hypertrophic growth required for lipid filling.

Key Words: miRNA, adipogenesis, qRT-PCR

W152 MicroRNA-21 and its messenger RNA targets Programmed Cell Death Protein 4 and Phosphatase and Tensin Homolog are expressed in bovine adipose tissue. S. L. Pratt*, E. Curry, T. A. Burns, and S. K. Duckett, *Clemson University*, *Clemson, SC*.

MicroRNA (miRNA) are small non-coding RNA that regulate adipocyte function, both in vivo and in vitro by translational repression or RNA interference of targeted messenger RNA. miR-21 expression increases in adipocytes compared with preadipocytes, and this miRNA promotes cell survival and hypertrophic growth, in part, by the translational inhibition of Programmed Cell Death Protein 4 (PDCD4) and Phosphatase and Tensin Homolog (PTEN). Neither PDCD4 nor PTEN has been reported to be expressed in, or involved in adipocyte function. Our objectives were to detect and quantify 1) miR-21 and 2) PDCD4 and PTEN in adipose tissue isolated from Angus steers (289 kg) finished on pasture only (PA; n = 6) or on a high-concentrate diet (C; 85% concentrate/15% roughage; n = 7). Fat samples (s.c.; 5 g per sample) were removed from the tail head area of each carcass at slaughter, rinsed with sterile saline, frozen in liquid nitrogen and stored at −80°C. Protein extracts were subjected to SDS-PAGE, Western blotting and immunodetection with PTEN and PDCD4 antisera. tcRNA was used in real time qRT-PCR to determine expression levels for miR-21, PTEN, and PDCD4. Western blotting and immunodetection with antisera to PTEN and PDCD4 detected proteins ~50 and 60 kDa, respectively. Message levels for PTEN and PDCD4 increased 3.2- and 6.7-fold, respectively in PA compared with C treatment ($P < 0.05$); in contrast miR-21 expression was repressed in PA compared with C ($P < 0.05$). These data show that miR-21, PTEN and PDCD4 are expressed in bovine adipose tissue. Message level for PTEN and PDCD4 in mature adipose tissue may be regulated at the transcriptional level, and low levels of concentrate in the diet may increase the PTEN and PDCD4 message under chronic conditions which would stimulate increased adipocyte cell mortality and turnover. PTEN and PDCD4 protein expression may be increased due to increased message levels and to the decrease in miR-21 expression which negatively regulates the translation of both messages.

Key Words: miRNA, adipose tissue, qRT-PCR

W153 Both growth hormone and signal transducer and activator of transcription 5b inhibit glycerol-3-phosphate dehydrogenase activity and CCAAT/enhancer binding protein α mRNA expression in differentiating bovine preadipocytes. L. Zhao*, B. A. Corl, and H. Jiang, *Virginia Polytechnic Institute and State University*, *Blacksburg*.

It has been long known that growth hormone (GH) inhibits adipogenesis in various animals, including cattle. However, the underlying mechanism remains poorly understood. The objective of this study was to determine if GH inhibits bovine adipogenesis by activating the signal transducer and activator of transcription 5b (STAT5b), a transcription factor known to be activated by GH in many tissues including the adipose tissue. Two studies were conducted to achieve this objective. In one study, preadipocytes from adipose tissue explants of cattle were induced to differentiate in the presence or absence of 10 ng/mL GH and 100 ng/mL GH for 6 d before differentiation assessment. In the other study, the preadipocytes were induced to differentiate in the presence of 10 or 100 multiplicities of infectivity (MOI) of adenovirus expressing constitutively active STAT5b (STAT5bCA) or β-galactosidase (LacZ) as a control for 6 d before differentiation assessment. Differentiation was assessed by measuring glycerol-3-phosphate dehydrogenase (G3PDH) activity, and mRNA expression of CCAAT/enhancer binding protein α (CEBPα), peroxisome proliferator-activated receptor γ (PPARγ), and fatty acid binding protein 4 (FABP4). Both concentrations of GH inhibited G3PDH activity ($P < 0.05$, n = 5) and decreased mRNA expression of CEBPα compared with the no-GH control ($P < 0.05$, n = 5). Neither GH concentration altered mRNA expression of PPARγ or FABP4 compared with the no-GH control. The STAT5bCA adenovirus at 100 MOI inhibited the G3PDH activity ($P < 0.05$, n = 4) and decreased mRNA expression of CEBPα compared with the LacZ adenovirus or the no-adenovirus control ($P < 0.05$, n = 4). The STAT5bCA adenovirus did not change mRNA expression of PPARγ or FABP4. In summary, both GH and STAT5bCA overexpression inhibited G3PDH activity and CEBPα mRNA expression in differentiating bovine preadipocytes.

Key Words: growth hormone, STAT5b, bovine preadipocyte

W154 Primary preadipocytes can be isolated, propagated, and differentiated from bovine intermusclar fat harvested 48 h postmortem. T. A. Burns*, S. K. Duckett, and S. L. Pratt, *Clemson University*, *Clemson, SC*.

Traditionally, primary cell cultures are isolated from tissues collected at slaughter using collagenase digestion or tissue explantation methods. Although we have previously been successful isolating and differentiating bovine preadipocytes from slaughtered cattle, the abattoir is not a conducive environment for aseptic tissue collection. Therefore, the objective of this study was to isolate, propagate, and successfully differentiate bovine preadipocytes collected from refrigerated rib sections 48 h postmortem. Sections of intermuscular fat were excised and minced using sterile instruments, rinsed with Hanks' Balanced Salt Solution (HBSS), and digested in 25 mL HBSS containing 2 mg/mL collagenase, type I, and 40 mg/mL bovine serum albumin under constant shaking at 37°C for 120 min. Cells were plated at 1×10^4 cells/cm^2, passaged every 2–4 d when 60% confluent, and were frozen after 4 passages. To test a cell line's ability to differentiate, cells were thawed, passaged 3 times, and seeded in wells at 1×10^5 cells/cm^2. Cells were allowed to reach confluence, held for 2 d, and differentiated on d 0 with Dulbecco's modified eagles medium containing 10% fetal calf serum, 2X antibiotic/antimycotic, insulin at 2.5 μg/mL, 0.25 μ*M* dexamethasone, 20 μ*M* troglitasone, 0.5 m*M* isobutylmethylxanthine, and 10 m*M* acetate. Undifferentiated cells were harvested on d 2 (CON) and treated cells were harvested on d 2 (D2), 6 (D6), and 12 (D12) for fatty acids and RNA. Gross morphology of differentiating cells displayed characteristic shape change from fibroblastic to spherical. Using GLM procedure of SAS, duplicate fatty acid data were analyzed across 3 cell lines by time. Total fatty acids were not different between CON and D2, but increased ($P < 0.05$) on D6 and D12 compared with CON. On a percentage basis, C16:0, C18:0, and C18:2 decreased ($P < 0.05$) and C18:1c9 increased ($P < 0.05$) by D12. In addition, differentiation-associated genes were increased ($P < 0.05$) in treated cells. This evidence suggests that cells harvested 48 h postmortem are capable of propagating and differentiating for use in in vitro studies.

Key Words: preadipocyte, isolation, differentiation

W155 *Trans*-10, *cis*-12 conjugated linoleic acid induces adipogenic gene expression in single and co-cultures of bovine preadipocytes and myoblasts. S. H. Choi*[1], K. Y. Chung[2], G. Go[1], C. W. Choi[3], B. J. Johnson[2], and S. B. Smith[1], [1]*Department of Animal Science, Texas A&M University*, *College Station,* [2]*Department of Animal and Food Science, Texas Tech University*, *Lubbock,* [3]*National Institute of Animal Science*, *Suwon, Gyunggi, Korea*.

A limited number of studies have investigated the differentiation of bovine adipocytes and myoblasts in single cultures, and there is even less information about the interaction between adipocytes and myoblastic cells in a coculture system. We hypothesized that preadipocyte differentiation would be depressed by differentiating myoblasts, where preadipocytes would promote adipogenic gene expression in myoblasts in a coculture system. We also determined the effects of arginine, a biological precursor of nitric oxide, and/or *trans*-10, *cis*-12 conjugated linoleic acid (CLA) on adipogenic gene expression of bovine preadipocytes and myoblasts. Muscle-derived satellite cells and preadipocyte were isolated from 14-mo old crossbred steers. Both bovine satellite (BSC) and preadipocytes (PA) cells were cultured with 10% FBS/DMEM and 1% antibiotics during the proliferation period (3 d). After proliferation, BSC and PA were treated with 3% of horse serum (HS) DMEM and 5% FBS/DMEM with antibiotics respectively, for 4 d. Finally, single or combined BSC and PA were cultured with 40 μ*M* *trans*-10, *cis*-12 CLA and/or 5 m*M* arginine for 2 h. Cocultured PA had significantly less AMPK ($P = 0.04$) and SCD ($P = 0.04$) gene expressive than single-cultured PA. Arginine stimulated, and CLA depressed SCD gene expression. Arginine significantly stimulated PPARγ gene expression ($P = 0.06$) in cocultured PA compared with other treatments. SCD gene expression was significantly increased by arginine in both single- ($P < 0.001$) and cocultured ($P < 0.01$) PA. Conversely, C/EBP-β gene expression was significantly enhanced by coculture in BSC in the absence or presence of arginine or CLA. PPARγ gene expression tended to be increased by coculture in BSC. We conclude that arginine and CLA had similar effects in single and cocultured PA and BSC, but the effects were stronger in cocultured cells.

Key Words: co-culture, preadipocytes, satellite cells

W156 Growth hormone stimulates liver expression of fibroblast growth factor 21 mRNA in cattle. J. Yu*[1,2], A. Wang[2], S. Eleswarapu[2], and H. Jiang[2], [1]*Sichuan Agricultural University*, *Yaan, Sichuan, China*, [2]*Virginia Polytechnic Institute and State University*, *Blacksburg*.

Fibroblast growth factor 21 (FGF21) is a novel endocrine regulator of glucose homeostasis, lipid metabolism, insulin sensitivity, and obesity. In addition, FGF21 is known to inhibit growth hormone (GH)-induced signaling through the signal transducer and activator of transcription 5 (STAT5). In the body, FGF21 mRNA is expressed predominantly in the liver. In this study, we tested the hypothesis that FGF21 expression in the liver is induced by GH. Nonlactating and nonpregnant cows were injected subcutaneously with 500 mg of recombinant bovine GH in a slow-release formula. Liver biopsy and blood samples were collected from each cow one week before and 24 h after the injection. Liver FGF21 mRNA abundance after GH injection was 21 times that before the injection ($P < 0.05$, n = 5), as measured by real-time RT-PCR. The GH injection tended to increase serum concentration of FGF21 ($P = 0.09$, n = 5), as measured by an enzyme-linked immunosorbent assay. The bovine FGF21 gene promoter contains 3 putative STAT5 binding sites. Electrophoretic mobility shift assays showed that all of them could bind to the STAT5 protein from bovine liver. Chromatin immunoprecipitation assays demonstrated that GH injection stimulated binding of STAT5 to the FGF21 promoter in the liver ($P < 0.05$, n = 4). Co-transfection analyses indicated that reporter gene expression from the bovine FGF21 promoter could be induced by GH in a STAT5-dependent manner. Taken together, these data suggest that GH stimulates expression of FGF21 mRNA in cattle and that the stimulation may be mediated by the transcription factor STAT5.

Key Words: growth hormone, fibroblast growth factor 21, STAT5

W157 Abundance of growth hormone secreteagogue receptor and PPARy2 in longissimus dorsi of beef cattle. C. L. Delvaux*, J. S. Jennings, and A. E. Wertz-Lutz, *South Dakota State University*, *Brookings*.

Objectives of this experiment were to determine the presence and abundance of growth hormone secreteagogue receptor (GHS-R) and PPARy2 in longissimus dorsi of beef cattle fed to achieve differences in composition of gain. Beef steers (n = 72) of similar age, weight (292 ± 1.44 kg), and genetic background were used. At trial initiation (d 0), 8 steers were harvested. The remaining 64 steers were allotted, by weight, to pen, and treatment was assigned randomly. Treatments were 1) 60% forage; 40% concentrate diet fed during the growing period (0–112 d) followed by 10% forage; 90% concentrate diet during the finishing period (113–209 d) (GRW-FNSH) or 2) 10% forage; 90% concentrate

diet fed for the duration of the experiment (0–209 d) (FNSH-FNSH). Steers were allowed ad libitum consumption regardless of dietary treatment. Eight steers per treatment were harvested on d 88, 116, 165, and 209. Tissue samples from the longissimus dorsi were collected 48 h subsequent to harvest and frozen. Protein separation and quantification was determined using SDS-PAGE and Western blotting techniques. Abundance of GHS-R and PPARy2 was quantified using the LI-COR system and standardized to β-Actin. Protein abundance data were analyzed statistically using the MIXED procedure of SAS evaluating diet, age at harvest, and their interaction. Differences in composition of gain have been reported previously. Abundance of GHS-R differed ($P < 0.001$) as a result of age at harvest, and dietary treatment tended ($P = 0.11$) to influence GHS-R abundance. Differences in GHS-R abundance relative to age at harvest, and potentially as a result of differential growth, warrants further investigation. The PPARy2 was not sufficiently abundant in longissimus dorsi and could not be quantified. The PPARy2 is exclusively associated with adipose tissue, and therefore not expected to be abundant in longissimus dorsi tissue. Degradation of PPARy2 also may have occurred as samples were not collected until 48 h postmortem.

Key Words: growth hormone secreteagogue receptor, PPARy2, longissimus dorsi

W158 Effect of estradiol-17β on protein synthesis and degradation rates in fused bovine satellite cell cultures. E. Kamanga-Sollo, M. E. White*, M. R. Hathaway, W. J. Weber, and W. R. Dayton, *University of Minnesota*, *St. Paul*.

Although androgenic and estrogenic steroids are widely used to enhance muscle growth and increase feed efficiency in feedlot cattle, their mechanism of action is not well understood. While in vivo studies indicate that Estradiol-17β (E2) affects muscle protein synthesis and/or degradation, in vitro results are inconsistent. We have examined the effects of E2 treatment on protein synthesis and degradation rates in fused bovine satellite cell (BSC) cultures. Additionally, to learn more about the mechanisms involved in E2-enhanced muscle growth, we have examined the effects of compounds that interfere with binding of E2 or IGF-I to their respective receptors on E2-induced alterations in protein synthesis and degradation rates in BSC cultures. Treatment of fused BSC cultures with E2 results in a concentration-dependent increase ($P < 0.05$) in protein synthesis rate and a decrease ($P < 0.05$) in protein degradation rate. The pure estrogen antagonist ICI 182 780 suppresses ($P < 0.05$) E2 -induced alterations in protein synthesis and degradation in fused BSC cultures. The G-protein coupled receptor (GPR)-30 agonist, G1, does not affect either synthesis or degradation rate establishing that GPR30 does not play a role in E2-induced alterations in protein synthesis or degradation. JB1, a competitive inhibitor of IGF-I binding to the Type 1 insulin-like growth factor receptor (IGFR-1), suppresses ($P < 0.05$) E2-induced alterations in protein synthesis and degradation. In summary our data show that E2 treatment directly alters both protein synthesis and degradation rates in fused BSC cultures via mechanisms involving both the classical ER and IGFR-1.

Key Words: estradiol-17β, satellite cells, protein turnover

W159 Effect of trenbolone acetate on protein synthesis and degradation rates in fused bovine satellite cell cultures. E. Kamanga-Sollo, M. E. White*, M. R. Hathaway, W. J. Weber, and W. R. Dayton, *University of Minnesota*, *St. Paul*.

Although androgenic and estrogenic steroids are widely used to enhance muscle growth and increase feed efficiency in feedlot cattle, their mechanism of action is not well understood. While in vivo studies have indicated that androgens affect protein synthesis and/or protein degradation rate in muscle, results from in vitro studies have been inconsistent. Consequently, we have examined the effects of trenbolone acetate (TBA), a synthetic androgen, on protein synthesis and protein degradation rates in fused bovine satellite cell (BSC) cultures. Additionally, we have examined the effects of compounds that interfere with binding of TBA or insulin-like growth factor (IGF)-I to their respective receptors on TBA-induced alterations in protein synthesis and protein degradation rates in BSC cultures. Treatment of fused BSC cultures with TBA results in a concentration-dependent increase ($P < 0.05$) in protein synthesis rate and a decrease ($P < 0.05$) in protein degradation rate, establishing that TBA has a direct effect these parameters. Flutamide, a compound that prevents androgen binding to the androgen receptor, suppresses ($P < 0.05$) TBA -induced alterations in protein synthesis and degradation in fused BSC cultures, indicating the androgen receptor is involved. JB1, a competitive inhibitor of IGF-I binding to the Type 1 IGF receptor (IGFR-1), suppresses ($P < 0.05$) TBA-induced alterations in protein synthesis and degradation indicating that this receptor also is involved in the actions of TBA on both synthesis and degradation. In summary our data show that TBA acts directly to alter both protein synthesis and degradation rates in fused BSC cultures via mechanisms involving both the androgen receptor and IGFR-1.

Key Words: trenbolone acetate, satellite cells, protein turnover

W160 Zilpaterol HCl enhances adenosine monophosphate-activated protein kinase α (AMPKα) expression in bovine skeletal muscle. R. J. Tokach*, K. Y. Chung, and B. J. Johnson, *Texas Tech University*, *Lubbock*.

Zilpaterol HCl (ZH), a β-2 adrenergic agonist, has been used for enhancing muscle growth in feedlot cattle. The aim of these in vivo and in vitro experiments was to determine the effect of ZH on changes in enzymes and growth factors important in skeletal muscle growth. We hypothesized that AMPKα expression increased in animals or cells treated with ZH. Thirteen month old calf-fed Holstein steers implanted with an estrogen-based implant were used in randomized complete block design with a 2 × 2 factorial arrangement of treatments. Main effects included; ZH 0 or 20 d before slaughter and either a 3-d or 10-d withdrawal period (WD). Semimembranosus muscle (SM) was collected within 10 min of harvest for analysis of AMPKα and IGF-I protein and mRNA abundance. Western blot analysis revealed that the protein content of AMPKα in muscle from ZH-treated cattle with a 3-d withdrawal increased ($P < 0.05$) as compared with the control group. There was no significant difference of AMPKα in muscle from the ZH-treated cattle with a 3-d withdrawal as compared with the ZH-treated cattle with a 10-d withdrawal. Real-time quantitative PCR was used to measure the relative level of mRNA. The mRNA for AMPKα tended to increase in muscle from ZH-treated cattle with a 3-d withdrawal ($P = 0.12$) as compared with the control group. Withdrawal time resulted in a decrease in IGF-I mRNA. Primary cultures of bovine satellite cells (BSC) isolated from the SM were harvested after 120 h of either ZH, ZH antagonist (ICI-118,551), or ZH plus ICI-118,551 exposure for AMPKα and IGF-I protein and mRNA analysis. AMPKα abundance increased in BSC treated with ZH as compared with the control, ICI-118,551, and ZH plus ICI-118,551 treated BSC. IGF-I mRNA relative units (3.7 ± 0.6) increased in BSC treated with ZH as compared with the control (0.8 ± 0.4) and the addition of ICI-118,551 (0.9 ± 0.2) ameliorated these changes ($P < 0.05$). These data indicate that ZH alters mRNA and protein concentrations of AMPKα in SM, and these effects may be mediated through the β 2 adrenergic receptor.

Key Words: AMPKα, bovine satellite cells, zilpaterol hydrochloride

W161 Steroidal implants and zilpaterol HCl alter serum urea-N and NEFA responses in finishing beef steers. S. L. Parr*[1], M. L. Galyean[1], K. Y. Chung[1], J. P. Hutcheson[2], and B. J. Johnson[1], [1]*Texas Tech University*, *Lubbock,* [2]*Intervet / Schering-Plough Animal Health*, *De Soto, KS*.

British × Continental steers (n = 168; 7 pens/treatment; initial BW = 362 kg) were used to evaluate the effect of dose of trenbolone acetate (TBA) and estradiol-17β (E_2) and feeding of zilpaterol hydrochloride (ZH) on serum urea-N (SUN) and NEFA concentrations. A randomized complete block design was used with a 3 × 2 factorial arrangement of treatments. Main effects were implant (no implant [NI]; Revalor-S [REV-S; 120 mg TBA + 24 mg E_2]; and Revalor-XS [REV-X; 200 mg TBA + 40 mg E_2]) and ZH (0 or 8.3 mg/kg of DM for 20 d with a 3-d withdrawal before harvest). Blood was drawn from 2 steers per pen (n = 84/d) on d −1, 2, 6, 13, 27, 55, 83, 111, and 131 relative to implanting and d −1, 11, and 19 relative to ZH supplementation. Steers were fed for 153 or 174 d depending on block. Overall ADG (1.4, 1.7, and 1.8 kg for NI, REV-S and REV-X, respectively) and G:F (0.16, 0.18 and 0.19) were increased ($P < 0.05$) as TBA and E_2 dose increased. Carcass-adjusted ADG (1.5 vs. 1.7 kg for 0 and 8.3 mg/kg ZH respectively) and G:F (0.17 vs. 0.19) were increased ($P < 0.05$) by ZH. Serum urea-N increased ($P < 0.05$) over time (no implant × day interaction, $P = 0.16$). Implanting decreased ($P < 0.05$) SUN from d 2 through d 131 and SUN tended ($P = 0.08$) to be less for REV-S than REV-X at d 13 but was otherwise not different among implants. Feeding ZH decreased ($P < 0.05$) SUN. Serum NEFA concentrations were not affected by implants ($P = 0.44$). There was a day × ZH interaction ($P = 0.06$) for NEFA; steers not fed ZH had similar ($P > 0.10$) NEFA concentrations on d −1, 11, and 19, whereas ZH steers had increased ($P < 0.01$) NEFA concentrations at d 11 of ZH feeding. We conclude that implanting decreased SUN but a greater dose of TBA and E_2 did not result in further changes in SUN. Moreover, feeding ZH affected steer metabolism by decreasing SUN and increasing serum NEFA. These metabolic responses during ZH may aid in explaining steer performance and carcass responses to ZH.

Key Words: beef steers, estradiol-17β, zilpaterol hydrochloride

W162 Canonical relationships of body shape of grazing bulls under tropical conditions. H. J. Fernandes*[1], L. O. Tedeschi[3], M. F. Paulino[2], M. O. Porto[2], and L. M. Paiva[1], [1]*State University of Mato Grosso do Sul*, *Aquidauana, Brazil*, [2]*Federal University of Viçosa*, *Viçosa, MG, Brazil*, [3]*Texas A&M University*, *College Station*.

The objective of this study was to analyze and compare the changes of body shape, using body measurements (BM) of Nellore crossbred bulls (n = 20) under grazing conditions using canonical equations. Animals were grazing *Brachiaria decumbens* Stapf and received either mineral (control; C) or 3 concentrate supplementation programs (different protein patterns). Animals in the programs T1, T2, and T3 received 1.2 kg of a concentrate containing 32, 25, and 9% of CP during the nursing phase, 1.5 kg of isonitrogenous concentrate (35% CP) with 8, 4, and 0% of urea during the dry season, and 2.0 kg of isonitrogenous concentrate (27% CP) with 6, 3, and 0% of urea during the rainy season; respectively. The BM were taken every 28 d and included hooks width, pins width, pelvic girdle length, rump height, abdomen width, body length, height at withers, and rib depth. The first and the second canonical variables for each phase and for the entire experimental period was developed using all BM. The most important BM to explain the differences in animal′s body shape were rump height, height at withers, pins width, and rib depth for the nursing phase; rib depth, body length, abdomen width, and pelvic girdle length for the dry season; rump height, body length, abdomen width, and hooks width for the rainy season; and rib depth, pins width, rump height, and height at withers for the complete experimental period. Dietary supplementation did not affect the animal′s body shape in the nursing phase. Animals in the C program had heavier hindquarter during the dry season, and during the rainy season they were higher, longer, and wider than animals receiving concentrate supplementations. The animals in the T1 program tended to be higher and longer than animals in the other supplementation programs (T2 and T3). The results of the complete experimental period indicated animals in the C program tended to be shorter and wider, suggesting animals with smaller mature size likely due to malnutrition. Further studies should evaluate the relationship between body shapes and variations in body composition of the animals.

Key Words: biometrics, cattle, growth

W163 Comparison of mathematical functions to describe the growth of grazing bulls in tropical conditions. H. J. Fernandes*[1], L. O. Tedeschi[2], M. F. Paulino[3], A. G. Silva[3], and L. M. Paiva[1], [1]*State University of Mato Grosso do Sul*, *Aquidauana, Brazil*, [2]*Texas A&M University*, *College Station*, [3]*Federal University of Viçosa*, *Viçosa, MG, Brazil*.

The availability of forage throughout the year is not constant and it can change the pattern of growth of grazing animals. The goal of this study was to evaluate different mathematical functions to characterize the growth of grazing Nellore crossbred bulls (n = 20) under tropical conditions. The animals had initial and final BW of 129 ± 28.1 and 405 ± 62.0 kg, initial age of 130 ± 30 d, and grazed *Brachiaria decumbens* Stapf during 420 d. BW was recorded every 28 d. Five mathematical functions (multiphase, linear, logarithmic, Gompertz, and Logistic) were used to describe the BW of the bulls. The multiphasic equation used 3 phases: 2 linear phases in which the difference was the ADG and a third phase represented by a Logistic model. The time points (thresholds) between these phases were assumed to be parameters of the function. The assessment of the adequacy of the mathematical functions was performed using the coefficient of determination, the simultaneous *F*-test of identity of the parameters, the concordance correlation coefficient, and the square root of the mean square error of prediction (MSEP). The analysis of the paired MSEP and the difference of Akaike′s Information Criterion (AIC) between mathematical functions were used to compare accuracy and precision of the functions. Adequacy of the mathematical functions (Table 1), the paired MSEP and the difference of AIC indicated the multiphasic function was more accurate and precise than the other functions in describing the growth of grazing beef cattle in tropical conditions. This was likely because of the effect of the dry season on the growth pattern of the animals. Other multiphasic functions should be evaluated to define the most appropriate equation for each production condition.

Table 1. Adequacy statistics of the functions[1]

Functions	r^2	P- value	CCC	RMSEP
Multiphase	0.993	0.617	0.996	6.83
Linear	0.961	0.678	0.980	16.1
Gompertz	0.916	< 0.001	0.945	25.0
Logarithmic	0.902	< 0.001	0.936	26.7
Logistic	0.861	< 0.001	0.886	34.0

[1]r^2 = coefficient of determination, *P* – value = probability of the *F*-test for intercept equal to zero and slope equal to one, CCC = concordance correlation coefficient, RMSEP = square root of the MSEP.

Key Words: beef cattle, grazing, seasonality

W164 Expression of specific genes regulating mammary growth in pre-pubertal Holstein heifers. F. Soberon*, M. J. Meyer, and M. E. Van Amburgh, *Cornell University*, *Ithaca, NY*.

In a previous study, we demonstrated that calves fed greater nutrients from milk replacer from birth to 100 kg BW had significantly increased mammary epithelial cell proliferation compared with calves fed a more restricted diet. Additional work has demonstrated the presence of a putative stem cell population that has been considered nutritionally responsive and might account for the observed cell proliferation. One objective of this study was to identify genetic markers of stem cells associated with the proliferation. Further, changes in mammary growth rate occur from birth to puberty, such as the change from allometric to isometric growth during the peri-pubertal period. The second objective of this study was to evaluate genes that might be responsible for signaling this change in mammary growth from an allometric to an isometric rate. Heifers (n = 66) reared on one of 2 dietary treatments (TRT), restricted (R) 650 g/d or elevated 950 g/d gain, were harvested at 100, 150, 200, 250, 300, or 350 kg BW. Mammary samples (n = 5 to 8) were excised from the mid parenchyma tissue (MPT) and extra parenchyma tissue (EPT), snap frozen and stored at −80°C. Gene expression in mammary tissue was determined by RT-PCR. Data were analyzed using a mixed model with 18S RNA as a covariate. Telomerase transcriptase was used as a marker for stem cells. Further SERPINB5 (maspin) was analyzed as a marker of myoepithelial cell development and a possible signal for changes in growth rate of the mammary gland. Telomerase expression in EPT was lowest ($P < 0.05$) at 100 kg BW for both treatments and tended ($P < 0.1$) to decrease in R at 350 kg BW. Telomerase expression did not differ between TRT in MPT but was lower at 100 and 150 kg BW ($P < 0.05$). Expression of SERPINB5 was significantly increased in EPT at 250 kg BW for both TRT whereas SERPINB5 expression in MPT remained constant among all weight groups. We suggest that SERPINB5 signals the end of allometric growth by arresting the effect of estrogen in the cells extending into the fat pad, but has no effect on the developed parenchymal tissue.

Key Words: mammary growth, calves, serpinb5

W165 Effects of meal timing on anabolic hormone status and energy metabolism in neonatal Holstein calves. K. C. Simon, C. C. Williams*, L. R. Gentry, B. F. Jenny, R. M. Doescher, and A. H. Dolejsiova, *LSU AgCenter*, *Baton Rouge, LA*.

A study was conducted to determine effects of feeding time on metabolic hormone secretion, growth, and energy metabolism in neonatal dairy calves. Twelve Holstein bull calves were randomly assigned to 1 of 2 dietary treatments which included milk replacer fed at a fixed meal time (REG) or a varied meal time (IRR). Body weights were measured every 2 wk from birth to 8 weeks. Serial blood collections were conducted biweekly from wk 2 through 8 at 0530, at 0, 15, 30, 45, 60, 75, 90, 105, 120, 135, and 150 min relative to regularly scheduled feeding time. Plasma was analyzed for ghrelin, leptin, growth hormone (GH), and insulin-like growth factor-1 (IGF-1). Rumen fluid was collected biweekly from wk 2 through 8 for analysis of volatile fatty acids (VFA) and pH. Treatment did not affect ($P > 0.10$) body weight or average daily intake. Mean plasma ghrelin, leptin, GH, and IGF-1 concentrations were not affected ($P > 0.10$) by treatment. A treatment by week interaction was observed ($P < 0.05$) for total plasma ghrelin concentrations, with total plasma ghrelin concentrations higher at wk 2 and 4 in REG calves. Total plasma ghrelin concentrations decreased ($P < 0.05$) in all calves as they aged. A treatment by time interaction was observed ($P < 0.10$) for IGF-1, and a treatment by week by time interaction was observed ($P < 0.10$) for GH and IGF-1. Growth hormone decreased as calves aged, while IGF-1 increased. There was no treatment effect ($P > 0.10$) on rumen VFA concentrations, but acetate, propionate, and butyrate increased ($P < 0.05$) with age. No treatment effect was observed ($P > 0.10$) on rumen pH. At wk 4 and 8, intravenous glucose tolerance tests were performed to assess glucose half life ($T_{1/2}$), glucose clearance rate (k), and insulin concentrations. REG calves had greater ($P < 0.05$) $T_{1/2}$ and lower ($P < 0.05$) k. Peak insulin concentrations were higher ($P < 0.05$) for REG calves. These data suggest that feeding time does not affect overall growth and feed intake but does have an effect on some of the regulatory mechanisms that control them.

Key Words: dairy calves, feeding times, energy metabolism

W166 Effect of supplementing fatty acids to prepartum Holstein cows and milk replacer enriched with linoleic acid on calf performance. M. Garcia*, L. F. Greco, M. G. Favoreto, R. S. Marsola, L. T. Martins, D. Wang, W. W. Thatcher, J. E. P. Santos, and C. R. Staples, *University of Florida*, *Gainesville*.

The aim of this study was to evaluate supplementing linoleic acid (LA) to cows during the last 2 mo of pregnancy and their calves from birth to 60 d of age on calf performance. Cows (n = 96) were fed diets formulated to supply minimum amounts of LA and supplemented without fat, with saturated fatty acids (SFA; Energy Booster 100, MSC) at 1.75% of dietary DM, or with Ca salts of unsaturated fatty acids enriched in LA (UFA; Megalac-R, Church and Dwight, Co.) at 2% of dietary DM. Within 2 h of birth, calves were fed 4 L of colostrum from their own dam or from a dam of the same dietary treatment using an esophageal feeder. Calves were blocked by gender and dam diet and assigned randomly to receive a milk replacer (MR) with low (0.56% LA) or high concentration of LA (1.78% LA, DM basis) for 60 d. Milk replacer (20% fat and 29% CP) was fed twice daily at 6.7 g of fat per kg of metabolic BW and amounts were adjusted weekly. A single grain mix of minimum LA concentration (18.7% CP and 4.2% fat) was offered in ad libitum amounts starting at 31 d of age. Calves fed the high-LA MR had greater ($P < 0.05$) ADG (0.50 vs. 0.45 kg/d) and efficiency of gain (0.63 vs. 0.58 kg of gain per kg of DMI) than calves fed the low-LA MR over the entire period. These benefits occurred during the period of feeding MR alone and during the period of feeding MR and grain mix. Calves born from cows fed SFA prepartum had better ($P = 0.01$) ADG than calves born from cows fed UFA (0.50 vs. 0.45 kg/d due to a tendency ($P = 0.07$) to consume more DM (1.45 vs. 1.40% of BW. Calves fed the high-LA MR had a lower ($P < 0.01$) mean concentration of plasma BHBA (0.9 vs. 1.4 mg/dL). Calves born from dams fed fat tended ($P = 0.07$) to have a greater concentration of BHBA (1.2 vs. 1.0 mg/dL). Mean concentration of plasma NEFA was not affected by MR or prepartum dam diet (190 mEq/L). Increasing average intake of LA from 2.8 to 8.8 g/d from the MR improved calf performance.

Key Words: calves, milk replacer, linoleic acid

W167 The effect of automated feeder system feeding curves (dilution/weaning age) on growth and health of calves fed milk replacer. T. J. Earleywine*, B. L. Miller, and T. E. Johnson, *Land O'Lakes, Inc.*, *Webster City, IA*.

Forty-seven (47) Holstein bull calves with an average initial weight of 43.7 kg were employed in a 49-d trial to evaluate 2 feeding curves on an automated milk replacer (MR) dispensing unit (Förster Technik, Vario Milk Powder Feeder). Calves were allotted to treatment based upon weight and blood gamma globulin status. Calves assigned to both curves were fed a 25% protein/20% fat MR powder to provide equal amounts (24.6 kg DM) through weaning. MR contained milk, soy and

plasma protein sources. Calves were fed either a 12% solids solution MR providing on average 676 g DM per d for 6 wk (12sol/6wk) or a 15% solids solution MR providing on average 822 g DM per d for 5 wk (15sol/5 wk). Calves were on test through 7 wk to limit the effect of weaning age on growth parameters. MR was medicated with 0.28 g neomycin and 0.14 g oxytetracycline/kg. Calf starter (20% CP as-fed) was fed throughout this 49 d trial. Calves were housed by treatment in 2 group pens. There was a trend for increased total gain ($P = 0.08$) for the 15%/5 week treatment. MR intakes and health data were similar ($P \geq 0.37$). Scour score is a 1 - 4 scale (1 = normal, 2 = loose, 3 = water separation, 4 = 3 with severe dehydration). Respiratory score equals days treated with antibiotics for respiratory infection. Data were analyzed by the MIXED procedure in SAS.

Table 1. Feeding Curve

Item	12 sol/6wk	15sol/5wk	P-value	CV
n	23	24		
MR (DM), kg	21.5	21.7	0.60	6.68
BW gain, kg	20.2	23.9	0.08	32.41
Scour score (4 wk)	1.28	1.23	0.37	14.65
Respiratory score (7 wk)	2.12	1.57	0.40	121.68

Key Words: calf, milk replacer, automated feeder

W168 The effect of automated feeder system feeding curves (weaning age) on growth and health of calves fed milk replacer. T. J. Earleywine*, B. L. Miller, and T. E. Johnson, *Land O'Lakes, Inc.*, *Webster City, IA*.

Thirty-six (36) Holstein bull calves with an average initial weight of 43.9 kg were employed in an 84-d trial to evaluate 2 feeding curves on an automated milk replacer (MR) dispensing unit (Förster Technik, Vario Milk Powder Feeder). Calves were allotted to treatment based upon weight and blood gamma globulin status (calf is experimental unit). Calves assigned to both curves were fed a 28% protein / 20% fat MR powder (15% solution) to provide equal amounts (49.1 kg DM) through weaning at 8 or 7 wk. 8-wk weaned calves were offered on average 1021 g MR daily. 7-wk weaned calves were offered on average 1262 g MR/d. MR was medicated with 0.22 g neomycin:0.11 g oxytetracycline/kg. Calf starter (22% CP as-fed) was fed throughout this 84 d trial. As calves were housed by treatment in 2 group pens, starter intake could not be statistically analyzed. 7-wk weaned calves had strong trends for increases in total 8 wk weight gain ($P = 0.06$) and in 12 wk weight gain ($P = 0.08$). Hip height had a strong trend for increase ($P = 0.07$) and heart girth gain was increased ($P = 0.03$) for calves assigned to the 7-wk feeding curve. Data were analyzed by the MIXED procedure in SAS.

Table 1. Weaning age

Item	8 Weeks	7 Weeks	P-value	CV
MR (DM), kg	48.3	46.7	0.01	3.82
Starter (DM, 12 wk), kg	123.4	148.5	- -	- -
BW gain (8 wk), kg	43.3	49.4	0.06	19.88
BW gain (12 wk), kg	80.3	90.0	0.08	18.69
Scour score (4 wk)	1.14	1.19	0.22	11.39
Respiratory score (12 wk)	2.35	1.05	0.25	199.22
Hip height gain, cm	16.35	18.42	0.07	19.00
Heart girth gain, cm	28.15	31.58	0.03	15.47

Key Words: calf, milk replacer, automated feeder

W169 Strategies for feeding full potential rates of calf milk replacer: Two feedings daily and weaned at 7 weeks vs. three feedings daily and weaned at 6 weeks. B. L. Miller*, T. J. Earleywine, and T. E. Johnson, *Land O'Lakes, Inc.*, *Webster City, IA*.

Thirty-eight (38) Holstein bull calves with an average initial weight of 47.9 kg were employed in an 83-d trial to evaluate 2 strategies for feeding full potential rates of milk replacer (MR). The strategies evaluated included: 2 feedings daily with calves weaned at 7 wk (2X/7wk) or 3 feedings daily with calves weaned at 6 wk (3X/6wk). Calves were allotted to treatment based upon weight and blood gamma globulin status. Calves were fed a milk replacer (28% protein / 20% fat) to provide equal total amounts (48.2 kg) of DM per strategy. Actual consumption of MR by treatment is provided. 2X/7wk calves were fed 568 g of MR per feeding or 1135 g of MR daily. 3X/6wk calves received 454 g of MR per feeding or 1362 g of MR daily. During the final wk, 2X/7wk and 3X/6wk calves were offered 568 or 454 g of MR respectively in one feeding (amount = to one feeding during the prior week). MR contained all milk protein and was medicated with 0.22 g neomycin and 0.11 g oxytetracycline/kg. Calf starter (22% CP as fed) was fed throughout this trial. Total gain and body measurements were improved for calves assigned to the 3X/6wk strategy. Data were analyzed by the MIXED procedure in SAS.

Table 1. Strategy

Item	2X/7wk	3X/6wk	P-value	CV
BW gain (7 wk), kg	33.2	36.3	0.6000	18.62
BW gain (12 wk), kg	67.8	77.2	0.0046	13.23
MR (DM), kg	41.8	44.9	0.0025	6.88
Hip height, cm	96.9	99.1	0.0182	2.73
Heart girth, cm	105.8	109.4	0.0004	2.60
Body volume gain, 1	174.2	198.2	0.0040	12.81

Key Words: calf, milk replacer, feedings

W170 Factors affecting pregnancy rate of recipient mares to embryo transfer. L. D. Wallace*, K. J. Stutts, and D. W. Ricks, *Sam Houston State University*, *Huntsville, TX*.

The objective of this study was to determine the effects of age of mare and degree of asynchrony between donor and recipient on pregnancy rate (PR) to embryo transfer in recipient mares. Light-horse mares (n = 34) between 3 and 16 yr of age were used as recipients. Mares were subjected to an artificial photoperiod. Cyclic recipients were examined by palpation and ultrasound at regular intervals and daily during estrus. Reproductive tracts of recipients were examined for follicular activity, ovulation, presence of a corpus luteum, uterine edema, and fluid in the uterine lumen. When necessary, ovulation was hastened by administration of hCG. Fresh, cooled, or frozen semen from various stallions was used to inseminate donors. Embryos were recovered 7 to 8 d after ovulation by non-surgical uterine lavage. Embryos were transferred non-surgically to recipient mares between 5 and 9 d post ovulation. Recipients were examined for pregnancy by ultrasound on d 25 and 110. PR was analyzed by chi-squared analysis using the frequency procedure. Pearson correlation coefficients were used to determine the relationship between PR and level of asynchrony. Age of recipient had a significant effect on PR to embryo transfer. Mares age 3–9 yr (76.0%) had a higher ($P < 0.02$) PR at d 25 of pregnancy than mares age 10–16 yr (33.3%). Mares age 3–9 yr also had a numerically higher PR at d 110; however this difference was not significant. A negative relationship ($P < 0.03$) existed between asynchrony and PR at d 25 ($r = -0.51$) and d 100 ($r = -0.39$) indicating a decrease in pregnancy rate as asynchrony between the estrous cycle of the donor and the recipient increased in terms of days. Level of asynchrony ranged from 0 to 6 d. Results of this study indicate that PR to embryo transfer is lower in older recipient mares (age 10–16 yr) compared with younger mares (age 3–9 yr) and PR is decreased as asynchrony between the donor and recipient increases from 0 to 6 d.

Key Words: equine, embryo transfer, recipients

W171 Growth models for horses differ based on date of birth. A. L. Graeff* and W. B. Staniar, *The Pennsylvania State University*, *University Park*.

Understanding growth patterns may be critical in balancing the economic and perceived athletic benefits of large size against the associated risk of skeletal abnormalities. Thoroughbred growth data indicate that models of growth should be different depending on the time of year an animal is born. Our objective was to compare parameter estimates of a sigmoidal (Richards) growth model fit to a large database of Thoroughbred weight and wither height measurements. Data for this study consisted of 35,285 weight measurements and 26,063 height measurements from 2,184 horses. Data were collected from 1977 to 2007 on farms located in the United Kingdom, Ireland, and the United States. Data were divided into consecutive 30 d periods approximating month of birth as January (J30), February (F60), March (M90), April (A120) and May (M150). Growth curves were fit to each data set using a nonlinear mixed model with fixed effects associated with the main parameters (A, b, k, M), and random effects associated with individual horses added to the A and M parameters. Differences in parameter estimates between data sets were evaluated by ANOVA with Bonferroni corrected multiple comparisons and considered significant at $P < 0.05$. There were differences in parameter estimates between all 5 data sets defining specific growth curves for each. Most striking were differences in the b, k, and M parameters, each representing shape characteristics of the growth curve over time. An overall representation of these may be described as a sequential change moving from relatively slow early and moderate later growth in the J30 and F60 to rapid early and slow later growth in the M150. The M90 and A120 data sets were intermediate. Little emphasis should be placed on the A parameter as it represents mature size and 99% of the data for this study is from horses < 4 years of age. The growth models developed in this study confirm the influence of month of birth on growth patterns demonstrated in previous Thoroughbred growth studies. Further, these models of growth will be useful in investigating hypotheses related to the impact of the environment, and more specifically management on modifying equine growth.

Key Words: equine, growth model, Thoroughbred

W172 The impact of molasses-based blocks versus sweet feed on blood glucose in horses. C. D. Gunkel*, J. S. Drouillard, L. W. Murray, and T. L. Slough, *Kansas State University*, *Manhattan*.

This study compared circulating blood glucose concentrations (GLC) in horses fed molasses-based blocks or a textured sweet feed. Six 4-yr-old Quarter horse geldings (488 ± 20 kg BW) equipped with continuous glucose monitors (Dexcom, San Diego, CA) were used in a switch back experiment conducted over 2 6-d periods with a 4-d washout phase between periods. Treatments consisted of a sweet feed concentrate (SF) fed twice daily or ad libitum access to a molasses-based block (BL) supplement. Long-stemmed prairie hay and salt blocks were offered ad libitum. SF was fed at 700 and 1400 h, gradually increasing meal size to 0.82-kg over the first 3 feedings. Motion-sensing cameras were placed above each block feeder, generating time-stamped photographs to document time and duration of BL usage. Horses consumed 1.2 kg/d of BL and had GLC of 75.4 ± 2.3 mg/dL. Horses consumed 1.46 kg/d SF and had mean GLC of 53.4 ± 4.2 mg/dL. In the BL group, daily min to max GLC values varied by 74.2 mg/dL, while the SF group varied by 86.7 mg/dL. Technical difficulties with glucose monitors resulted in large blocks of missing data for 2 animals, so 4 of 6 animals were modeled. The ARIMA procedure of SAS Version 9.1 was used to examine cross-correlations between min spent at BL and GLC per 15-min period, providing information on the delay between BL intake and glucose appearance in blood. No significant correlation was detected in one horse, while 3 horses showed significant correlation ($P \leq 0.05$). Lag patterns varied from an instantaneous effect to delays of 15 min to 4.5 h. The ARIMA procedure was used to obtain a Box-Jenkins model of GLC measurements and GLC per 15-min period with a SEM that accounted for serial correlation (non-independence) among GLC readings over time, and a 95% confidence interval was calculated. Mean, min, and max GLC values and SEM were highly variable among horses, thus no significant treatment effects were detected.

Key Words: low-moisture block, glucose, molasses

W173 Short-term selenium depletion and oxidative stress in the horse. M. Brummer*, S. H. Hayes, J. E. Earing, S. M. McCown, and L. M. Lawrence, *University of Kentucky*, *Lexington*.

Various compounds such as vitamin A, E and C, catalase, superoxide dismutase and the seleno-enzyme, glutathione peroxidase (GSH-Px) contribute to the total antioxidant capacity (TAC) of the body. Our objec-

tive was to investigate the relationship between Se status and indicators of antioxidant defense and oxidative damage in adult, idle horses. We hypothesized that low Se status would result in lower TAC and more oxidative damage. Serum malondialdehyde (MDA) concentration was used as indicator of oxidative damage. Twenty 4 mature horses were kept on low Se pasture (0.04 ppm Se; DM) with access to salt. Sixteen of these horses received no supplementation (P), while 8 horses (PC) received 1.8 kg concentrate per day (0.3 ppm Se; DM). Blood samples were obtained from all horses after 4 mo on their respective diets. Data were analyzed using the PROC CORR and PROC TTEST procedures of SAS 9.1. Serum Se concentration ranged from 69 – 193 ng/mL and were higher for horses in PC ($P < 0.0001$). A serum Se concentration above 130 ng/mL is indicative of adequate Se status. All horses in P had serum Se concentration below 130 ng/ml and were considered to have low Se status. Serum GSH-Px activity was not correlated with serum Se and no difference existed between P and PC. TAC was not correlated with serum Se or serum GSH-Px activity and did not differ between P (mean ± SE; 1.011 ± 0.43 m*M* Trolox equivalents) and PC (0.981 ± 0.45 m*M* Trolox equivalents). No correlation was found between MDA concentration and serum GSH-Px activity or serum Se concentration. A trend existed ($P = 0.078$) for higher MDA concentration in PC (28.89 ± 0.041 μMol MDA) than P (27.59 ± 0.021 μMol MDA). It has been suggested that GSH-Px may play a small role in the total cellular antioxidant system, and based on these results, the same may be true for the extracellular total antioxidant system. In addition Se status did not affect the measure of oxidative damage used in this study, possibly because the horses were not challenged by an oxidative stressor such as exercise or infection.

Key Words: glutathione peroxidase, TBARS, antioxidant

W174 In vivo digestibility and mean retention time estimates of young and mature horses receiving the same diet. J. E. Earing*, S. H. Hayes, M. Brummer, S. M. McCown, A. G. Parks, and L. M. Lawrence, *University of Kentucky*, *Lexington*.

Forages are important sources of nutrients for mature horses, however little research has been conducted to evaluate fiber utilization in young, growing horses. This study compared in vivo digestibility and mean retention time (MRT) estimates in yearling and mature horses fed the same diet. Six yearling colts and 6 mature geldings (average age, 14 y) were used. Horses received a 75%:25% forage: concentrate diet consisting of timothy cubes (9.8% CP, 63.7% NDF, 38.0% ADF), sweet feed (20.9% CP, 19.7% NDF, 9.7% ADF), and supplement pellet (35.0% CP, 13.5% NDF, 7.9% ADF). Yearlings and geldings were offered the same amount of feed on a metabolic body weight (MBW; $BW^{0.75}$) basis. All animals were dosed with Yb-labeled hay and CoEDTA. Feces were collected in a collection harness every 4 h for 3 d. Each 4 h subsample was analyzed for Yb and Co content. The remaining fecal material was compiled daily by horse; a subsample was retained for dry matter digestibility (DMD), NDF digestibility (NDFD), and organic matter digestibility (OMD) analysis. The MRT was estimated using the equation of Blaxter et al. (1956). The effect of age on digestibility and passage was determined using Proc GLM of SAS; each pair of animals was treated as a block. Feed refusals were minimal and marker dose was completely consumed. Feed intake (as % MBW) was similar between the yearlings and geldings. Mean in vivo DMD, NDFD, and OMD were 62.7% and 55.6% ($P = 0.019$), 47.7% and 36.9% ($P = 0.014$), 65.6% and 57.6% ($P = 0.031$) for the yearlings and geldings, respectively. The MRT of the fluid phase of digesta was 23.5 h for the yearlings and 21.4 h for the geldings ($P = 0.149$). The MRT of the particulate phase was 26.2 h and 22.7 h for the yearlings and geldings, respectively ($P = 0.019$). Yearlings in this experiment were better able to digest the forage-based diet than the geldings. This difference may be due to the longer MRT for the particulate phase in the yearlings and may be a biological mechanism which allows for increased nutrient digestion during growth.

Key Words: yearlings, markers, passage rate

W175 Effect of grazing fall pasture on indicators of hindgut pH and fermentation characteristics in horses. A. C. Pearson, P. D. Siciliano*, S. J. McLeod, and V. Fellner, *North Carolina State University*, *Raleigh*.

Six stock-type geldings ranging in age from 5 to 8 yr and weighing 553 ± 37 kg (mean ± SD) were used in a completely randomized 2-period switch-back design to determine the effect of grazing fall pasture having moderate non-structural carbohydrate concentration (NSC; 11.3 ± 1.4%), or fed hay made from the same pasture having lower NSC concentration (6.8%), on parameters reflecting hindgut pH and fermentation characteristics. Horses were initially assigned to one of 2 dietary treatments: pasture fed (PF; n = 3) or hay fed (HF; n = 3). The PF horses had access to tall fescue pasture from 1300 to 700 the following day, followed by stall confinement from 700 to 1300 each day for 14 d. The HF horses were fed tall fescue hay at a rate of 2% of body weight (as-fed) one time per d at 1300 each day for 14 d. Following the first 14-d period treatments were switched for an additional 14 d period so that all horses receive all treatments. At 700 on d-7 of each period pH was measured in feces of individual horses and individual batch cultures using each horse's fresh feces as inoculum and alfalfa meal as substrate were performed. Acetate, propionate and butyrate concentrations were measured in culture media following 48 h of incubation. Differences in response variables between treatments within horses were analyzed using a paired *t*-test and results are expressed as the mean of differences between treatments within horses (±SE). Fecal pH was 0.30 ± 0.14 pH units lower ($P = 0.042$) when horses consumed pasture compared with hay. Batch culture media acetate and butyrate concentration, expressed as a molar percent, did not differ between treatments. Batch culture media propionate concentration decreased ($P = 0.002$) by 5.1 ± 1.1 molar % and the acetate:propionate ratio increased ($P = 0.02$) by 0.55 ± 0.21 when horses were fed pasture compared with hay. These results suggest pasture containing moderate amounts of NSC can alter indicators of hindgut pH and some fermentation characteristics. The implications of these findings on hindgut health requires further investigation.

Key Words: horse, non-structural carbohydrates, pasture

W176 Summary of equine pastures utilizing a line point transect to measure vegetative cover to reduce sediment and nutrient losses, enhancing pasture quality. A. Swinker*[1], D. Foulk[1], J. Malot[2], S. Truax[2], J. Weld[1], and M. Harper[1], [1]*Pennsylvania State University*, [2]*USDA Natural Resources Conservation Service, Harrisburg, PA*.

Twenty horse farms representative of the industry (7 to 99 horses) from Pennsylvania, northern Virginia and Maryland were surveyed. Farm surveys were conducted to quantify equine pasture quality, to analyze the pasture conditions under the management systems and the "efficiency" of those practices. Data were recorded using an Excel spread sheet; SPSS was used to determine frequencies. Existing pasture condition tools used for conservation and sediment loads were evaluated. None of the surveyed horse farms utilized an intensive grazing system, 2 (10%) of the farms used a pasture grazing system that grazed 24 h 7 d /week and were overstocked; 80% of the farms limited grazing or restricted the horse's grazing times. Only 3 farms rested pastures for at least 2 weeks before re-grazing. Equine pasture data were obtained using the

"Line Point Transect" and "Pasture Condition Scoring" methods. Percent vegetative canopy cover, % basal stem cover, % pasture forage, % forage canopy, number of forage species and the Pasture Condition Score were recorded. Overall, surveyed farms averaged 87% canopy cover (range 53–100%), 45% basal stem cover (69–21%), 56% good quality forage (89–11%), 63% canopy from good forage (97–13%), 19 plant species including weeds (range 35–12), 5 forage species (7–2) and averaged 25.5 on Pasture Condition Score with a range of 5–40. Past studies report soil loss reduction will be greater if the initial canopy cover is less than 70%. One of the surveyed farm's pastures contained 53% cover; this contributed to a loss of 30 tons of sediment per hectare per year; a second farm with a 75% canopy had a 10-ton loss; and there were 7 farms with percent canopy in the 80s resulting in a 5-ton loss. The remaining 9 farms had over 90% vegetative canopy. Eighty percent of the surveyed horse farms maintained acceptable vegetative cover of desirable and weed species reducing nutrient and sediment loss. More strategies are needed to preserve vegetative cover to enhance pasture quality and help to reduce sediment and nutrient loss.

Key Words: equine pasture, condition, sediment loss

W177 Segregation of AB_098561: c.1470G>A SNP of the serotonin transporter gene (*SLC6A4*) in Mangalarga Brazilian horses. L. Arneiro*[1,2], M. Mota[1,2], and R. Curi[2], [1]*Universida Estadual Paulista*, *Jaboticabal, São Paulo, Brasil*, [2]*Universidade Estadual Paulista*, *Botucatu, São Paulo, Brasil*.

In equines (*Equus caballus*), behavioral changes are important because of the uses of these animals in different modalities such as jumping, running, dressage, etc. It is considered that the gene coder of serotonin transporter has influence on behavioral traits in animals, controlling the serotonin reabsortion in the synaptic gaps. The aim of this study was to evaluate the segregation of SNP AB_098561: c.1470G > A of gene SLC6A4 in a representative sample of Mangalarga bred in São Paulo state. The idea was to determine if there is application potential of the association studies between molecular markers and economic interest traits for this breed. Thus, 151 animals of both sexes were genotyped by PCR-RFLP from the amplification of 359-bp gene fragment and digestion with *Hha*I restriction enzyme. Using PopGene 1.32 program, allele frequencies (0.079 for the A allele and 0.921 for the G allele), chi-squared (1.075), observed (0.159) and expected heterozygosity (0.147), Shannon gene diversity index (0.277), fixation index F (−0.086) and Ewens-Watterson selective neutrality (0.853), were estimated. From the results it was concluded that the studied population is in Hardy Weinberg equilibrium for the locus in question, showing the absence of selection in favor of one allele. However, the observed value for the selective neutrality test is near the superior limit (0,99), not excluding the possibility of using the marker in association studies with behavioral traits. However, it must be emphasized that due to the extremely low frequency of allele A, studies involving a larger sample of animals should be done.

Financial support: Fundunesp and CNPq

Key Words: equine, gene, serotonin

W178 The use of equine blood parameters to identify chronic exposure to feed-borne *Fusarium* mycotoxins: A field study. M. Mortson*, C. K. Girish, and T. K. Smith, *University of Guelph*, *Guelph, Ontario, Canada*.

Feed-borne mycotoxins consumed at low levels over an extended period of time may have an effect on equine performance and breeding ability and may potentially cause immunosuppression. An equine biomarker that indicates an exposure to a wide range of *Fusarium* mycotoxins including deoxynivalenol (DON, vomitoxin), zearalenone, and T-2 toxin has not yet been identified. A field study was conducted to identify a potential biomarker in equine blood that reflects chronic exposure to low levels of feed-borne *Fusarium* mycotoxins. This was done by identifying any correlation between serum gamma-glutamyltransferase (GGT), urea, and immunoglobulin A (IgA), and the presence of naturally occurring *Fusarium* mycotoxins in forages and concentrates. A total of 30 horses from 18 Ontario horse farms and 1 New Jersey horse farm participated in the study. Blood samples were collected from each horse as well as a sample of hay and concentrate. Serum GGT, urea, and IgA were measured and a correlation analysis was completed. Mycotoxin concentrations were determined by a combination of HPLC and GC/MS methodology. DON was present in feed samples collected at 18 farms with an average concentration of 0.48 mg/kg. The range was from 0.13 mg/kg to 1.5 mg/kg. 15-acetyl DON was the second most prevalent *Fusarium* mycotoxin in feed samples (n = 6) followed by zearalenone (n = 5). No significant correlations were identified between the concentrations of *Fusarium* mycotoxins in the samples collected and the equine blood parameters analyzed. It can be concluded that feed-borne mycotoxins are present in many horse feeds on farms in Eastern North America. Biomarkers for chronic *Fusarium* mycotoxicoses, however, remain to be identified.

Key Words: *Fusarium*, mycotoxins, equine

W179 Influence of velocity on stride variables of the Wilbur-Cruce Mission horse intermediate gait. M. Nicodemus*[1] and J. Beranger[2], [1]*Mississippi State University*, *Mississippi State,* [2]*American Livestock Breeds Conservancy*, *Pittsboro, NC*.

Wilbur-Cruce Mission horse (WCM) is a strain of Spanish Colonial horse that originated from the Arizona mountains. Due to the breed's sure-footedness, the WCM is assumed to be gaited like other Spanish Colonial breeds. Study objectives were to determine the relationship between trotting velocities and the WCM stride variables and whether at trotting velocities the WCM can perform a 4-beat stepping gait. Nine WCM were worked from the ground along the arena railing at both a slow (3.0 ± 0.3 m/s) and fast (4.7 ± 0.4 m/s) trotting velocity. Horses were filmed along the long side of the arena. Frame-by-frame analysis was performed documenting hoof contact and lift-off for 10 strides for both velocities. Stride variables were given as a % of stride duration. Student's paired *t*-tests were performed to determine gait symmetry and differences between stride variables at the slow and fast velocity ($P < 0.05$). Stance durations between left and right variables were not significantly different indicating gait symmetry, and thus, left and right stride variables were collapsed ($P < 0.05$). At the fast velocity the WCM performed a shorter stride duration and suspension, while demonstrating a longer stride length and diagonal bipedal support ($P < 0.05$, Table 1). Stance durations, stride rate, and diagonal advanced placement (DAP) and completion (DAC) remained consistent between velocities. While other Spanish Colonial horses were found to perform 4-beat stepping gaits at similar velocities, the WCM performed at both velocities a trot. Although similarities can be found between this study and other trotting studies, velocity changes for the WCM, unlike that of other trotting studies, did not impact stance durations, DAP, and DAC. With less than 100 horses representing the breed, these stride variables can be applied in distinguishing the WCM from other Spanish Colonial breeds and assist in further breed development.

Table 1. Means ± SD for WCM stride variables at a slow and fast trotting velocity

	Slow Velocity	Fast Velocity
Stride Duration (ms)	783 ± 25[a]	689 ± 26[a]
Stride Length (m)	2.3 ± 0.2[b]	3.2 ± 0.2[b]
Stride Rate (strides/s)	1.3 ± 0.1	1.4 ± 0.1
Fore Stance (%)	43 ± 3	42 ± 3
Hind Stance (%)	43 ± 3	42 ± 3
DAP (%)	0 ± 0	0 ± 0
DAC (%)	0 ± 0	0 ± 0
Diagonal Bipedal Support (%)	85 ± 1[c]	83 ± 1[c]
Suspension (%)	15 ± 1[d]	17 ± 1[d]

Similar superscripts indicate significant differences ($P < 0.05$) between velocities.

Key Words: Spanish Colonial horse, stride variables

W180 Nutraceutical extracts affect oxidative stress and antioxidant status in intensely exercising horses. D. Smarsh*, N. Liburt, J. Streltsova, K. McKeever, and C. Williams, *Rutgers, The State University of New Jersey*, *New Brunswick*.

Many nutraceuticals are used as equine supplements without their efficacy having been scientifically tested. Black tea, cranberries, orange peel and ginger are a few of those nutraceuticals that warrant further study. The objective of this study was to test the effects of single doses of black tea, cranberry, orange peel and ginger extract on markers of oxidative stress and antioxidant status following exercise in horses. Study 1: Nine mature, healthy unfit Standardbred mares were administered 2 L of either placebo (water; W), orange peel extract (O; 30g extract), or decaffeinated black tea extract (T; 28g extract). Study 2: the same mares were administered 2 L of either placebo (water; W), cranberry extract (C; 30g extract), or ginger extract (G; 30g extract). In each study mares were given the extracts via nasogastric tube 1 h before performing a graded exercise test (GXT), in a randomized crossover design with at least 7 d between GXTs. Blood samples were collected at rest, at fatigue, 1, and 24-h post-exercise and analyzed for lipid hydroperoxides (LPO), total glutathione (GSH-T), glutathione peroxidase (GPx), α-tocopherol (TOC), β-carotene (BC), and retinol. Data was statistically analyzed using a repeated measures ANOVA. Study 1: There was no effect ($P > 0.05$) of treatment for LPO, GSH-T, GPx, TOC or BC. Retinol was higher for both T ($P = 0.0006$) and W ($P = 0.004$) than for O. Study 2: There was no treatment effect ($P > 0.05$) for LPO, GPx, GSH-T, RET, BC or TOC. These results show that a single dose of black tea may be beneficial in increasing antioxidant status in exercising horses, however, effects on oxidative stress were not found with any of the nutraceuticals. Further investigation is needed as to whether long-term supplementation would enhance these effects.

Key Words: antioxidant, black tea, equine

W181 Whole farm balance of nitrogen and phosphorus on horse farms in the Chesapeake Bay watershed. M. T. Harper*, A. Swinker, and K. B. Kephart, *Pennsylvania State University*, *University Park*.

Whole farm nutrient balances of inputs and outputs can be used to assess the risk of non-point source pollution and identify pollution reduction strategies. Many nutrient balance studies have been conducted on livestock and poultry farms. To our knowledge this is the first study to characterize nitrogen (N) and phosphorus (P) balance on horse farms. Nitrogen and P inputs and outputs on 13 horse farms in the Chesapeake Bay watershed were estimated to determine the risk of non-point source pollution. Annual amounts of imported fertilizer, hay, concentrate, and bedding were recorded for each of the farms based on estimates reported by farm managers. Samples of hay, concentrate, and bedding from each farm were analyzed for N and P. Small square bales were weighed and multiplied by the number of bales received. Bedding volumes were multiplied by respective nutrient concentrations to estimate mass values. Manure nutrient exports but not the sale of horses were included in the calculation of nutrient output. Four of the 13 farms did not export manure. Four farms exported a portion of their manure estimated by the farm owner. Five farms exported all collected manure which was estimated to be (24 kg/d/head) × (% time in a stall). Nutrient exports were estimated by multiplying the manure amount by the analyzed nutrient value of the composite manure samples or fecal samples from each farm. The mean farm balance ((import-export/import) × 100) of N and P for all farms was 75 ± 7.9% and 52 ± 17%, for farms exporting some manure was 87 ± 11% and 80 ± 17%, and for farms exporting all manure was 46 ± 6.8% and −8 ± 23.3%, respectively. The overall mean balance per animal unit was 42.8 ± 6.7 kg for N and 7.3 ± 2.7 kg for P. The overall mean balance per hectare was 118.7 ± 21.7 kg for N and 17.2 ± 5.7 kg for P. No farms achieved N balance. Only farms exporting all collected manure were able to be in P balance. Manure must be exported and/or fewer nutrients must be imported to approach nutrient balance. It appears that to achieve whole farm nutrient balance, horse operations must export a large proportion of the manure generated by the farm.

Key Words: nitrogen and phosphorus, horse, nutrient balance

W182 Effect of dietary energy manipulation on mares and their foals: Foaling parameters. K. N. Winsco[1], J. L. Lucia*[1], C. J. Hammer[2,3], and J. A. Coverdale[1], [1]*Department of Animal Science, Texas A&M University*, *College Station,* [2]*Department of Animal Sciences, North Dakota State University*, *Fargo,* [3]*Center for Nutrition and Pregnancy*, *Fargo, ND*.

To determine the effect of dietary DE manipulation on foaling parameters, 30 Quarter Horse mares (538 to 695 kg of BW and 4 to 19 yrs of age) were blocked by expected foaling date. All mares were allowed ad libitum access to coastal bermudagrass pasture and randomly assigned within block to 1 of 2 dietary treatments: pasture (P) or pasture + concentrate (PC; concentrate fed at 0.75% BW on an as-fed basis). Dietary treatments began 110 d before expected foaling date and were terminated at parturition. When parturition was observed, the following foaling parameters were recorded: time of water break to birth, time to stand, and time of birth to placenta expulsion. Total length of gestation was calculated and placenta weight was recorded. Additionally, total volume, specific gravity, and Brix % of colostrum were measured. Physical measurements were also obtained which included mare BW, foal BW, foal wither and hip height, and foal body length. All data were analyzed using PROC GLM of SAS. There was no influence of dietary treatment on foaling parameters; however, time from birth to placenta expulsion tended ($P = 0.06$) to be longer in P mares. There was also no effect of treatment ($P \geq 0.46$) on foal physical measurements obtained following parturition, although foals from P mares tended ($P = 0.06$) to exhibit greater hip height compared with foals from PC mares. Ratio of placenta to mare BW, placenta to foal BW, and the ratio of foal BW to mare BW were not affected by treatment ($P \geq 0.16$). There was no influence of dietary treatment on total colostrum volume ($P \geq 0.56$). There was an influence of DE manipulation on colostrum quality indicated by greater specific gravity and refractometer values (Brix %; $P \leq 0.01$) in P mares compared with PC. In summary, these data indicate that dietary

DE manipulation of mares in late gestation affects colostrum quality, but not volume. Furthermore, maternal DE manipulation did not influence foaling parameters or foal physical characteristics.

Key Words: mares, energy, foaling

W183 Comparison of a commercially available glucometer to a standardized laboratory method for glucose analysis in healthy horses. K. O'Diam*[1], J. Sylvester[2], and K. Cole[1], [1]*The Ohio State University*, *Columbus*, [2]*MARS Horsecare US, Inc.*, *Dalton, OH*.

Extremes in blood glucose concentrations can be detrimental to a horse's health. Elevated blood glucose and insulin levels for extended periods of time are associated with equine metabolic syndrome and laminitis while decreased blood glucose concentrations may result in seizures. The ability to quickly and accurately determine blood glucose levels in the field can facilitate important management decisions. Blood samples (n = 432) obtained from 6 healthy horses for use in a separate study were used to determine the accuracy of a commercially available hand-held point-of-care (POC) glucometer in comparison to a standard laboratory method for glucose analysis. Blood samples were collected via jugular catheter into heparinized tubes and 0.6 μL of whole blood was immediately analyzed by a POC glucometer (POC/WB). Plasma was separated by centrifugation and analyzed using an automated biochemistry analyzer (CHEM). In addition, plasma glucose concentrations were also determined using the POC glucometer (POC/PL), although the POC glucometer was designed for use with whole blood. Statistical analyses were performed on paired data using correlation and mixed procedures of SAS. Overall, mean glucose concentrations determined by POC/PL, CHEM and POC/WB were 101.4mg/dL, 97.0 mg/dL and 95.5 mg/dL, respectively. Both POC/PL and POC/WB were positively correlated with the standard laboratory method (CHEM; r = 0.78 and 0.73, respectively; $P < 0.0001$). A positive correlation was also observed, to a lesser extent, between POC glucometry using whole blood (POC/WB) and plasma (POC/PL; r = 0.59; $P < 0.0001$). These data suggest that hand-held POC glucometers may be useful in the field for determining blood glucose levels in horses.

Key Words: glucose, glucometer, horse

W184 Effects on lactation performance when slick hair gene is simulated in dairy cattle in the tropics. R. M. Mejía*[1,2], J. A. Ortuño[1], G. J. Lascano[2], and M. Vélez[1], [1]*Zamorano University*, *El Zamorano, Honduras*, [2]*The Pennsylvania State University*, *University Park*.

In the tropical and subtropical regions, high temperatures affect dairy cattle, reducing the metabolic activities of the animal and decreasing the blood flow to the udder. Cattle with the slick hair gene tolerate high temperatures and humidity much better than normal haired cows. The objective of the present study was to determine if the effect on lactation performance of slick hair gene cows can be simulated through hair clipping. The experiment was conducted in Zamorano University, Honduras located at 800 m.a.s.l. (average year-round temperature of 23° C). Thirty two multiparous crossbred, Holstein, Jersey and Brown Swiss lactating cows were monitored through 140 d of lactation. Cows were blocked according to their age, body condition score and milk production and assigned randomly to two different coat treatments. Treatments consisted of normal-haired (NH; n=16) and clipped-hair lactating cows (CH; n=16). Hair was clipped from the cow′s barrel, neck and legs at the beginning of the experiment and on d 60. CH and NH cows were kept under the same environmental conditions. Rectal temperature (at 1400 h) and milk yield (kg/d) were measured once weekly. All data were analyzed according to a randomized complete block design with repeated measures using the MIXED procedure of SAS. NH cows had lower temperatures (35.2 vs.36.4° C ± 0.58; P = 0.01). There was a significant interaction effect between time and treatment (P = 0.05) that was maintained consistently throughout the experiment. Milk yield (kg/day) was higher when cows were clipped (13.4 vs. 10.8 ± 0.26; P = 0.003). The decrease in rectal temperature and increase in milk production reflects the capacity of CH cows to mimic lactation performance of slick-haired gene cows resulting in an enhanced lactation performance.

Key Words: slick hair gene, clipped-haired cows, lactation performance

W185 Effects of a direct-fed microbial product on milk production by crossbred dairy cows in the Brazilian Cerrado. R. D. Sainz*[1], C. U. Magnabosco[2,3], R. A. Carnevalli[3], R. Guimamães Jr.[2], M. M. S. Mamede[4,3], J. R. Costa Jr.[5,3], and E. A. Filgueiras[6], [1]*University of California*, *Davis,* [2]*Embrapa Cerrados*, *Planaltina, DF, Brazil*, [3]*Embrapa Arroz e Feijão*, *Santo Antonio de Goiás, GO, Brazil*, [4]*Associação Goiana de Criadores de Zebu*, *Goiânia, GO, Brazil*, [5]*Universidade Estadual de Goiás*, *Goiânia, GO, Brazil*, [6]*Bioformula*, *Goiânia, GO, Brazil*.

Thirty-two Girolando (crossbred Holstein x Gir) dairy cows were randomized as to percentage Holstein, age, parity, stage of lactation and current production level into control and treated groups. Cows averaged 63% Holstein, 2.6 parities, 174 days of lactation and 13.3 kg/d milk. Treated group cows received 2 g/d of a product (Bioformula, Goiania, Brazil) containing live yeast (1×10^9 CFU/g), mannan oligosaccharide (10%), and *Lactobacillus acidophilus*, *Bacillus subtilis*, and *Enterococcus faecium* (2×10^7 total CFU/g), whilst controls received 2 g/d of the carrier alone. Cows grazed *Brachiaria brizantha* pastures and received up to 5 kg/d grain supplement according to production level. Milk production was monitored weekly for six weeks. Five control and four treated cows had mastitis during the experiment and their data were excluded. Data were analyzed by ANOVA, with treatment as main effect and previous level of production as the covariate. When previous level of production was included, all other factors (percentage Holstein, age, parity and stage of lactation) became non-significant. Average milk yields for the first three weeks were 11.1 and 11.7 kg/d (SD = 0.97) for control and treated cows, respectively (P = 0.15). For the second three weeks, average milk yields were 10.8 and 11.9 kg/d (SD = 0.86) for control and treated cows, respectively (P = 0.01). Therefore, direct-fed microbials had no effect in the first three weeks of treatment, but for the second three weeks milk production was increased by 10%. These results suggest that probiotics have the potential to increase milk production by crossbred dairy cows under tropical conditions.

Key Words: probiotics, dairy, tropical

W186 Digestibility of fresh sugarcane-based diets with slow-release non protein nitrogen addition for limit-fed dairy heifers in the tropics. G. J. Lascano*[1], M. Velez[2], J. M. Tricarico[3], and A. J. Heinrichs[1], [1]*The Pennsylvania State University*, *University Park*, [2]*Zamorano University*, *El Zamorano, Honduras*, [3]*Alltech Inc.*, *Nicholasville, KY*.

Sugarcane presents interesting characteristics for feeding ruminants in the tropics, such as perennial growth, reduced harvesting requirements, and peak yield and nutritive value that coincide with dry periods when forage is scarce. An experiment was conducted to determine the effect of replacing soybean protein (SBM) with non-protein N in limit-fed dairy heifers in the tropics. Eight Holstein heifers (237.6 ± 5.45 kg BW) were allocated to 2 dietary treatments in a cross over design. Treatments were control (C; 23% SBM) and O (Optigen, fed at 3% of DMI; Alltech Inc.). The forage to concentrate ratio was 50:50 (DM-basis) and fresh chopped sugarcane the sole source of forage. Each experimental period (2) lasted 15 d with 4 d of total feces and urine collection. Diets provided similar intakes of ME, allowed for 800 g/d of ADG, and chemical composition was held constant across all diets. Data were analyzed using a mixed-effects model with repeated measures. Compared to O, diet C tended to have greater total tract apparent digestibility (TAD) of DM (71.2 vs. 68.6 ± 0.63%; P = 0.06) and ash (47.4 vs 38.3 ± 3.81%; P = 0.08). Total tract apparent digestibility values in C-fed were greater than in O-fed heifers for OM (73.9 vs. 71.3 ± 0.64%; $P < 0.01$), CP (76.9 vs. 75.2 ± 0.72%; P = 0.04), hemicellulose (50.5 vs. 43.3 ± 1.89%; $P < 0.01$), and starch (98.6 vs. 97.2 ± 0.48%; P = 0.03). However, TAD of NDF was similar (44.9 ± 1.93%; P = 0.26) and TAD of ADF was lower (P = 0.03) in C (27.7± 2.15%) than in O heifers (33.3 ± 2.15%). Excretion of urine, wet and dry feces, and water intake were similar between treatments. Retained N was similar between treatments (65.5 ± 3.53%; P = 0.47), and thus no differences were found in N dynamics. We conclude that when O replaced SBM it tended to decrease DM and decreased OM, CP, hemicellulose, and starch TAD, but did not affect NDF and increased TAD of ADF. Even though control diets were more digestible overall, individual nutrient digestibility was not greatly affected, suggesting that replacing SBM with slow-release non-protein N is possible in sugarcane-based diets in the tropics.

Key Words: sugarcane, tropics, limit-feeding, dairy heifer

W187 System dynamics ex ante decision support for caprine initiatives in Southern Mexico. K. C. McRoberts*[1], C. F. Nicholson[4], R. W. Blake[3,1], T. W. Tucker[1], and G. Díaz Padilla[2], [1]*Cornell University*, *Ithaca, NY*, [2]*Instituto Nacional de Investigaciones Forestales, Agrícolas y Pecuarias*, *Xalapa, Veracruz, México*, [3]*Center for Latin American and*

Caribbean Studies, Michigan State University, *East Lansing*, [4]*California Polytechnic State University*, *San Luis Obispo*.

Researchers and development practitioners at the Instituto Nacional de Investigaciones Forestales, Agrícolas y Pecuarias (INIFAP) Xalapa team were trained in systems thinking and dynamic modeling techniques during an institutional capacity-building course. Course participants contributed expert knowledge to improve a system dynamics model designed to assess impacts on farmer profits of value-added agricultural production by a smallholder marketing cooperative. The dynamic biophysical and socioeconomic model consisted of nine modules that represented the aggregate community goat flock and a processing and marketing cooperative. The primary objective of the model was to assess strategies to increase net income from caprine production in highland communities. This adaptable model was designed as an *ex ante* impact assessment mechanism for INIFAP to evaluate the opportunities and limitations of value addition. Model analyses indicated that manufacture of goat's milk products by the cooperative could increase community net income from caprine activities under a wide variety of environmental and market conditions. Increases in net income from dividend payments during the dry season could partially mitigate seasonality from other income sources. Model sensitivity analyses indicated that the exogenous effects of seasonal rainfall on forage supply were more important to system performance than feedback processes (e.g., reinvestment of profits). System performance was measured by elements that likely influence farmer and cooperative decision-making: returns to labor, time required until the cooperative was financially solvent, dividend payments, and buyer orders for aged cheese cancelled due to supply delays. The analyses also indicated potential risks and factors that could limit cooperative success. The most important included the size and reliability of the market for premium aged cheese, the cooperative's policy of payments for milk and dividends, milk production costs, cheese production costs, and the composition and productivity of the goat flock. These factors and forage quality should receive priority in future research.

Key Words: caprine production, system dynamics, processing cooperative

W188 Biomass production and nutritional value of wheat and oat hydroponic forages sowed at three densities. J. A. Rivera-Ahumada[1], A. S. Juárez-Reyes[1,4], H. Bernal-Barragán[2,4], M. A. Cerrillo-Soto*[1,4], F. G. Ríos-Rincón[3,4], A. Estrada-Angulo[3,4], and M. Guerrero-Cervantes[1,4], [1]*Universidad Juárez del Estado de Durango*, *Durango, Dgo., México*, [2]*Universidad Autónoma de Nuevo León*, *Monterrey, Nuevo León, México*, [3]*Universidad Autónoma de Sinaloa*, *Culiacán, Sinaloa, México*, [4]*Red Internacional de Nutrición y Alimentación en Rumiantes*, *Durango, Dgo, México*.

A study was conducted to evaluate the biomass yield, CP, ME, metabolizable protein (MP) content, and gas fermentation parameters of wheat and oat hydroponic forages. Seeds were sowed at three densities (400, 600 and 800 g seeds) and manually placed in 40 × 40 cm plastic trays in triplicate. A controlled 5 × 4 m green house was used to grow the germinated hydroponic seeds and after 10 and 12 d, the forages were harvested. Two hundred mg of samples were incubated by triplicate in 100 ml calibrated glass syringes for 0, 3, 6, 9, 12, 24, 48, 72 and 96 h. Data were fitted to the equation: $Y=a + b*(1-e^{-ct})$ to estimate the gas produced from the soluble fraction *a*, the gas produced from the slowly degradable fraction *b* and the constant rate of gas production *c*. The ME content (Mcal kg^{-1} DM) was calculated by: $(2.20+0.136Gas\ production_{24h}+0.057CP+0.0029EE^2)/4.184$. The MP content was estimated according to the Intestinal Digestible Protein French System. Data were analyzed according to a factorial design to test the effects of 3 seed densities (400, 600, 800 g), 2 species (wheat and oat) and their interactions. There was a species × density interaction for biomass yield, CP and *b* fraction ($P < 0.05$). Biomass yields of wheat hydroponic forage with the higher density was 3.7 fold of that grown with the lower density, whereas an increment of 1.8 fold was registered in the oat hydroponic forage. Higher seed density in oats resulted in decreased CP (from 18.0 to 13.2%) and ***b*** (from 58.9 to 45.5ml of gas/200 mg DM) values, respectively. Values for in vitro gas production at 24 h, constant rate of gas production ***c***, ME and MP contents were higher ($P < 0.01$) for hydroponic wheat (60.5 mL/200 mg DM, 6.7% h^{-1}, 2.7 Mcal ME kg^{-1} DM and 80.6 g MP kg^{-1} DM) than for hydroponic oat (44.3 mL/200 mg DM, 5.7% h^{-1}, 2.2 Mcal ME kg^{-1} MS and 64.2 g MP kg^{-1} DM). According to our results, wheat hydroponic forage has a better nutritive value than its counterpart.

Key Words: hydroponic forage, in vitro gas production, nutritive value

W189 Growth potential of village chicken in Nigeria. J. A. Olupona*, O. O. Adejinmi, and A. M. Raji, *Federal College of Animal Health and Production Technology, Institute of Agricultural Research and Training*, *Ibadan, Oyo, Nigeria*.

The growth potential of village chickens in Nigeria was evaluated by comparing their growth performance under intensive and semi-intensive system of management. Preliminary investigation by the author revealed that 86.75% of village chickens are kept under semi-scavenging system of management in Ibadan southwest local government of Nigeria whereas birds are provided with small amount of grains and by-products to supplement their scavenging. Chicks (n=52), 8 wk old were collected from villages in Ibadan south west local government and individually raised in cages. Chicks (n=56) remained with the farmers and were raised under semi- scavenging conditions. On-farm made growers mash (18%CP) was fed to chicks raised under intensive condition and birds were treated against common diseases and parasites. Data were collected on feed intake, weight gain and feed efficiency. All measured and calculated parameters were tested for normality using proc univariate, normal and plot procedure of SAS and later analyzed using ANOVA. Village and system of management significantly ($P < 0.05$) influenced growth rates. Feed intake, weight gain and feed efficiency for birds under intensive conditions were significantly ($P < 0.05$) greater than for birds under semi-scavenging conditions. Phenotypic variance for daily weight gains, and growth rate were lower for intensively managed birds than for semi intensive system Correlation coefficients of growth traits measured between intensive and semi-scavenging conditions were low (r=0.16-0.49; $P < 0.05$), probably indicating that the effect of environment and its interaction on genotype had a strong impact. It is concluded that growth potential of village chicken can be enhanced by providing sufficient feed under semi- scavenging conditions.

Key Words: village chicken, semi-scavenging, intensive

W190 Effects of demographic characteristics and attitudes of consumers on table egg consumption. M. Bejaei* and K. M. Cheng, *The University of British Columbia*, *Vancouver, BC, Canada*.

In addition to regular (white and brown) eggs, alternative types of table eggs (e.g., free-run, free-range, organic eggs) are also available in Canadian market and their market growth rate has been high during the last decade in British Columbia (BC). Despite this growth there is insufficient data about consumers' attitudes and preferences relating to this differentiated egg market. The objective of our research was

to identify the consumers' attitudes and demographic characteristics toward different types of table eggs. We used an online interactive survey questionnaire to gather information from adult BC residents. Email addresses of 1027 potential subjects were randomly selected and 702 completed surveys were processed. The survey was conducted in June 2009 according to the regulations of UBC Behavioural Research Ethics Board. PASW Statistics 17 (SPSS) was used to analyze the survey data. Different statistical tests were applied to the responses (e.g. ANOVA, Pearson correlation, Bonferroni correction). Our results indicated that the consumption of cage-free eggs has changed in BC in 2009 in comparison to a Print Measurement Bureau consumer survey in 2007. Almost a third of the consumers used free-range eggs at home in BC in 2009. Individuals with a higher educational level or higher income consumed more free-range eggs and fewer white regular eggs than those with a lower educational level or lower income. Consumers who rated the nutritional value of white regular eggs as high (score 4 or 5 in a five point Likert scale) consumed more white regular eggs. Consumers did not act according to the same priorities when they were selecting different types of eggs. Price was the main factor in selection of white regular or brown regular eggs; bird welfare, environmental concerns and having access to healthy food were main factors in the selection of cage-free eggs; and nutritional value and having access to healthy food were main factors in consumption of nutrient enhanced eggs. Because of the results of this research egg producers are more capable of designing a marketing mix plan to develop their market share in the future.

Key Words: table eggs, consumer attitudes, demographic characteristics

W191 Effect of dry ammoniation on the chemical composition and digestibility in vitro in the mesocarp of the fruit and empty bunches of African oil palm. N. Castro-Ucross[1], J. Vergara-Lopez[2], and O. Araujo-Febres*[1], [1]*Universidad del Zulia, Facultad de Agronomía, Departamento de Zootecnia*, *Maracaibo, ZU, Venezuela*, [2]*Instituto Nacional de Investigaciones Agricolas*, *Maracaibo, ZU, Venezuela*, [3]*Universidad del Zulia, Facultad de Agronomía, Departamento de Zootecnia*, *Maracaibo, ZU, Venezuela*.

Venezuela has about 52,384 ha planted with African oil palm, of which 27,100 ha had a total production of fresh empty fruit bunch of about 334,262 MT (with empty bunches representing 25% and mesocarp 11% of total weight). This study was conducted to evaluate the effect of dry ammoniation on the chemical composition and digestibility in vitro of the mesocarp of the fruit and the empty fruit bunches of african oil palm at Catatumbo municipality of Zulia state, Venezuela. Five levels of urea (0, 15, 30, 45 and 60 g/kg DM) and two incubation times (14 and 28 d) were applied to the products. The study was conducted as complete randomized experiment with a factorial arrangement 2×2×5, with 3 replications. Dry matter (DM), crude protein (CP), neutral detergent fiber (NDF), acid detergent fiber (ADF), lignin (Lig) and in vitro dry matter digestibility (IVDMD) were determined. Data were analyzed using ANOVA. Dry matter content decreased ($P < 0.01$) as urea levels increased. The lowest values of NDF, ADF and Lig were found in the empty fruit bunch (32.9, 29.6 and 7.1%, respectively) and the correlation analysis demonstrated a downward trend in fiber content as urea levels and incubation time increased. The CP content was greatest ($P < 0.01$) in the mesocarp at 28 d of incubation, and it increased 4% units when comparing 0 vs 60 g of urea addition. The IVDMD was greater in the empty fruit bunch (61.7%, $P < 0.01$) than in the mesocarp (39.5%). Dry ammoniation positively changed the chemical composition and digestibility of oil palm by- products, with the empty fruit bunch being the most affected of the byproducts.

Key Words: African oil palm, dry ammoniation, dry matter digestibility

W192 Nutritive value of Henequen (*Agave fourcroydes* Lem.) pulp as ruminant feed. E. González–García*[1,2], O. Cáceres[2], F. Ojeda[2], and R. Delgado[2], [1]*INRA, UMR 868, Élevage des Ruminants Regions Chaudes*, *Montpellier 34090, France*, [2]*Estación Experimental de Pastos y Forrajes 'Indio Hatuey'*, *Matanzas 44280, Cuba*.

Henequen (*Agave fourcroydes* Lem.) is a highly resistant and succulent plant (genus *Agave*; family Agavaceae) with sword-shaped leaves of 1.2 to 1.8 m long in a form of rosette. It's extensively planted in Mexico (Yucatan) and Cuba (Varadero) basically to profit their leaves′ fiber (so-called Henequen) for rope and twine productions. The remained pulp is an industrial by-product that, if not used, may constitute an environmental problem. We evaluated its nutritive value (NV), fresh (HPF) or ensiled (HPE), as a ruminant feed with potential to be used in a planned integration of livestock and agro industry productions locally in the north-center of Matanzas, Cuba (23°08′22″N 81°17′10″W). Two metabolic trials of 21 d each (14 d adaptation, 7 d data collection) were conducted for evaluating HPF and HPE, respectively. For each trial, 6 adult castrated Pelibuey wethers (BW = 35 ± 2.3 kg) were used, randomly housed in individual metabolism crates and the INRA French system of ad libitum (10% of refusal from previous day) feed supply and total feces collection was implemented. Feeds (HPF or HPE) were daily and individually distributed into 2 equilibrated meals (0800 and 1630). Data were analyzed for each trial by separate using an ANOVA. The experimental unit was the wether, included in the model as a random effect. Comparisons between HPF and HPE were avoided. Despite a limiting DM content (16.8 and 20% for HPF and HPE, respectively), either HPF or HPE showed acceptable NV for ruminants due to good voluntary intake (Ø: 96% of reference feedstuff) which was likely due to the high energetic potential (>2.5 mcal/ kg DM) (Table 1). However, CP content was low for both states of presentation (72 and 60 g/ kg DM for HPF and HPE, respectively) which also determined low levels of protein arriving to the small intestine (PDIMN and PDIME). This by-product of Henequen industrial processing (pulp) could be considered as an energetic raw material for ration formulation in ruminant feeding systems. However, some strategies such as drying (i.e. meal) are recommended to increase feasibility of manipulation and conservation during long periods of time.

Table 1. Nutritive value of henequen pulp, fresh (HPF) or ensiled (HPE)

State of presentation	DM, %	CP, g/kg DM	CF, g/kg DM	ME, mcal/ kg DM	PDIMN, g/kg DM	PDIME, g/kg DM	Ca, g/kg DM	P, g/kg DM
HPF	16.8	72	204	2.62	51.1	73.1	58.0	4.0
HPE	20.0	60	280	2.50	48.0	68.0	50.0	0.4

PDIMN, microbial protein to be synthesized from degraded dietary N when energy is not limiting; PDIME, microbial protein synthesized from rumen fermented OM when degraded N is not limiting.

Key Words: nutritive value, ruminant, Henequen

W193 Economic weight of some production and functional traits of dairy cattle. F. Szabó*[1], Z. Fekete[1], J. Wolf[2], and M. Wolfová[2],

[1]*University of Pannonia Georgikon Faculty*, *Keszthely, Hungary*, [2]*Institute of Animal Science*, *Uhrinéves, Prague, Czech Republic*.

The objective of this study was to evaluate the marginal and relative economic values of 7 traits for dairy cattle. The importance of the study derives from more than 68% of cattle in Hungary belonging to the dairy industry. The study was conducted in 2009 using a bioeconomic model based on the program ECOWEIGHT (Wolf et al., 2005). Data were collected for typical dairy farms of about 330 Holstein- Friesian cows with annual milk yield close to 7,000 kg. Cows were managed in loose-housing systems with parlor milking, representing current commercial dairy enterprises. A total mixed ration based on maize silage and concentrates with some alfalfa hay was offered to 4 groups (first-, second-, third- phases of the lactation and a dry group). Besides the dairy enterprise, calf and replacement rearing were also taken into consideration. Income came from milk, calves, culled cows, and sale of manure. About 50% of the total cost was related to feed and the remainder was due to factors such as management, reproduction and health services, labor, interest and amortization. Annual revenues and costs were used for the economic calculations. Gross margin was the difference between income and variable costs. Marginal economic value of a given trait was defined as the partial derivative of the profit function and was standardized by multiplying by the genetic standard deviation of the trait. The relative economic values for traits were expressed as percentages of the standardized economic value of 305-d milk yield. The relative economic importance of the traits were as follows: 305-d milk yield, 100%; length of productive life, 52%; conception rate of cows, 35%; 305-d protein yield, 35%; 305-d fat yield, 21%; stillbirth, 13%; and pregnancy rate of replacements, 3%. It can be concluded that milk yield is currently the most economically important trait in Hungary.

Key Words: 305-d milk-, protein- and fat yield, length of productive life, conception rate

Lactation Biology 2

W194 Effect of feeding level and milking frequency in early lactation on milk production in dairy cattle. A. G. Rius*, J. K. Kay, C. V. C. Phyn, S. R. Morgan, and J. R. Roche, *DairyNZ*, *Hamilton, New Zealand*.

The objective was to evaluate the effects of feeding level (FL) and milking frequency (MF) in early lactation on milk production in grazing dairy cattle. Multiparous Holstein-Friesian cows (n = 120; ~31 DIM) offered an unrestricted allowance of fresh pasture (UnRes) and milked twice daily (2X) were randomly assigned to one of 4 treatments for 21 d in a 2 by 2 factorial arrangement - 2 FL of pasture (UnRes or a 50% restriction: Res) and 2 MF (once daily: 1X or 2X). After the treatment period, all animals received a generous allowance of pasture and were milked 2X for the remainder of lactation. Body weights (BW) and body condition scores (BCS) were recorded and milk samples collected once weekly. Main effects and interactions during treatment, and for 8 wk post-treatment, were tested using mixed models (GenStat 12.1). Interactions between FL and MF were detected ($P < 0.01$) for milk and protein yields during the treatment period. Decreases due to 1X were greater ($P < 0.01$) in UnRes than in Res cows for milk (4.8 vs. 2.2 kg/d), and protein (0.17 vs. 0.06 kg/d) yields. Upon cessation of treatments milk production was greater ($P < 0.01$) in UnRes cows compared with Res cows (18.4 vs. 17.1 kg/d) and in 2X compared with 1X (18.3 vs. 17.2 kg/d), but there was no interaction. Similarly, UnRes cows had greater ($P < 0.01$) fat (0.79 vs. 0.74 kg/d) and protein (0.67 vs. 0.62 kg/d) yields and 2X cows had greater ($P < 0.01$) fat (0.78 vs. 0.75 kg/d) and protein (0.66 vs. 0.63 kg/d) yields. Relative to their UnRes comparison, Res cows were lighter and thinner ($P < 0.01$; BW: 440 vs. 484 kg and BCS: 3.86 vs. 4.03; 10-point scale) and relative to 1X, 2X cows were lighter ($P < 0.01$; 460 vs. 468 kg) by the end of the treatment period. In summary, reducing milking frequency and the level of nutrition for 21 d in early lactation impaired milk production.

Key Words: milking frequency, grazing, milk production

W195 Expression of key metabolic indicators of energy metabolism across mammary gland development and lactation in dairy cows. L. J. Ren, H. L. Tong, Q. Z. Li, and X. J. Gao*, *Key Laboratory of Dairy Science of Education Ministry, Northeast Agricultural University*, *Harbin, China*.

Appropriate energy supply is critical to normal growth and development of the mammary gland. To understand how key indicators of mammary gland metabolism change with physiological state, 39 primiparous dairy cows were allotted in 13 groups according to stage of mammary development (mo 2, 12, 14 of virgin, mo 2, 4, 6 of pregnancy, d 7, 50, 140, 280 of lactation and d 3, 30 of involution, and 3 animals per group). Mammary gland tissue samples were collected by paracentesis and the contents of important indicators in different periods including hexokinase(HK), glucose-6-phosphatase dehydrogenase (G-6-PDH), isocitrate dehydrogenase(ICDH), Na^+K+-ATPase, $Ca^{2+}Mg2$+-ATPase, triglyceride(TG), glucose(Glc), lactose(LAC), energy charge and NADPH were detected. LAC, energy charge and NADPH were detected by HPLC. Others were detected by the testing kits. In this test, qRT-PCR was used to detect those important genes which were related to lactation, including β–actin, sterol regulatory element binding protein-1(SREBP-1), acetyl CoA carboxylase(ACC), D-glucose transport 1(Glut1), AMP-activated protein kinase(AMPK), phosphoenolpyruvate carboxykinase(PEPCK), β–casein and signal transducers and activators of transcription 5(Stat5) in different mammary gland development periods of dairy cow. The results showed the different indicators reached the highest at different periods. For example, the activities of ICDH and G-6-PD both reached the highest at d 7 of lactation, but the activity of Na^+K+-ATPase reached the highest at d 280 of lactation. qRT-PCR showed that the expression of these genes was significantly higher at the period of lactation than other periods. In conclusion, according to the changes of metabolism indexes and the expression of these important genes, we can conclude energy metabolism in the course of mammary gland development and lactation of dairy cows.

Key Words: dairy cow, mammary gland, energy metabolism

W196 Insulin stimulates glucose uptake by regulating cell viability and expression of glucose transporter 8 gene in bovine mammary epithelial cells. K. Zhao, H. Y. Liu*, and J. X. Liu, *Institute of Dairy Science, MOE Key Laboratory of Molecular Animal Nutrition, Zhejiang University*, *Hangzhou 310029, P.R. China*.

Glucose transporter 8 (GLUT8) is expressed at high levels in the bovine mammary gland. Because the classical insulin responsive glucose transporter GLUT4 is not detected in the mammary gland of dairy cows, GLUT8 is postulated to be an alternative insulin responsive transporter. In this study, bovine mammary epithelial cells (BMEC) were used to examine the effect of insulin on cell viability and glucose uptake, and to verify the possible role of GLUT8 in insulin-regulated glucose uptake. The BMEC were cultured in DMEM/F12 medium containing 10% FCS, and treated with different levels of insulin (0, 5, 50, and 500 ng/ml) for 48 h after 24 h starvation without FCS. Viability of the cells was determined by MTT method. Glucose uptake and mRNA expression were determined by enzymatic coloring glucose oxidase/peroxidase assay, and by SYBR green method of real-time PCR, respectively. The viability of the cells was enhanced with the increasing level of insulin ($P < 0.05$), with highest value at 500 ng/ml. Compared with control, insulin (500 ng/ml) increased glucose uptake ($P < 0.05$), while expression of GLUT8 gene was elevated in all insulin-treated groups ($P < 0.05$). As predicted, expression of the GLUT1 gene, the predominant glucose transporter, was not affected by insulin ($P > 0.05$). In addition, insulin-induced glucose uptake was totally suppressed by the protein synthesis inhibitor, cycloheximide ($P < 0.05$). Pretreatment with LY294002, a specific inhibitor of PI3-K, for 30 min, significantly reduced the insulin-stimulated glucose uptake ($P < 0.05$). In contrast, SB203580, an inhibitor of p-38 MAPK, did not influence the insulin-induced glucose uptake ($P > 0.05$). These results indicate that GLUT8 is an insulin responsive transporter in BMEC. Insulin may stimulate glucose uptake primarily via regulating cell viability and thus expression of GLUT8 in BMEC. This effect may be mediated through PI3-K- linked signaling pathways.

Key Words: insulin, glucose transporter 8, bovine mammary epithelial cell

W197 Pathogen-specific and dose-dependent response of the bovine mammary gland to lipopolysaccharide from *E. coli* and lipoteichoic acid from *S. aureus*. R. M. Bruckmaier*, E. T. Arnold, and O. Wellnitz, *Veterinary Physiology, Vetsuisse Faculty, University of Bern*, *Bremgartenstr. 109a, 3001 Bern, Switzerland*.

Lipoteichoic acid (LTA) and lipopolysaccharide (LPS) are proinflammatory cell wall components expressed by gram-positive or gram-negative

bacteria, resp. This study was performed to investigate if intramammary challenge with LTA from S. aureus or LPS from *E. coli* elicits a different immune response. Five cows per group with somatic cell counts (SCC) below 100 × 103/ml were intramammarily challenged in one quarter with 10 or 20 μg of LTA or 0.2, 1, or 10μg LPS in 10 mL saline solution (0.9%). At 0, 6, and 12 h after challenge biopsy samples of the mammary gland or milk cells from 1 L of milk were taken for mRNA expression measurements of immune factors by quantitative RT-PCR. Additionally, from cows that received no biopsy small milk samples (~5mL) were taken hourly. Differences between treatments and time points were considered as significant if $P \leq 0.05$. SCC increased in all treatments within 4 h. The increase of SCC, tumor necrosis factor α (TNFα), and lactate dehydrogenase (LDH) in milk was dose dependent. TNFα concentration in milk did not increase in LTA-treated quarters. mRNA expression of TNFα, interleukin (IL)-8 and IL-1β increased dose dependently in mammary tissue and in milk cells. This effect was more pronounced in milk cells compared with the tissue within the same dosage. The results show that LPS induced a stronger response of the measured factors than LTA in dosages with the induction of a similar SCC response. A low dosage of LTA induced a SCC increase but hardly any response of the measured factors. In addition, milk cells showed a stronger immune response to the same concentration of LPS than the mammary tissue. This reflects the situation during an infection of the mammary gland where the first reaction of the immune system is realized by the somatic cells which are already present in the milk before challenge. Then the bacteria or endotoxins must exceed a certain level to induce an immune response of milk cells as well as of mammary tissue. In conclusion, the immune response of the mammary gland is dependent on toxin type and dosage.

Key Words: mastitis, lipoteichoic acid, lipopolysaccharide

W198 Greater milk yield is related to increased DNA and RNA content but not to mRNA abundance of selected genes in sow mammary tissue. C. Farmer*[1], M. F. Palin[1], J. F. Trott[2], and R. C. Hovey[2], [1]*Agriculture and Agri-Food Canada, Dairy and Swine R & D Centre*, *Sherbrooke, QC, Canada*, [2]*Dept. of Animal Science, University of California*, *Davis*.

The relationship between greater sow milk yield and mammary development, expression of selected genes in mammary tissue and serum hormone concentrations in lactating sows was studied. Crossbred sows were separated into 2 groups according to weight gains of their piglets up to d 21 of lactation. Groups were: 1) lower milk yield (LOW, n = 14) or 2) higher milk yield (HI, n = 14), representing lactation weight gains of 4.47 and 5.24 kg/pig, respectively. Jugular blood samples were obtained from all sows on d 3 (for prolactin determination) and 23 (for measures of prolactin, leptin, insulin, glucose and free fatty acids) of lactation. Milk samples were collected on d 3 and 22 of lactation for compositional and leptin analyses. At weaning (d 23), sows were killed and their mammary glands collected, dissected and composition determined. Mammary parenchymal tissue was analyzed for the mRNA abundance of selected genes, namely, porcine prolactin (pPRL), pPRL receptor (all isoforms and the long isoform alone), STAT5A, STAT5B, whey acidic protein and leptin. On d 3 of lactation, jugular concentrations of prolactin tended to be greater ($P = 0.1$) while dry matter and leptin in milk were less ($P < 0.05$) in HI than LOW sows. There was a tendency for HI sows to have more parenchymal tissue per teat ($P < 0.1$) than LOW sows. Parenchymal tissue contained less fat ($P < 0.05$) and there was more DNA and RNA per teat in HI than LO sows ($P < 0.05$). On the other hand, the expression of selected genes within mammary tissue was unaffected ($P > 0.1$) by treatment. Sow milk yield therefore directly reflects mammary gland composition in late lactation.

Key Words: genes, milk yield, sow

W199 5′-untranslated region haplotypes of beta-2-microglobulin exon IV in Chinese Holstein dairy cows and its association with IgG1 concentration and mass in milk. C. Zhang*1,2, G. Liu[1], J. Wang[1], D. Bu[1], L. Zhou[1], S. Zhao[1], and Y. Yang[1], [1]*State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences*, *Beijing, China*, [2]*College of Animal Science and Technology, Yangzhou University*, *Yangzhou, China*.

Production and transfer of IgG into milk is an important area of study because of its biological functions including opsonization, complement fixation, prevention of adhesion of pathogenic microbes to endothelial lining, inhibition of bacterial metabolism, agglutination of bacteria, and neutralization of toxins and viruses. In the mammary gland, IgG is transferred selectively from serum into milk by a neonatal Fc receptor (FcRn)-mediated mechanism. Beta-2-microglobulin (β2MG) is an integral component of the FcRn heterodimer, which has prominent roles in IgG transfer across mammary epithelial cells. This study examined mutations in the 5′-untranslated region (5′UTR) of β2MG exon IV and its association with variation of IgG1 concentration and mass in milk. One hundred and eighty-nine Holstein dairy cows in lactation were used to determine the genetic diversity of 5′UTR. Two single nucleotide polymorphisms (SNPs) and insertion/deletion (indel) of 2 base pairs were identified by sequencing the 5′UTR of β2MG exon IV and were assigned into 4 haplotypes. These haplotyes were evaluated with respect to IgG1 concentration and mass in the milk. These results demonstrated a significant association between β2MG genotypes and concentration and mass of the milk IgG1 ($P < 0.05$). Dairy cows homozygous with a double base-pair deletion (H3H3) had similar serum IgG1 concentration with other genotypes, but significantly lower milk IgG1 concentration and mass ($P < 0.05$). These results suggest that β2MG genotypes might serve as a marker of IgG1 production and distribution.

Key Words: beta-2-microglobulin gene, immunoglobulin G1, path analysis

W200 How does increased milking frequency stimulate milk production? M. Dehghan-Banadaky*, M. Eslamizad, K. Rezayazdi, H. Kohram, and R. Heydari, *University of Tehran*, *Karaj, Tehran, Iran*.

We tested the hypothesis that frequent milking stimulates milk production through increased prolactin secretion. Multiparous (n = 105) and primiparous (n = 15) Holstein cows were used in a completely randomized design and assigned at calving to 1 of 3 treatments as follows: 1) 6 times a day milking for the entire lactation (6X); 2) 6 times a day milking for 90 DIM, then switched to 3 times subsequently (6X-3X); and 3) 3 times a day milking for the entire lactation (3X). Milk production was recorded every other day for the first 60 DIM and subsequently on 2 consecutive days a week. Blood samples were taken from each cow on 15, 30, 60, 90, 120, 150, 210, and 270 DIM. Plasma prolactin concentrations were determined using a double antibody radioimmunoassay procedure. Data were statistically analyzed using the repeated measures option in Proc Mixed of SAS with cow as a random effect. Milk and fat corrected milk (FCM 3.5%) yield were greater in 6x and 6x-3x cows than in 3x treatments (41.03, 42.3; 40.11, 40.60 VS 37.97, 38.40 kg/d, respectively). Plasma concentrations of prolactin were 57.73 ± 1.32, 59.62 ± 1.64, and 58.87 ± 1.73 ng/ml in 6x, 6x-3x, and 3x cows, respectively. Increased milking frequency did not alter the concentration of plasma prolactin at any sampling time ($P = 0.53$). In

conclusion, results of the present study did not support the hypothesis that increased milking frequency stimulates milk production through increased prolactin.

Key Words: milking frequency, prolactin, Holstein cow

W201 Impact of duration of milk storage in the mammary gland on milk composition throughout milking . M. Dutreuil[1,2], C. Cébo[3], J. Guinard-Flament[2,1], and C. Hurtaud*[1,2], [1]*INRA UMR1080 Production du lait*, *Saint-Gilles, France*, [2]*Agrocampus Ouest UMR1080 Production du lait*, *Rennes, France*, [3]*Unité GABI*, *Jouy-en-Josas, France*.

Our objective was to study the effect of duration of milk storage in the mammary gland on milk composition throughout milking. Three durations of milking storage were studied on 6 dairy cows averaging 118 ± 22 DIM: 13-, 20-, and 24-h. The trial was carried out according a double Latin square 3′3 with 14 d periods. Yield and composition were measured on milk samples collected every min during morning milking on d 10 of each period. Statistical analysis was carried out using the Proc Mixed procedure in SAS software with repeated statement. Milk yield, lactose content, milk protein yield and content remained unchanged between treatments. Milk fat content and lipolysis did not vary according to the duration of milk storage. In contrast, there is a significant interaction between duration of milk storage and kinetics of milk ejection for 2 parameters: fat yield and specific MFG area. Milk fat yield increased during the whole milking for the 13-h milk storage whereas it started to decrease at the end of milking for 20- and 24-h milk storages. The specific MFG area decreased less during milking for the 24-h milk storage. The lipolysis, measured by method of copper soap, decreased during milking whereas the milk fat content and milk fat globule diameter increased (respectively from 1.45 to 7.55% and from 3.1 to 4.1 μm). Variations in the profile of milk fatty acids were also noticed as an increase in desaturation activity of the mammary gland (increase of C14:1/C14:0 ratio) during milking. In conclusion, there is a great change in milk composition during milking. But duration of milk storage in the mammary gland induced no important change on the kinetics of milk secretion.

Key Words: milk composition, milk fat globule, milking

W202 Effects of Actigen supplementation on mRNA levels of mucin and markers of gut health in the jejunum of broiler chicks. K. M. Brennan*, T. Ao, J. L. Pierce, and K. A. Dawson, *Center for Animal Nutrigenomics and Applied Animal Nutrition, Alltech Inc.*, *Nicholasville, KY*.

Previous studies in our lab have indicated that the addition of Actigen, a yeast-derived feed supplement, to the diet positively affects gut health including increasing goblet cell size and small intestinal mucin secretion. Based on these data, the objective of this study was to compare the effects of supplementing Actigen and bacitracin methylene disalicylate (BMD) in the diet on mRNA levels of mucin and mucin-regulating genes in the jejunum of 6-week old chickens. Dietary treatments included 1) corn-soy control diet; 2) Diet 1 plus Actigen; 3) Diet 1 plus BMD. Chicks (n = 7) from each dietary treatment were randomly selected and killed at d42. Jejunum samples were rinsed and placed in RNAlater, then transferred to −20°C freezer until further analysis. Total RNA was isolated from stored tissue, treated with DNase and reverse transcribed into cDNA. mRNA levels of target genes were measured using real-time PCR and normalized to the housekeeping gene mitochondrial ribosomal protein L48 (MrpL48). Target genes included mucin 2 (cMUC2), keratinocyte growth factor 7 (KGF7), interleukin 18 (IL18), tumor necrosis factor α (TNFα) and toll-like receptors 2 and 5 (TLR2 and TLR5), 2 key markers for pathogenic insult in the gut. cMUC2 mRNA levels tended to be 1.29-fold greater in Actigen and BMD-treated birds than controls ($P < 0.10$). mRNA levels of mucin-regulating genes, IL18 and KGF7, were similar between Actigen and BMD treated birds. TLR2 and TLR5 mRNA levels were greater (1.20-fold and 1.23-fold, respectively) in BMD-treated birds than control. These data indicate that Actigen and BMD have similar effects on the mRNA levels of mucin and mucin-regulating genes in the jejunum of broiler chicks.

Key Words: mucin, broiler, gene expression

W203 Age changes in gastrointestinal pH in broilers. R. Angel*[1], B. Humphrey[2], and W. Saylor[3], [1]*University of Maryland*, *College Park,* [2]*California Polytechnic State University*, *San Luis Obispo,* [3]*University of Delaware*, *Newark*.

pH was measured in the different segments (crop, proventriculus, gizzard, duodenum, jejunum, ileum, ceca, large intestine) of the gastrointestinal tract (GIT) of broiler chickens, at different ages over 15 studies done over 2 years. Direct comparisons (same source of birds, same water and feed) of intestinal pH between broilers in batteries and floor pens were done. At least 2 and up to 5 birds by age and study were sampled. In 3 initial studies the pH was measured using 2 protocols: In situ, by inserting the pH probe (2 measurements) into the middle area of each region; and Ex situ, by inserting the pH probe (2 measurements) into intestinal contents diluted in distilled, deionized water (1:2.5 wt:wt ratio). Feed was also diluted in water (1:2.5 feed to water ratio) for pH determination (2 measurements) and facility water pH documented. Statistical analysis was run within study and between studies as one way ANOVA. Facility water pH was used as a covariate. The in situ method resulted in lower pHs for most GIT segments measured and always resulted in lower standard deviations. Given this the remaining of the work was done using only in situ measurements. Variability between birds was high. For example, at 5 d of age, where 5 birds were sampled, crop, gizzard, proventriculus, duodenum, jejunum, and ileal pH was 5.32, 2.37, 2.14, 5.99, 6.07, and 7.12, respectively and the standard deviation was 0.54, 0.92, 0.24, 0.28, 0.14, 0.12. pH decreased $P < 0.05$ after 5 d of age primarily in the proventriculus and gizzard (pH at 14 d of age was 1.15 and 1.90 in the proventriculus and gizzard, respectively). By 18 d of age the pH in the proventriculus and gizzard was similar ($P > 0.05$) to that at 5 d of age (2.50 and 2.64, respectively). By 46 d of age crop, gizzard, proventriculus, duodenum, jejunum, and ileal pH was not different ($P > 0.05$) from those at 5 d (5.85, 2.04, 2.36, 5.87, 5.97, and 7.15, respectively). It is possible that differences between ages were not found due to the high variation seen between birds. No clear patterns of change were seen between battery and floor pen raised broilers. Facilities water pH has the most impact on crop pH.

Key Words: broilers, gastrointestinal, pH

W204 Adaptive response in intestinal function in species with different dietary habits. D. J. Batchelor*[1], J. Brand[2], and S. P. Shirazi-Beechey[1], [1]*University of Liverpool*, *Liverpool, UK*, [2]*Monell Chemical Senses Center*, *Philadelphia, PA*.

The domestic cat (*Felis catus*) a carnivore, naturally eats a very low carbohydrate diet. In contrast the dog (*Canis familiaris*) a carno-omnivore is adapted to eat a varied diet. While cats appear to suffer from carbohydrate malabsorption following ingestion of high carbohydrate meals, dogs are able to cope with the diet containing higher levels of carbohydrate. The major aims were to determine expression (this includes function) of intestinal sodium/glucose cotransporter, SGLT1, and the brush border membrane disaccharidases, sucrase, lactase and, maltase in response to such contrasting diets. We first cloned and sequenced cat SGLT1, to determine its amino acid sequence and facilitate the production of a suitable antibody to cat SGLT1. We then measured the expression, and/or kinetics of SGLT1, sucrase, maltase and lactase, as appropriate, either by quantitative immunohistochemistry of fixed tissues or in purified brush border membrane vesicles. Intestinal tissues of healthy cats, n = 10 and dogs, n = 12 were provided by the University of Pennsylvania School of Veterinary Medicine and Monell Chemical Senses Center in Philadelphia. Animals had been euthanized, with the approval of the University Animal Care and Use Committee, for using the tissues for research purposes. Results: Feline SGLT1 amino acid sequence is closely related to that in other species; most notably to canine SGLT1. SGLT1 expression is 2-fold higher in the intestine of dogs compared with cats ($P < 0.001$), this is reflected in 2-fold increase in Vmax. Sucrase and maltase activity are (both 3-fold, $P = 0.0015$ and < 0.001, respectively) higher in dog intestine compared with cat; with dogs also retaining higher (1.6-fold, $P = 0.019$) lactase activity. The higher expression of SGLT1 and disaccharidases in dog intestine is not due to any structural changes; villus height and crypt depth are the same in cats and dogs. This study shows that dogs, in contrast to cats, have a higher capacity to digest and absorb carbohydrates.
Financial support of the Biotechnology and Biological Sciences Research Council and Pfizer Ltd is gratefully acknowledged.

Key Words: intestinal adaptation, glucose transport, disaccharidase

W205 Performance, nutrient utilization and gizzard development of broiler starters fed diets containing ground or whole corn. Y. Singh, T. J. Wester, G. Ravindran, and V. Ravindran*, *Massey University, Palmerston North, New Zealand*.

The influence of including 20% whole corn, differing in grain hardness, on the performance, nutrient utilization and gut characteristics of broiler starters was investigated. The experimental design was a 3 × 2 factorial arrangement of treatments evaluating corn hardness (hard, semi hard or soft) with diets based on ground corn or 20% of ground corn replaced by whole corn. The 3 corn cultivars were ground in hammer mill to pass through a 4 mm sieve and 6 diets were developed. Following mixing, all diets were cold pelleted. Each diet was fed to 6 replicate cages (8 birds per cage) from d 1 to 21 post hatch. Body weights and feed intake were recorded on a cage basis at weekly intervals. Mortality was recorded daily and data was corrected for mortality. Corn hardness and whole corn inclusion had no effect ($P > 0.05$) on the weight gain. Corn hardness had significant effect ($P < 0.05$) on feed intake and feed per gain, while these 2 parameters were unaffected ($P > 0.05$) by the inclusion of whole corn. Birds tended ($P = 0.08$) to consume more of the diets based on hard-corn than those based on soft-corn. Feed intake of diets based on semihard-corn did not differ ($P > 0.05$) from those based on hard- or soft-corns. Feed per gain of birds fed diets based on soft-corn was lower ($P > 0.05$) than those fed diets based on semihard-corn. Feed per gain of birds fed diets based on hard-corn was similar ($P > 0.05$) to those fed diets based on hard- and soft-corn. Inclusion of whole corn increased ($P < 0.05$) relative gizzard weights. The relative gizzard weights of birds fed hard- and semihard corn diets were higher ($P < 0.05$) than those fed the soft corn diets. Dietary AME was not influenced by dietary treatments. Ileal nitrogen digestibility was influenced ($P < 0.05$) by hardness, with soft corn diets having higher digestibility. Overall, these results indicate that 20% of whole corn can be substituted for ground corn in broiler starter diets with no adverse effects on growth performance

Key Words: whole corn, gizzard, broiler

W206 The effect of dietary vitamin C on growth performance, meat quality, immune function and antioxidant capacity of broilers. F. Z. Liu*, Z. Y. Niu, X. H. Wang, Y. N. Min, and H. Y. Wang, *College of Animal Science and Technology, Northwest A &F University, Yangling,Shaanxi, 712100 P. R. China*.

The purpose of this study was to evaluate the effect of dietary vitamin C on growth performance, meat quality, immune function and antioxidant capacity of 42-d-old broilers. Two hundred forty one-day-old broiler chicks were randomly divided into 3 treatments with 8 replicates of 10 birds. Birds were fed a corn-soybean meal basal diet supplemented with 0, 150, or 300 mg/kg vitamin C. The trial period was 42 d. We determined the index of growth performance, meat quality, immune function and antioxidant capacity of broilers in the experiment. Dietary Vitamin C supplementation significantly increased the ADG and ADFI of broilers ($P < 0.05$), but feed/gain ratio was not significantly affected ($P > 0.05$). Compared with the control diet, adding 300 mg/kg of vitamin C increased the breast muscle weight, declined the abdominal fat weight and liver weight ($P < 0.05$). The trail groups significantly increased the b* value of breast muscle, reduced the L* value of leg muscle ($P < 0.05$), and also had beneficial effect on the water-holding capacity and tenderness of leg muscle, and improved the quality of the chicken meat. Adding 300 mg/kg of vitamin C improved thymus index, bursa of Fabricius index and Newcastle disease antibody level compared with control-fed birds ($P < 0.05$). Compared with the control group, the vitamin C concentration in serum and breast muscle, the SOD, GSH-PX activity and A-TOC level were significantly higher in the 300 mg/kg supplementation ($P < 0.05$).

Key Words: vitamin C, growth performance, broilers

W207 Quality and oxidative stability of vitamin E enriched chicken meat. Z. Y. Niu[1], X. H. Wang[1], Y. N. Min[1], F. Z. Liu*[1], and H. Y. Wang[2], [1]*College of Animal Science and Technology, Northwest A &F University, Yangling, Shaanxi, 712100 P. R. China*, [2]*Yulin Municipal Animal Husbandry Bureau, Yulin, Shaanxi, 719300 P.R. China*.

The objective of this work was to evaluate the quality and oxidative stability of vitamin E enriched-chicken meat. Two hundred forty one-day-old Avian broiler chicks were allocated to 3 treatments, one is the control group fed the basal diet, the other 2 fed the dietary vitamin E supplementation diet, containing 100, 200 mg/kg vitamin E respectively. Broilers were raised to 42 d. We determined the meat quality, the activities of antioxidant enzymes in serum and tissues and the MDA concentration of the breast muscle during the refrigeration. The result showed the dietary vitamin E supplementation has a positive effect on the meat quality of broiler chickens. The 100 mg/kg vitamin E supplementation increased the tenderness, yellowness (b*) of the breast muscle, declined the water-loss rate, lightness (L*) and yellowness (b*) of the leg muscle significantly ($P < 0.05$). Dietary vitamin E supplementation increased the concentration of vitamin E in serum and muscle, and then took effect on the antioxidation enzyme system, improved the activity of SOD and T-AOC, declined the MDA generation. The 200 mg/kg vitamin E supplementation had significantly improved the antioxidation ($P < 0.05$) and had more active effect than the 100 mg/kg supplementation. Dietary vitamin E supplementation improved the oxidative stability of meat refrigerated at 4°C, deferred the lipid oxidation. The TBARS in breast muscle of the dietary vitamin E supplementation group was significantly lower than the control group at the 8th d ($P < 0.05$).

Key Words: vitamin E, meat quality, broilers

W208 Dietary preferences of acids and salts in piglets. J. A. Suárez*[1], E. Roura[2], and D. Torrallardona[1], [1]*IRTA-Centre Mas de Bover, Constantí, Spain*, [2]*Lucta S.A., Barcelona, Spain*.

Compromised voluntary feed intake of piglets in the post-weaning period might be improved by increasing feed palatability. Eighteen double choice tests with a total of 600 post-weaned pigs (20–25 kg BW), were conducted to determine preference for 14 acids and 4 salts compared with a control (REF) diet. Each test was performed using 8 or 9 pens (replicates) of 3–4 pigs that were offered simultaneous access to 2 feeding hoppers (REF diet or diet containing one of the products (AC) being tested). Each test was performed during 3 consecutive 4d-periods, in which low, medium and high inclusion rates of the AC were evaluated, respectively. The AC were tested at 0.5, 1 and 1.5% of inclusion, except for benzoic and succinic acids that were tested at 0.25, 0.5 and 1%, and potassium diformate that was tested at 0.5, 1 and 2%. The preference for each AC and dose compared with REF was calculated as the percentage contribution of the AC diet to total feed intake. Mean preference values were compared with the neutral value of 50% using the Student's *t*-test. Values are presented in brackets ordered by increasing doses and those

with an asterisk are significantly ($P < 0.05$) different from 50%. Acids that improved feed preference (%) include the medium doses of citric (59.0, 69.8*, 56.8) and tartaric acids (54.2, 73.4*, 67.5) and the high doses of potassium diformate (57.2, 58.5, 65.9*) and sodium propionate (55.1, 58.1, 58.2*). There were no significant effects on feed preference with ascorbic (47.8, 49.6, 41.9), benzoic (45.0, 48.4, 50.8) and malic (50.0, 48.9, 34.8) acids or sodium butyrate (42.4, 51.1, 48.3). Finally, negative effects on feed preference were found with all the doses of acetic (32.5*, 29.9*, 16.6*) and caproic (29.1*, 27.8*, 22.1*) acids and some doses of butyric (35.9, 43.5, 21.2*), caprilic (33.0, 33.2*, 14.7*), formic (39.9, 35.6*, 24.9*), lactic (51.3, 38.4, 35.6*), phosphoric (28.9*, 34.4*, 35.6), propionic (52.1, 37.0, 25.6*) and succinic (36.9*, 41.6, 51.9) acids and calcium formate (29.9*, 35.8*, 38.1). We conclude that some AC significantly affect feed preference in pigs.

Key Words: acidifiers, palatability, feed intake

W209 Impact of different nutrients on the development of hyperhomocysteinemia in neonatal piglets. M. E. Côté-Robitaille*[1,2], C. L. Girard[1], F. Guay[2], and J. J. Matte[1], [1]*Dairy & Swine R & D Centre, Agriculture and Agri-Food Canada*, *Sherbrooke(STN-Lennoxville), QC, Canada*, [2]*Department of Animal Sciences, Laval University*, *Quebec city, QC, Canada*.

The present experiment aimed to determine if the rapid post-natal development of hyperhomocysteinemia in piglets can be regulated by exogenous dietary provision of nutrients involved in homocysteine (Hcy) metabolism as methyl donors (betaine and choline), methyl user (creatine), or for catabolism (vitamin B_6). Those nutrients were given either separately or in association. Twenty sows were artificially inseminated and fed gestation and lactation diets supplemented with folic acid (10 mg/kg) and vitamin B_{12} (200 ug/kg). At birth, piglets were identified and weighed. A blood sample was also taken before ingestion of colostrum to measure plasma Hcy concentration. Eight piglets in each litter received daily an oral liquid bolus of one of the 8 following treatments: 1) saline, 2) betaine (50 mg/kg BW), 3) choline (70 mg/kg BW), 4) creatine (300 mg/kg BW), 5) pyridoxine (200 ug/kg BW), 6) treatments 2 and 5, 7) treatments 3 and 4, 8) treatments 2, 3, 4 and 5. During lactation, piglets were weighed and blood samples were collected on d 1, 7, 14 and 21. Growth from birth to 21 d of age was not influenced by treatments ($P = 0.13$). Overall plasma concentration of Hcy was very low at birth (2.49 ± 0.17 μ*M*), increased sharply at 8.33 ± 0.93 μ*M* within 24 h and at 14.21 ± 0.99, 18.28 ± 1.00 and 18.05 ± 0.81 μ*M* at 7, 14 and 21 d of age, respectively. Treatment 8 decreased ($P = 0.05$) plasma Hcy concentration by 23% as compared with treatment 1 but there was no interaction between treatments and age ($P = 0.11$). Hcy profiles in other treatments did not differ ($P = 0.09$) from that of saline. Therefore, plasma Hcy concentrations were markedly reduced by combination of all nutrients. Nevertheless, even minimum values remained high (over 15 μ*M*) as compared with other species (3 to 10 μ*M*, in cows, rats and humans) and the question remains, as whether hyperhomocysteinemia, an unhealthy condition for those young and fragile animals, is harmful for piglets or inversely, whether a greater reduction of plasma Hcy is beneficial. This need to be assessed with further criteria of post-natal growth and development using a large number of animals.

Key Words: homocysteine, growth, suckling piglets

W210 Effects of fermented soybean meal on growth performance, nutrient digestibility, blood profiles and fecal microorganisms in weanling pigs. J. H. Lee*, J. S. Yoo, H. J. Kim, Q. W. Meng, S. M. Hong, and I. H. Kim, *Department of Animal Resource and Science, Dankook University*, *Cheonan, Choongnam, Korea*.

This study was conducted to evaluate the effects of 2 types of fermented soybean meal on growth performance, nutrient digestibility, blood profiles and fecal microorganisms in weanling pigs. A total of 144 [(Landrace × Yorkshire) × Duroc] pigs (6.66 ± 0.29kg) were randomly allocated to 6 treatments with 6 replications per treatment and 4 pigs per pen. The experiment lasted for 6 weeks and consisted of 2 phases. The dietary treatments were as follows: Phase1 (0–3 wk) 1) FSA1 (basal diet + 5% fish meal + 5% fermented soybean meal with *Aspergillus oryzae*), 2) FSB1 (basal diet + 5% fish meal + 5% fermented soybean meal with *Bacillus subtilis*), 3) SPC (basal diet + 5% fish meal + 5% SPC), 4) FSA2 (basal diet + 2.5% fish meal + 7.5% fermented soybean meal with *Aspergillus oryzae*), 5) FSB2 (basal diet + 2.5% fish meal + 7.5% fermented soybean meal with *Bacillus subtilis*), 6) FSB3 (basal diet + 1% fish meal + 9% fermented soybean meal with *Bacillus subtilis*); phase 2 (3–6 wk) 1) FSA1 (basal diet + 2% fish meal + 4% fermented soybean meal with *Aspergillus oryzae*), 2) FSB1 (basal diet + 2% fish meal + 4% fermented soybean meal with *Bacillus subtilis*), 3) SPC (basal diet + 2% fish meal + 4% SPC), 4) FSA2 (basal diet + 1% fish meal + 5% fermented soybean meal with *Aspergillus oryzae*), 5) FSB2 (basal diet + 1% fish meal + 5% fermented soybean meal with *Bacillus subtilis*), 6) FSB3 (basal diet + 6% fermented soybean meal with *Bacillus subtilis*). During phase 1 (0–21d), the ADG was higher ($P < 0.05$) in the SPC group than the FSB3 group and its G:F ratio was increased ($P < 0.05$) when compared with other treatments. The DM and N digestibility was highest ($P < 0.05$) in the FSB1 group during wk 0–3. The DM and N digestibility were highest in the FSB2 group. Fermented soybean meal had no effects on the blood profiles except that it led to lower creatinine levels ($P < 0.05$) in the FSM group. Overall, the results of this experiment revealed that fermented soybean meal could partially replace fish meal in the diets of weanling pigs.

Key Words: fermented soybean meal, digestibility, weanling pigs

W211 Effects of probiotics (Agarie) supplementation on growth performance, nutrient digestibility, fecal microbial, fecal noxious gas emission and blood characteristics of finishing pigs. J. H. Jung*, J. H. Lee, J. P. Wang, X. Ao, S. M. Hong, and I. H. Kim, *Department of Animal Resource and Science, Dankook University*, *Cheonan, Choongnam, Korea*.

This study was conducted to evaluate the effects of probiotics (Agarie) supplementation on growth performance, nutrient digestibility, fecal microbial content, fecal noxious gas emission and blood characteristics of finishing pigs. A total of 60 pigs [(Landrace × Yorkshire) × Duroc, initial body weight 56.48 ± 1.66kg)] were used for this 42 d feeding trial. Dietary treatments included 1) CON (basal diet), 2) P1 (CON + 0.1% probiotics) and 3) P2 (CON + 0.2% probiotics). There were 3 dietary treatments with 5 replicate pens per treatment and 4 pigs per pen. There was no significant difference in the ADG observed among the groups ($P > 0.05$). The G:F ratio was higher in the P2 group than the CON group ($P < 0.05$). P2 treatment showed a higher dry matter and energy digestibility value than the CON and P1 groups ($P < 0.05$). No significant differences were observed in the fecal Lactobacillus levels among the groups; however, the fecal *Escherichia coli* levels were lower in the P2 group than the CON group ($P < 0.05$). The ammonia, H_2S and total mercaptan levels were higher in the P1 and P2 groups than the CON group ($P < 0.05$). Blood characteristics were not affected by probiotics ($P > 0.05$). In conclusion, the results showed that supplementation of the diet with 0.2% probiotics influenced the G:F ratio, dry matter,

energy digestibility, fecal *Escherichia coli* and fecal noxious gas levels in growing pigs.

Key Words: probiotics, digestibility, pigs

W212 Effect of type of grinding of barley and alfalfa hay on jejunal histology and crude mucin excretion of growing rabbits. C. Romero[1], N. Nicodemus[1], J. D. Rodriguez[1], A. I. Garcia[2], G. G. Mateos*[1], and C. de Blas[1], [1]*Universidad Politecnica de Madrid*, *Madrid, Spain*, [2]*NUTRECO Poultry and Rabbit Research Center*, *Casarrubios del Monte, Spain*.

The aim of this work was to test the effects of particle size of barley and alfalfa hay on jejunal histology and mucin dynamics in fattening rabbits. The basal diet contained 27.5% alfalfa hay, 24.0% barley, 19.9% sunflower meal and 15.0% sugar beet pulp. There were 4 treatments arranged in a factorial structure 2 × 2 with grinding (coarse, 4.5 mm vs. fine, 1.5 mm) and ingredient (barley vs. alfalfa hay) as main effects. Percentage of large particles (>0.315 mm) ranged from 48.8 to 54.1% DM as diets contained finely or coarsely ground ingredients. Thirty-two rabbits (8 rabbits/treatment) were fed these diets from weaning (35 d; 877 ± 81 SD g BW) to slaughter (46 d; 1430 ± 180 SD g BW). Villi height decreased by 13.1% when rabbits received the diet containing alfalfa hay ground coarsely (704 vs. 612 μm; $P < 0.05$). Moreover, rabbits fed diets including coarse alfalfa hay had deeper crypts (121 vs. 92.1 μm; $P < 0.05$) and lower villus to crypt ratios (5.08 vs. 7.66; $P < 0.001$) compared with those fed the diets based on fine alfalfa hay. An increase in crude mucin excretion (from 12.6 to 21.7 g DM; $P < 0.01$) was observed in rabbits fed the coarse barley diet when alfalfa hay was ground coarsely. Nitrogen concentration in crude mucin excreted was unaffected by treatment (4.00% DM on average). In parallel with results for crude mucin, an increase in sialic acid excretion (from 43.2 to 72.2 mg; $P < 0.01$) was observed in rabbits fed the coarse barley diet when alfalfa hay was also ground coarsely. The present work determines a mean value of 4.45 g N/kg DMI for endogenous ileal nitrogen flow in growing rabbits when results of both crude mucin excretion and its N content are considered. In conclusion, the diet containing coarsely ground barley (4.5 mm) and finely ground alfalfa hay (1.5 mm) slightly enhanced jejunal mucosa morphology and decreased ileal crude mucin excretion.

Key Words: growing rabbit, dietary particle size, crude mucin

W213 Effects of freeze-dried *Lactobacillus reuteri* M8 on growth performance and intestinal microflora in broiler chickens. D. Y. Zhang, H. F. Ji*, S. X. Wang, J. Wang, and Y. M. Wang, *Institute of Animal Husbandry and Veterinary Medicine, Beijing Academy of Agriculture and Forestry Sciences*, *Beijing, China*.

The objective of this study was to evaluate the effect of supplementation of freeze-dried *Lactobacillus reuteri* M8 on growth performance and intestinal microflora of broilers. The strain M8 was isolated from the cecum mucosa of healthy Beijing You Fowl in our laboratory. Ninety, one-day-old, unsexed Avian broilers (45.20 ± 0.10 g BW) were randomly distributed into 3 groups with 3 replicates per group and 10 broilers per replicate comprising of control (basal diet), 20 mg/kg zinc bacitracin supplementation (antibiotic diet), and 0.3% freeze-dried *L. reuteri* M8 supplementation treatment. The experiment lasted 42 d. The ADG, ADFI, and feed conversion ratio were determined at 21 and 42 d, the intestinal microflora was measured at the end of the experiment. The results showed that there were no significant differences on ADG, ADFI, and feed conversion ratio among the treatments during the first 3 wk. However, birds fed the diet containing freeze-dried *L. reuteri* M8 had improved ($P < 0.05$) ADG compared with control fed broilers (82.77 vs. 77.85 g/d) and the antibiotic fed group (82.77 vs. 79.55 g/d) during 21 to 42 d of age, and there was no difference between control diet and antibiotic diet. Feeding the diet containing freeze-dried *L. reuteri* M8 significantly increased the number of *Lactobacilli* in the cecum mucosa compared with either control (9.87 vs. 8.76 cfu/g, $P < 0.01$) or antibiotic (9.87 vs. 9.68 cfu/g, $P < 0.05$) groups. While no difference in the number of *Lactobacilli* existed in faeces. The numbers of *Escherichia coli* in the cecum mucosa and feces were not significantly affected by diet. This experiment indicated that *L. reuteri* M8 would be a beneficial bacterium with regard to enhancing growth performance and improving intestinal bacteria of broilers.

Key Words: *Lactobacillus reuteri*, growth performance and intestinal microflora, broiler chickens

W214 Weaned piglet responses to *Escherichia coli* K88$^+$ (ETEC) oral challenge when fed diets containing a *Saccharomyces cerevisiae* fermentation product with or without in-feed antibiotics. E. Kiarie*[1], S. Bhandari[1], D. O. Krause[1], M. Scott[2], and C. M. Nyachoti[1], [1]*University of Manitoba*, *Winnipeg, MB, Canada*, [2]*Diamond V Mills*, *Cedar Rapids, IA*.

Ninety weaned piglets (17 d of age; 5.5 ± 0.19 kg BW) were used to investigate the effects of a *Saccharomyces cerevisiae* fermentation product on the growth performance and gastrointestinal (GIT) measurements upon *Escherichia coli* K88$^+$(ETEC) oral challenge. Pigs (3/pen) were randomly allotted to one of 6 diets with 5 replicate pens/diet. Treatments were: negative control (NC, no additives), positive control (PC, 0.04% chlortetracycline + 0.004% Denagard, Novartis Inc., Canada), *S. cerevisiae* fermentation product (NC+0.2% XPC, Diamond V Original XPC, Cedar Rapids, IA), and PC+XPC (0.1, 0.2, or 0.4% XPC). On d 7, pigs were orally inoculated with a 6 mL dose of 2×10^9cfu/ml of ciprofloxacin-resistant ETEC. On d 10 and 14, performance measures were recorded and GIT samples were obtained. Before challenge, pigs receiving additives (PC, XPC, PC+XPC) had higher ($P < 0.05$) ADG and G:F compared with NC pigs (227, 194, 234, 242, 237 vs. 161 g/d; 0.79, 0.77, 0.85, 0.82, 0.88 vs. 0.66 g/g, respectively). Pigs fed NC+0.2% XPC did not differ ($P > 0.10$) in performance from PC+0.2% XPC pigs. After challenge (d 8–10), ADG and ADFI were higher ($P < 0.05$) for pigs receiving additives compared with NC (187, 170, 371, 231, 233 vs. 138 g/d; 291, 357, 409, 351, 397 vs. 312 g/d, respectively). Day 8–14, ADG and ADFI were higher ($P < 0.05$) for pigs receiving all additives compared with NC (348, 260, 369, 362, 364 vs. 222 g/d, 344, 379, 434, 399, 416 vs. 331 g/d respectively). Large intestine mass tended to be less ($P < 0.10$) for pigs receiving additives (19.5 vs. 22.8 g/kg BW). Pigs fed NC+0.2% XPC had less ($P < 0.05$) large intestine mass than those receiving PC+XPC (16.4 vs. 17.7, 23.4, 18.6). Results suggest that XPC supports weaned piglet growth performance during an ETEC challenge with or without in-feed antibiotics.

Key Words: *E. coli* K88, piglet performance, *S. cerevisiae* fermentation product

W215 Developing an efficient *E. coli* expression system for producing a recombinant antimicrobial peptide plectasin. M. Y. Xie[1], L. H. Sun[1], Z. Zhao[1], X. J. Xia[1], and X. G. Lei*[1,2], [1]*Int. Ctr. of Future Agriculture for Human Health, Sichuan Agri. Univ.*, *Chengdu, China*, [2]*Cornell University*, *Ithaca, NY*.

Plectasin is the first identified defensin-type antimicrobial peptide and was isolated from the saprophytic ascomycete fungus *Pseudoplectania nigrella*. Because plectasin has potent activity against gram-positive

bacteria, in particular *Streptococcus pneumonia*, with no hemolytic effect and low toxicity, it has great nutritional and therapeutic potentials. The objective of this study was to develop an efficient *E. coli* expression system to produce a recombinant plectasin. Based on the published plectasin sequence, we obtained the full-length double-stranded gene by PCR after we synthesized and annealed 2 overlapping single-stranded DNA fragments. The full-length DNA fragment was ligated into an expressing vector pET-32a(+) (Merck, Shanghai, China) and delivered into the *E. coli* strain Rosetta cells (DE3) (Merck, China). A Trx-plectasin fusion protein with a molecular mass of approximately 22.4 kDa was produced by the transformants, and represented over 60% of the total bacterial protein. This fusion protein was readily cleaved by enterokinase, resulting in the designated plectasin peptide with a molecular mass of approximately 4.4 kDa. Using a microdilution broth method, we found similar antimicrobial activity between our recombinant and the native plectasin. In conclusion, we have successfully developed an efficient *E. coli* expression system to produce a functional antimicrobial peptide plectasin for further animal tests and industrial applications.
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Key Words: plectasin, gene expression, protein purification, antimicrobial peptide

W216 In vivo evaluation of charcoal to prevent post-weaning pig diarrhea in an *Escherichia coli* K88 challenge experiment. C. Ionescu*[1], S. Meshkibaf[2], S. Bhandari[2], F. Zhu[2], E. Khafipoor[2], M. C. Nyachoti[2], D. Bravo[1], and D. O. Krause[2,3], [1]*Pancosma*, *Geneva, Switzerland*, [2]*Department of Medical Microbiology and Infectious Diseases, University of Manitoba*, *Winnipeg, MB, Canada*, [3]*Department of Animal Science, University of Manitoba*, *Winnipeg, MB, Canada*.

Pig post-weaning diarrhea is a leading cause of morbidity and mortality in the industry. The pathophysiology is commonly linked to *Escherichia coli* K88 (ETEC). Sub-therapeutic doses of antibiotics in diets has traditionally been used to prevent disease. With the rise of resistance, this practice is no longer acceptable. An ETEC challenge model was used to investigate the efficacy of non-activated charcoal (NAC) to prevent disease. The NAC had been selected for its binding properties to ETEC. Thirty-six pigs (19 ± 2 d old) were allotted to 6 treatments in a completely randomized design. The treatments were as follows: Basal diet (NC); NC + 0.15% Aureo SP-250 (PC); NC + 0.1, 0.5, 1, or 2% NAC. Pigs initial weights were 6.19 ± 0.22 kg. On d 7, all pigs were orally challenged with 6 mL of ETEC (≈109/mL). Post-challenge, fecal scours were measured daily (0, normal to 3, severe diarrhea). Seven days post-challenge, the pigs were euthanized and gut samples taken to enumerate ETEC and generic E. coli. The ETEC was levofloxacin resistant allowing for differential enumeration. ANOVA was made for treatment comparison and linear correlation coefficients were calculated between NAC doses and the different parameters. PC had the best ADG, ADFI, and G/F ($P < 0.05$). There was no correlation between NAC dose and ADG ($P = 0.43$) or ADFI ($P = 0.12$). There was a correlation between NAC doses and fecal scours ($R^2 = 0.96$, $P < 0.01$). This data was confirmed by correlation observed between NAC dose and ETEC counts in colon ($R^2 = 0.75$, $P = 0.055$) but not generic E. coli ($P = 0.32$). We conclude that NAC can be an effective dietary agent to reduce scouring in ETEC infected piglets. NAC does not appear to have negative effects on ADG and ADFI in antibiotic free diets.

Key Words: charcoal, ETEC, pig

W217 Effects of feed-borne *Fusarium* mycotoxins and an organic mycotoxin adsorbent on immune cell dynamics in the jejunum of broiler breeder pullets infected with *Eimeria maxima*. G. N. Girgis*, J. R. Barta, N. A. Karrow, H. J. Boermans, C. K. Girish, and T. K. Smith, *University of Guelph*, *Guelph, Ontario, Canada*.

Adverse effects of feed-borne *Fusarium* mycotoxins on the performance and metabolism of poultry have been described in the literature. There is a lack of information, however, regarding the effects of these mycotoxins on intestinal immune response to infections. Intestinal epithelium could be exposed to high concentrations of mycotoxins following ingestion of contaminated feed. An experiment was conducted to investigate the effects of feed-borne *Fusarium* mycotoxins and a polymeric glucomannan mycotoxin adsorbent (GMA) on immune cell dynamics in the jejunum of broiler breeder pullets using an *Eimeria maxima* infection model. Four groups of female Ross 308 broiler breeder chicks were fed a control diet, a diet naturally contaminated with *Fusarium* mycotoxins, contaminated diet plus GMA, or control diet plus GMA. Contaminated diets contained up to 6.5 μg/g deoxynivalenol (DON), 0.47 μg/g 15-acetyl-DON and 0.73 μg/g zearalenone. Pullets received a primary oral inoculation (1,000 oocysts/bird) with *E. maxima* USDA strain 68 at 2 weeks of age and a secondary oral inoculation (30,000 oocysts/bird) with the same strain at 4 weeks of age. The percentages of immune cell subsets in jejunal tissues collected at d 0, 3, 6 and 14 post-primary infection and d 0, 1, 2, 3 and 6 post-secondary infection were evaluated by immunohistochemistry and image analysis using ImageScope software. Data were analyzed by ANOVA and Tukey's test was used to compare least squares means among treatments ($P \leq 0.05$). Diet-related differences in $CD4^+$ cell, $CD8^+$ cell and macrophage recruitment pattern into the jejunum were observed following both the primary and secondary infections. It could be concluded that feed-borne *Fusarium* mycotoxins and GMA have the potential to modulate immune response to coccidial infections.

Key Words: *Fusarium* mycotoxins, coccidia, immune cells

W218 The granulated barley provided during growing or finishing period improves the carcass quality and increases the intramuscular fat content in muscle of heavy pigs. A. Daza[1], M. A. Latorre*[2], and C. J. López-Bote[3], [1]*Universidad Politécnica de Madrid*, *Spain*, [2]*Universidad de Zaragoza*, *Spain*, [3]*Universidad Complutense de Madrid*, *Spain*.

A total of 48 Duroc × (Large White × Landrace) gilts of 46.8 ± 1.39 kg of body weight (BW) were used to study the effect of the diet on growth performance, carcass characteristics and intramuscular fat content in the Longissimus dorsi muscle. Experimental diets were provided ad libitum according to the following treatments: i) a control diet with 3,210 kcal metabolizable energy (ME)/kg, 13.73% crude protein (CP) and 0.62% digestible lysine (Lys) from 45.6 to 127.8 kg BW (group C), ii) the control diet from 47.0 to 91.8 kg BW and granulated barley with 3,020 kcal ME/kg, 10.2% CP and 0.26% Lys from 91.8 to 129.7 kg BW (group C+GB) and iii) granulated barley from 47.9 to 93.1 kg BW and the control diet from 93.1 to 135.1 kg BW (group GB+C). The dietary treatment was replicated 8 times and the replicate was a pen with 2 gilts. The C group grew faster ($P \leq 0.05$) and tended to have better feed conversion ratio ($P \leq 0.10$) than GB+C group with C+GB group being intermediate. The GB+C gilts showed a compensatory growth during the finishing period. Although no effect was observed on carcass weight and yield, carcass length was higher ($P \leq 0.01$) in GB+C and C+GB than in C group and ham length and weight were higher ($P \leq 0.05$) in GB+C than in C gilts. Also, C group had lighter ($P \leq 0.001$) forelegs, loins and sirloins than GB+C and C+GB groups. The weight

and yield of total main lean cuts (ham+foreleg+loin+sirloin) was higher ($P \leq 0.001$) in GB+C than in C gilts with C+GB being intermediate. The subcutaneous backfat thickness was higher in C+GB than in C gilts with GB+C being intermediate ($P \leq 0.001$) and the C+GB and GB+C gilts had higher intramuscular fat content in meat than C gilts ($P \leq 0.001$). The dietary treatment had no influence on color, shear force or cooking losses of the loin but thawing losses were lower ($P \leq 0.05$) in GB+C and C+GB than in C gilts. It is concluded that gilts fed granulated barley during growing period had the best carcass quality characteristics. Also, granulated barley provided during growing or finishing period increased intramuscular fat percentage in gilt meat.

Key Words: barley, carcass quality, pigs

W219 Broiler energy choice feeding with same protein levels and ambient housing temperatures. S. Cerrate*, R. Ekmay, C. Salas, and C. Coon, *University of Arkansas*, *Fayetteville*.

Cobb male broilers (28 d of age) previously fed same starter diet were offered a single diet (control) and isoproteic choices between 2.950 and 3.250 kcal/g diets from 29 to 50 d. The control and dietary energy choices were fed to broilers housed in one of 2 ambient temperatures: 21 ± 1°C (normal temperature) and 30 ± 0.6°C (heat stress). Broilers housed at 21°C fed isoproteic choices varying in ME content had similar BW gain, feed intake (FI), feed conversion, ME intake and energy conversion as did birds fed the control diet. Broilers housed at 30°C fed the isoproteic choices varying in ME content had better BW gain, feed conversion and energy conversion compared with broilers fed the control diet. There was a marked preference (78.9% of FI) for the high energy diet (3.250 kcal/g) over the low energy diet (2.950 kcal/g) for broilers housed at 21°C, but this preference was less accentuated for broilers housed at 30°C (65.2% of FI). A potential explanation for broilers selecting diets with less ME in heat stress conditions compared with diet selection for broilers housed at 21°C may be related to the broiler trying to reduce gastrointestinal energy cost especially if hot ambient temperatures decrease fat and protein digestion as suggested by previous research. These data indicate that broilers in heat stress prefer reduced ME diets compared with broilers housed at 21°C.

Key Words: choice feeding, environmental temperature, energy requirement

W220 Effects of dietary creep feeding on performance, blood characteristics and behavior in sows and piglets. H. D. Jang*, J. H. Lee, T. X. Zhou, L. Yan, S. M. Hong, and I. H. Kim, *Department of Animal Resource and Science, Dankook University*, *Cheonan, Choongnam, Korea*.

This study was conducted to evaluate the effects of dietary creep feeding on performance, blood characteristic and behavior in sows and piglets. In total, data were obtained from 30 sows (Landrace × Yorkshire) and their litters. Sows were randomly assigned with 1, 2 or 3+ parities to 1 of 3 creep feeding treatment groups. Dietary treatments included 1) CON (no creep feeding), 2) TRT1 [creep feed (DE 4,000kcal/kg) from 5d of age until weaning (21d)], and 3) TRT2 [high energy creep feed (DE 5,000kcal/kg) from 5d of age until weaning (21d)]. The behavior of sows (nursery, eating, standing) and piglets (sucking, sleeping, fighting) in each treatments was observed throughout this experiments. Each piglet was weighted and bled on 5, 10, 15 and 21 d after birth to evaluate the ADG and IgG concentration of piglet. In addition, all sows were also bled on the lactation and weaning day to evaluate, epinephrine, nrepinephrine and cortisol concentration, rectal temperature of each sows was also measured at the same time. In herein study, dietary TRT1 and TRT2 significantly decreased the Epinephrine, norepinephrine and cortisol concentration compared with the control group ($P < 0.05$). Higher piglet IgG concentration was observed in the TRT1 and TRT2 group compared with the control ($P < 0.05$). Dietary TRT1 and TRT2 led a lower diarrhea score of piglets than those of the control treatment ($P < 0.1$). A higher piglet ADG was detected in the TRT2 ($P < 0.1$) compared with the CON treatment. No significant difference was observed on the rectal temperature of sows, the behavior of the piglet and sows among treatments. In conclusion, creep feeding can increase the immunity of piglet and decrease the diarrhea score of piglets. A higher energy creep feeding can significantly increase the growth performance of piglet compared with the those without creep feeding, while the creep feeding with lower energy show intermediate.

Key Words: creep feed, behavior, sow

W221 Crude glycerin in market turkey diets. S. L. Noll*[1], K. Koch[2], and J. Brannon[1], [1]*University of Minnesota*, *St. Paul,* [2]*North Dakota State University*, *Fargo*.

Crude glycerin (CG) is produced as a co-product of the conversion of fats into biodiesel and contains 80–88% glycerol. Two studies were conducted to examine CG as a source of energy in growing diets of market turkey toms. In the first trial, CG replaced an equivalent amount of corn in diets of low and high nutrient density (LND vs. HND). Glycerin was added at levels of 2, 4, 6, and 8%. As glycerin replaced corn, diet Lys, Met, and Thr were adjusted to the control diet (0% CG) for each nutrient density series. The base diet contained corn, soybean meal, poultry byproduct meal, and distillers dried grains with solubles (20%). Diets were adjusted for age and fed to toms during 8–19 wks of age. Diets were fed as mash. A factorial analysis included CG and nutrient density. In Trial 2, the objectives were to compare performance of toms fed diets with CG replacing fat and corn in diets fed as mash or pellets and to determine the effect of CG on pellet quality. The base diet was similar to Trial 1. The source of fat was sunflower oil. The study was of a factorial design with factors of feed form (mash or pellets) and CG (0, 3, and 6%). Each diet was fed to 8 replicate pens of tom turkeys (Large White, Nicholas) during 11–19 wks of age. In trial 1, BW was decreased by 2.9% at 19 wks for the LND series as compared with the HND regimen or by feeding CG in excess of 4% ($P < 0.05$). Cumulative feed efficiency during 8 to 19 wks of age was increased for the LND as compared with HND (2.85 vs. 2.59) while no effect was observed for CG addition ($P < 0.05$). A significant interaction of nutrient density and CG was observed during 17–19 wks of age for feed/gain. In Trial 2, BW was not affected by diet. Pellet quality in general was poor. A significant interaction of feed form and CG occurred for cumulative feed efficiency ($P < 0.05$). The interaction was primarily due to a lowered feed intake of the pelleted diet containing 6% glycerin as compared with the response at 0 and 3% CG. The improvement in feed/gain with pelleting indicated an important role of reduction in feed wastage by the feeding of pellets even if they are of poor quality. Inclusion of up to 6% crude glycerin was possible without a negative effect on performance.

Key Words: turkey, glycerin, feed form

W222 The effect of vetch heat treatment on free amino acids profile in plasma, muscle and liver of growing chickens. I. Fernandez-Figares*, M. Lachica, R. M. Nieto, and J. F. Aguilera, *CSIC, Spanish National Reseach Council*, *Granada, Spain*.

The aim of the present work was to evaluate the effect of feeding heat processed vetch meal to growing chickens on free amino acid (AA) levels in different tissues. Eight 4-week-old White Rock male growing chickens (mean LW 500 (s.e. 9.3) g) were given, for 3 d by crop intubation in 2 daily meals, 2 isoenergetic (13.1 MJ ME/ kg DM) and isonitrogenous (120 g CP/ kg DM) semisynthetic diets based on vetch seed meal, as a single source of protein, untreated or previously autoclaved at 120°C for 30 min. The paired-feeding level used was above that of maintenance (684 kJ EM/kg $LW^{0.75}$; Arch. Zootec. 36: 165–72). Four hours after the last meal, they were slaughtered by cervical dislocation and samples of

right biceps muscle and liver were frozen in liquid nitrogen and stored at −20°C until analysis. Also, heparinized blood samples were taken and plasma was obtained by centrifugation and finally frozen at −20°C. Samples were homogenized and deproteinized (by ultrafiltration) before analysis for free AA by HPLC, using the Waters Pico Tag method. Data were analyzed as one-way ANOVA using SAS software. The chickens were in a positive energy balance, but the diets supplied insufficient amounts of all essential AA, with an imbalanced profile (Anim. Prod. 57: 309–18). Heat treatment increased significantly ($P < 0.05$) plasma His and Met and decreased Ile, Ser and Pro. In muscle, birds fed heat-treated vetch had a tendency ($P = 0.05$–0.10) to increase Met and Trp and to decrease Thr and Lys. In liver, heat treatment increased ($P = 0.01$–0.05) free essential AA with the exception of Arg, Ile ($P = 0.013$–0.14) and Thr ($P = 0.99$). Previous work of this laboratory has shown that heat treatment increases the digestion and net absorption of total N and AA of some grain legumes, presumably by destruction of toxic constituents which stimulate endogenous protein excretion (Anim. Sci.60: 493–7). Consequently, liver free amino acid pool was more sensitive than muscle or plasma pools to this increased net AA absorption.

Key Words: free amino acids, legume, chicken

W223 Use of near infrared spectroscopy and color for identification of soybean meals by origin. P. García-Rebollar, N. Núñez-Romero, S. Santos-Rosell, R. Lázaro, and G. G. Mateos*, *Universidad Politécnica de Madrid*, *Madrid, Spain*.

Recent work has shown that chemical composition and nutritional value of soybean meals (SBM) differ among origins. Near-infrared reflectance spectroscopy (NIRS) has demonstrate its potential to identify and classify food products, and color has also been used to detect improper processing conditions. The objective of this work was to evaluate NIRS and color methods and its application in the feed mill industry to permit rapid and accurate origin (Argentine, ARG; Brazil, BRA; USA) identification of commercial SBM. A total of 290 SBM unground samples of known origin (ARG, n = 84; BRA, n = 74; USA, n = 132) were scanned using a spectrophotometer (Foss NIRSystems 5000) over the range 1100–2500 nm. Color (CIELAB system) was recorded using a Minolta colorimeter (model CR-300). On the basis of spectral data, a Principal Component Analysis was performed and outliers with a Mahalanobis distance greater than 3 were removed. The 3 sets of SBM spectra were split using the CENTER algorithm (WinISI v.1.50) into a calibration set (ARG, n = 61; BRA, n = 53; USA, n = 86) used to develop linear discriminant models (PLS2-DA procedure), and an external validation set (ARG, n = 20; BRA, n = 16; USA, n = 43). The best discriminant model yielded a SECV of 0.2515 and over 97% of correctly classified samples in the training set (100% for ARG; 96% for BRA, and 98% for USA, respectively), whereas in the validation step 100% of the samples were correctly classified. Color parameters of SBM samples differed ($P < 0.001$) among origins, with the BRA meals being redder than the ARG and USA meals (7.6 vs. 6.5 vs 5.9, respectively). The yellowness and luminosity were higher for the USA meals (26.5 and 71.1) than for the South American meals (25.1 and 67.3 for ARG; 24.4 and 65.3 for BRA), respectively. The results obtained show that NIRS is a reliable method of origin identification of commercial SBM samples at the reception stage in the feed mill industry, and that color can help to confirm these results.

Key Words: soybean meal origin, color, near infrared spectroscopy

Nonruminant Nutrition: Mineral

W224 Bioavailability of copper sources to broiler chicks when fed below the copper requirement. K. C. Klasing* and A. Naziripour, *University of California*, *Davis*.

Tribasic copper chloride (TBCC) has been shown to have better bioavailability than copper sulfate pentahydrate (CS) when fed at levels in excess of the requirement. Our objective was to determine if this relationship holds at levels below the Cu requirement. After depleting Cu levels for 7 d, 3 pens of 4 chicks/pen were fed a purified diet or a sorghum-soy diet supplemented with either 0, 1, 3, 4.5 or 6 ppm Cu. LPS was injected in order to initiate an acute phase response and bioavailability was calculated by common-intercept multiple linear regression. Prior to LPS, TBCC resulted in greater ($P < 0.05$) bioavailability as indicated by weight gain and tendon Cu levels with both diet types. Following LPS injection, TBCC resulted in greater bioavailability based on the plasma acute phase protein, ceruloplasmin ($P = 0.01$; slope ratio = 1.26). Bioavailabilities of the Cu sources did not differ for hematocrit or liver Cu. In general, these results indicate higher bioavailability of TBCC when dietary Cu is deficient in both healthy and inflammatory-stressed chicks.

Key Words: copper, bioavailability, poultry

W225 Effects of tribasic copper chloride on intestinal absorption ability and mucosal immunity of broiler chickens. Y. Ding[1], R. She*[1], H. Bao[1], D. Han[1], Z. Yue[1], J. Tian[1], P. Yu[1], R. Li[1], J. Yin[1], and C. Liang[2], [1]*China Agricultural University, Beijing, China,* [2]*Micronutrients, Indianapolis, IN.*

In recent years there has been increasing interest in the growth-promoting effect and immune-enhancing role of the copper. The objective of this study was to determine the effect of tribasic copper chloride (TBCC) on intestinal absorption ability and mucosal immune responses in chickens. One hundred and eighty 1-day-old broiler chickens were randomly divided into 4 groups, and were fed the following diets respectively: a basal diet with no supplemental copper (negative control), a basal diet + 188 mg of Cu/kg of diet from TBCC (TBCC group), a basal diet + subtherapeutic antibiotics (positive control), and a basal diet + TBCC+ subtherapeutic antibiotics(mixed addition group). Fifteen chickens of each group were randomly selected and killed on day 7, 21, 35, and samples of the duodenum were immediately collected and fixed. The height and width of the villus and the crypt depth were measured and the number of goblet cells, which determined the absorptive capacity of intestine, was counted. The results showed that the TBCC group had significantly increased villus height and crypt depth at the age of 7 day compared with the control group ($P < 0.05$). The number of goblet cells of duodenum was higher ($P < 0.05$) in the TBCC group than in the negative control group at the age of 7 day. The number of intestine intraepithelial lymphocyte (iIEL) cells and the IgA-secreting cells were counted to reflect the mucosal immunity level. The results showed that the numbers of iIEL in duodenum of TBCC group were increased significantly than the control groups ($P < 0.05$) on day 7. In the duodenum, the IgA-secreting cells of TBCC group were increased significantly compared with the other three groups ($P < 0.01$) on day 35. In conclusion, the results of the experiment indicated that TBCC could effectively enhance the small intestine to absorb nutrients and improve the mucosal immunity of the chickens, especially for the young chicks. These findings demonstrated that TBCC could be considered to replace antibiotics in modulation of the immune response for animal health.

Key Words: copper, broiler chicken, absorption ability and mucosal immunity

W226 Productive performance and egg quality of laying hens as a response to dietary copper supplementation. M. J. González*[1], J. J. Bañuelos[1], M. Huerta[1], S. Carrillo[2], and J. M. Cuca[3], [1]*Universidad Autónoma Chapingo*, *Texcoco, México, México*, [2]*INCMNSZ*, *México, DF, México*, [3]*Colegio de Posgraduados*, *Texcoco, México, México*.

This study was carried out to: 1) Evaluate the productive performance and egg quality as a response to dietary copper (Cu) supplementation, and to 2) Calculate the dietary optimal Cu levels to minimize feed conversion (DOLFC) and to maximize egg mass (DOLEM) or profits (DOLP). Methodology: 250 Hy-Line W36 hens, from 23 to 34 weeks of age, were allocated in five treatments with five replicates each. Treatments consisted of five supplemented Cu levels (0, 75, 150, 225 and 300 mg Cu/kg diet) from copper sulfate as a source of Cu. A sorghum-soybean basal diet was calculated to fulfill the Hy Line W36 nutrient requirements. A completely randomized design, with an orthogonal contrast analyses, was used to detect linear and quadratic tendencies of the experimental variables as a response to Cu levels. Econometric and regression models were applied to calculate DOLFC, DOLEM and DOLP. Results of contrast analyses showed ($P \leq 0.05$) linear and quadratic effects on feed intake (FI), egg mass (EM), feed conversion (FC) and laying percentage (LP). The dietary Cu optimal levels were calculated at 129.5 mg Cu/kg diet for DOLFC; 117.1 mg Cu/kg diet for DOLEM, and 120.6 mg Cu/kg diet for DOLP. The DOLP was sensible to egg price variation. A comparison of the dietary Cu optimal levels with the control values for FC (2.07), EM (44.2 g), and LP (79.6%) showed a performance improvement of 13.5%, 13.1% and 11.3%, respectively. Egg quality showed no effect ($P > 0.05$) for egg weight. Nevertheless, height of albumin and Haugh units diminished ($P \leq 0.05$) with increasing dietary Cu levels. Shell thickness improved ($P \leq 0.05$) with Cu supplementation. Conclusions: 1) Dietary Cu supplementation improves productive performance and shell thickness; 2) Dietary Cu optimal levels are specific for each biological or economic goal.

Key Words: hens, copper, performance

W227 Effect of organic trace mineral sources on production and egg quality of white egg laying hens. L. M. Macalintal*, A. H. Cantor, T. Ao, J. L. Pierce, A. J. Pescatore, K. A. Dawson, M. J. Ford, W. D. King, and H. D. Gillespie, *Alltech-University of Kentucky Nutrition Research Alliance*, *Lexington*.

The effects of supplementing white laying hens with graded levels of organic and inorganic sources of Cu, Mn, Fe, Zn and Se on egg production and quality were studied. The organic sources used were proteinates of Cu, Mn, Fe and Zn (Bioplex, Alltech, Inc.) and selenium yeast (SelPlex, Alltech, Inc.). Seven treatments consisted of feeding corn-soybean meal diets alone (basal) or supplemented with Cu, Mn, Fe and Zn at 25, 50, or 100% of the NRC (1994) requirements provided by either inorganic salts or organic sources. Selenium was provided at 0.075, 0.15 and 0.3 mg/kg as either sodium selenite or selenium yeast in the diet containing 25, 50 and 100% of the NRC requirements, respectively. At each stage of growth or production, other nutrient levels were adjusted to meet the dietary requirements. Eight replicate groups of 16 chicks at day 1 of age were randomly assigned to each treatment. At 17 weeks of age, pullets were transferred to laying cages using 12 pullets per replicate and the mineral treatments were continued for 28 weeks of production. Egg quality parameters were assayed monthly on samples of six eggs per replicate group. During the 28 weeks of production, overall body weight gain (465 g/hen), feed intake (93.0 g/hen/d) and hen-day egg

production rate (85.0%) were not affected by treatments. During Weeks 17-20, hens fed organic minerals at 50% of the NRC requirement had higher egg production (94.2%) than those fed the basal diet (90.3%) or inorganic minerals at the 25% level (90.4%). Average egg weight at 26 wk of production was significantly higher for hens fed organic minerals at the 100% rate compared with all other treatments. Compared with the basal treatment, no improvements in shell breaking strength, % shell and specific gravity were observed due to mineral supplementation.

Key Words: trace minerals, mineral proteinates, egg production

W228 Layer excreta mineral content: Organic versus inorganic dietary trace mineral sources. S. Leeson[1], A. E. Sefton*[2], and K. A. Jacques[2], [1]*University of Guelph*, *Guelph, ON, Canada*, [2]*Alltech Inc.*, *Nicholasville, KY*.

Regular inorganic mineral premixes used in layer diets can result in levels of mineral in manure that are of environmental concern. Previous trials have shown that reduced levels of more available organic mineral forms do not harm performance or well being and can substantially reduce manure minerals. This experiment evaluated performance, egg quality and mineral excreta content of Lohmann layers fed inorganic or reduced amounts of organic copper (Cu), manganese (Mn) and zinc (Zn) sources over a laying cycle. Hens (720) at 18 wks of age were randomly allocated to cages of 5 birds assigned to diets containing either inorganic (sulfate) or organic (Bioplex, Alltech Inc.) sources of Cu, Mn and Zn. Mineral concentrations from supplemental sources in the inorganic control and organic mineral diet, respectively, were Cu, 5 and 0.6; Mn, 100 and 12.6; Zn, 60 and 14 ppm. The experiment consisted of 13, 28 day periods. Response variables were egg production, total egg number, egg weight, shell deformation, albumen height, feed intake, body weight, feather scoring and excreta mineral content. The data were subjected to ANOVA with means separated using Tukey's test. In general, diet treatment did not affect bird performance. Body weights, feed intake and feather scores were similar for both treatments ($P > 0.05$). There were marked reductions in the levels of Zn, Mn and Cu in excreta ($P < 0.01$) when birds were fed Bioplex vs. inorganic minerals (Zn, 149 vs. 354; Mn, 116 vs. 407; Cu, 18 vs. 38 ppm). It was concluded that layers performed equally well throughout a laying cycle when fed a diet containing either inorganic or Bioplex mineral sources. There was a very significant decrease in Zn, Mn and Cu in excreta when hens were fed a diet containing Bioplexes during the laying cycle.

Key Words: layers, trace minerals, excreta

W229 The effect of selenium source and supplementation level on vitelline membrane strength and glutathione peroxidase activity in the liver and shell gland of laying hens. A. A. Aljamal*[1], C. A. Fassbinder-Orth[2], and S. E. Scheideler[1], [1]*University of Nebraska-Lincoln*, *Lincoln,* [2]*Creighton University*, *Omaha, NE*.

The objective of this study was to investigate the effects of selenium source and level on production parameters of laying hens, effects on vitelline membrane strength, and effects on GSH-Px activity in the liver and shell gland of hens. A total of 120 White Bovan hens were fed the experimental diets for 8 weeks from 35 to 42 wks of age. A total of 30 cages were used in the trial with 6 cages/ treatment. Cages were blocked by side, north and south, each side with a total of 15 cages. Hens were fed a corn-soybean meal basal diet supplemented with: (0, 0.2 ppm Sel-Plex, 0.2 ppm sodium selenite, 0.4 ppm Sel-Plex, or 0.4 ppm sodium selenite) for a total of 5 dietary treatments, with the basal level of Se in the diet being 0.2 ppm. Feed intake and egg production were measured daily. Egg weights, specific gravity, and Haugh units were taken weekly. Aged and fresh albumen and yolk pH were measured biweekly. The experimental design of the trial was a randomized completely blocked design. Vitelline membrane strength was measured at weeks 5, 6, 7, and 8 of the trial. At the end of the study, 2 hens/ cage were euthanized to measure GSH-Px activity of the liver and shell gland tissues. Feed intake and egg production increased as dietary Sel-Plex supplementation increased in the diet ($P < 0.05$). Dietary treatments had no significant effect on egg weight, specific gravity, Haugh unit, or hen weight. Using Selenite at 0.2 ppm or Sel-Plex at 0.4 had the same effect to improve the VMS ($P = 0.0592$). Using 0.4 ppm Sel-Plex had a significant effect in decreasing the aged albumen pH but this was only significantly different from the treatment supplemented with 0.4 ppm selenite ($P = 0.0577$). Neither Sel-Plex nor selenite had any effect on GSH-Px activity in the liver and shell gland of the hens. Our research indicates that 0.4 ppm Se from Sel-Plex significantly improved egg quality in aged albumen pH and VMS measurements.

Key Words: laying hens, Sel-Plex, egg production

W230 Effects of altered calcium and phosphorus intake on growth performance and bone characteristics in growing pigs. L. A. Pettey*, K. M. Martorana, T. D. Moore, and J. M. Krumheuer, *California Polytechnic State University*, *San Luis Obispo*.

A two stage growth study was conducted to quantify the effects of altered calcium (Ca) and phosphorus (P) levels on growth performance and bone characteristics in growing pigs and to compare the sensitivity of various bones to changes in Ca and P intake. Pigs (n=112; 21.4 kg BW) were randomly allotted by weight to one of two dietary treatment groups: 1) NRC levels of Ca and P as control; and 2) as 1 with Ca and P increased to 120% of NRC. Pigs were fed diets for 2 weeks before six pigs from each group were harvested for collection of all skeletal bones. Increased Ca and P intake had no effect ($P > 0.10$) for ADG or Ca and P content of leg bones. Following the feeding of high and low Ca and P diets, 96 of those pigs were randomly allotted in a RCB design to one of three diets: 1) a corn-SBM based diet as control (0.62% Ca, 0.54% P), 2) as 1 with 0.74% Ca and 0.63% P, 3) as 1 with 10% added soybean hulls to decrease ME by 100 kcal/kg. Prior level of Ca and P intake was used as a blocking factor. Pigs were fed diets for 4-wk prior to collection of all skeletal bones. As expected, soy hull addition increased ($P < 0.05$) ADFI, thus increasing Ca and P intake ($P < 0.05$) compared with pigs fed the control, but similar ($P > 0.10$) to pigs fed a high Ca and P diet. Pigs with increased Ca and P intake (Diets 1 and 2) had greater ($P < 0.05$) ADG compared with pigs fed the control diet. Prior level of Ca and P intake had no effect ($P > 0.10$) on growth or bone traits. Increasing Ca and P intakes tended to increase ($P < 0.08$) the weight of ribs, metacarpal, metatarsal, humerus and femur. On a concentration basis (g/kg) all bones from pigs with increased Ca and P intakes were higher ($P < 0.05$) in ash, Ca, and P compared with pigs fed the control diet. The percentage increase in bone ash most closely correlated to Ca and P intake for rib bones ($R^2 = 0.92$), yet positive correlations were observed for femurs ($R^2 = 0.82$), humerus ($R^2 = 0.78$) and metacarpal/metatarsal bones ($R^2 = 0.74$). Overall, mineral content of specific bones increase differently to increasing levels of Ca and P intake in growing pigs.

Key Words: calcium, phosphorus, bone

W231 Effect of mineral source and mannan-oligosaccharide supplementation on mineral metabolism on young growing pigs. A. Lebel*[1], F. Guay[1], and P. Groenewegen[2], [1]*Universite Laval*, *Quebec, Qc, Canada*, [2]*Alltech Canada*, *Guelph, On, Canada*.

The objective of this study was to evaluate the effect of mineral source and mannan-oligosaccharide supplementation on the digestibility and net utilization of zinc and copper in young growing pigs. Twenty eight barrows (25.7 kg, SEM 1.2) were assigned to one of 4 diets in a randomized complete block design. Corn soybean diets were supplemented with 10 ppm of copper and 100 ppm zinc from organic (Bioplex) or inorganic (Sulfate) sources, and with (0.1%) or without mannan-oligosaccharide (Bio-Mos, MOS) according to a 2 x 2 factorial design. Animals were maintained in individual metabolic crates for an adaptation period of 3 days following by a collection period of 5 days for the total collection of urine and feces. Pigs fed organic mineral supplemented diets had higher feed intake (2,247 vs. 2,068 g/d, SEM 86, $P < 0.05$), copper intake (56.5 vs. 50.7 mg/d, SEM 2.2, $P < 0.07$) and zinc intake (325 vs. 293 mg/d, SEM 10, $P < 0.04$) than those fed diets supplemented with the inorganic minerals. The higher zinc and copper intakes in the organic treatment led to higher copper retention (32.0 vs. 22.4 mg/d, SEM 2.5, $P < 0.01$) and a trend for higher zinc retention (170 vs. 142 mg/d, SEM 10, $P < 0.07$). There was also a trend for a reduction in fecal copper excretion (23.8 vs. 27.7 mg/d, SEM 1.5, $P < 0.09$). These results explain the increased digestibility (45 vs. 56%, SEM 2, $P < 0.01$) and net utilization (44 vs. 55%, SEM 2, $P < 0.01$) of copper when fed in the organic form. However, these effects tended to be more pronounced when the diet did not contain MOS (interaction, mineral form × MOS, $P < 0.09$, without MOS 41 vs. 59% and with MOS 48 vs. 54%, SEM 3 for digestibility; without MOS 40 vs. 57% and with MOS 48 vs. 54% for net utilization). Mineral form and MOS supplementation had no significant effect on zinc digestibility or net utilization. These results suggest that organic mineral supplementation is an effective method to improve the digestibility and net utilization of copper, and reduce its total excretion but these effects would be less pronounced when the diet is supplemented with MOS.

Key Words: copper, zinc, mannan-oligosaccharide

W232 Enrichment of Japanese quail eggs with organic selenium. R. A. Gravena, R. H. Marques, J. D. T. Silva, F. H. Hada, J. Picarelli, J. Roccon, S. A. Queiroz, and V. M. B. Moraes*, *São Paulo State University*, *SP - Brazil*.

The aim of this study was to evaluate the effect of diets supplemented with organic selenium (Se) on the deposition of this mineral in the yolk and albumen of Japanese quail eggs. One hundred 92 quail were randomly distributed into 4 treatment groups with 6 replicates of 8 birds in each pen. The birds were placed on 1 of 4 dietary treatments (0, 0.35, 0.70 and 1.05 mg organic Se/kg feed) for 4 lay cycles. Three eggs were collected per treatment at 56 d. The Se content of egg yolks and albumen were determined using microwave digestion followed by AAS. The Se concentration in egg yolk was not affected by supplementing diets with organic Se ($P > 0.05$). The Se levels in albumen increased linearly ($y = 3.09308 + 9{,}63459x$; $r^2 = 0.52$) with the increase of supplemented Se in diets ($P < 0.0001$), which can be explained by the interaction of organic Se deposition with the proteins in albumen. These results suggest that supplementing the diets of Japanese quail with organic Se can improve the nutritional value of their eggs.

Table 1. Se concentration in the yolk and albumen in quails eggs supplemented with organic Se

	Se concentration		
Se levels (mg/kg diet)	Yolk (µg/kg yolk)	Albumen (µg/kg albumen)	Se concentration in albumen (%)
0	68.60	3.07	–
0.35	89.27	6.47	110.75
0.70	67.25	9.90	222.47
1.05	72.41	13.16	328.66
CV (%)	25.68	46.73	–
P value	0.76^{ns}	0.0001*	–

Key Words: albumen, organic selenium, quail

W233 Improved piglet birth weight by feeding sows an organic trace mineral blend. J. Zhao*[1], L. Greiner[2], M. Vazquez-Anon[1], C. D. Knight[1], and R. J. Harrell[1], [1]*Novus International Inc.*, [2]*Innovative Swine Solutions*.

The objective of this study was to examine the benefits of feeding sows an organic trace mineral blend (OTM, Mintrex, Novus International Inc.) on piglet birth weight and uniformity. Two sister farms with a common grandparent farm were fed either an inorganic control (ITM) or an OTM blend (Zn, Mn, and Cu), which replaced 50% of the ITM, with the target levels of Zn, 165ppm, Cu, 16.5ppm, and Mn, 38.5ppm in final diets. Treatment was initiated at weaning and continued through growing and entry into the breeding herd. After 2.5 years, about 30 litters were selected for each parity (P1, P2, P3+4, P5 and above). Individual piglet weight (within 24 hours after birth and before cross-fostering) was collected in a two-week period in August and December, 2009. The number of total born was not different on selected litters (12.9 vs. 13.0 ± 0.27, $P = 0.84$). The mean piglet weight was greater for sows fed OTM (1.36 vs. 1.25 vs. ± 0.02 kg, $P < 0.001$). Piglet uniformity was not different between treatments ($P = 0.45$). Benefits of OTM on piglet weight were more profound from P2 to P4 with average piglet weight of 1.13 vs. 1.22 kg for P1 ($P = 0.15$), 1.27 vs. 1.38 kg for P2 ($P = 0.04$), 1.23 vs. 1.38 kg for P3+4 ($P = 0.002$), and 1.19 vs. 1.25 kg for P5 and above ($P = 0.50$) for sows fed the control and OTM, respectively. In summary, sows fed OTM had heavier piglets compared to sows fed ITM and there is no difference on piglet uniformity between treatments.

Key Words: birth weights, sow, organic trace mineral,

W234 Dietary calcium affects neonatal bone development and mesenchymal stem cell activity. A. Mahajan[1], L. S. Alexander[1], B. S. Seabolt*[1], D. E. Catrambone[2], J. P. McClung[2], J. Odle[1], T. W. Pfeiler[3], E. G. Loboa[3], and C. H. Stahl[1], [1]*Laboratory of Developmental Nutrition, North Carolina State University*, *Raleigh,* [2]*Military Nutrition Division, US Army Research Institute of Environmental Medicine*, *Natick, MA,* [3]*Joint Department of Biomedical Engineering at University of North Carolina-Chapel Hill and North Carolina State University*, *Raleigh*.

Effects of dietary calcium (Ca) deficiency on skeletal integrity and endocrine parameters are well characterized in growing and mature pigs; however, little work has examined Ca nutrition during the neonatal period. We examined the effects of neonatal Ca nutrition on bone integrity, endocrine parameters, and mesenchymal stem cell (MSC) activity. Neonatal pigs (24 ± 6h post-partum) were pair-fed either a Ca adequate (Ca+) or a 30% Ca deficient (Ca-) liquid formula diet for 18 d. There were no differences in growth rate or feed efficiency based on dietary Ca level and all pigs grew at a rate similar to sow-reared pigs.

As anticipated, Ca deficiency reduced (P < 0.05) both BMD and bone flexural strength. The anticipated increase ($P < 0.05$) in plasma PTH levels was not evident until the end of the study. Surprisingly, dietary Ca level did not affect plasma Ca or 1,25(OH){2} vitamin D concentrations throughout the study. Calcium deficiency reduced ($P < 0.05$) the in vivo proliferation of MSC isolated from bone marrow by approximately 50%. To further assess the impact of Ca nutrition on MSC activity, cells isolated from these pigs were cultured in homologous sera, under both proliferative and adipogenic conditions for 6d. Under proliferative culture conditions, Ca- sera reduced MSC proliferation and Ca+ MSC had greater expression of osteocalcin and Runx2 mRNA. Under adipogenic culture conditions, MSC cultured in Ca- sera had greater Oil Red O staining and Ca+ MSC also had greater Oil Red O staining than did there Ca- counterparts. Ca- MSC cultured with Ca- sera under adipogenic conditions had 2-fold greater expression of PPARG2 mRNA than any other treatment group. Concentrations of calcitropic hormones were not different between Ca+ and Ca- sera, but we identified 22 differentially expressed proteins in these sera. The results indicate that neonatal Ca restriction may have long-term effects on bone integrity via programming of MSC. The results indicate that neonatal Ca nutrition is crucial for bone integrity and suggest that early life Ca restriction may have long-term effects on bone integrity via its effects on MSC activity.

Key Words: calcium, mesenchymal stem cells, pig

W235 Serum from pigs fed a high-Se diet inhibits growth of human lung cancer cells. J. G. Li[1], J. Shi[1], K. N. Wang[1], G. Gao[2], X. J. Xia[1], and X. G. Lei*[1,3], [1]*Int. Ctr. of Future Agriculture for Human Health, Sichuan Agri. Univ.*, *Chengdu, China*, [2]*Chengdu Municipal Ctr for Disease Control and Prevention*, *Chengdu, China*, [3]*Cornell University*, *Ithaca, NY*.

Supranutritional levels of Se may decrease risks of human lung cancer, but may increase risks of diabetes. Pigs are an excellent model for humans. The objective of this study was to determine if serum from pigs fed a high-Se diet inhibited growth of human lung cancer cells. A total of 16 weanling pigs were fed a Se-deficient (0.03 mg Se/kg) corn-soy basal diet and the basal diet plus 3 mg Se/kg (as sodium selenite) for 16 wk. At the end, serum collected from individual pigs was pooled by the treatment groups and filtered through a 0.22-μm membrane for cell culture. While serum insulin and insulin-like growth factor 1 concentrations were similar between the two groups of pigs, serum Se concentration and serum lactate dehydrogenase (LDH) activity was lower ($P < 0.05$) and higher ($P < 0.05$), respectively, in the Se-deficient pigs than those fed 3 mg Se/kg. Based on cell viability, the optimal serum level for the cell growth was 17 and 15%, respectively, for serum from pigs fed the basal diet and the diet plus 3 mg Se/kg. Compared with the Se-deficient serum (16%), the high-Se serum (16%) from pigs fed 3 mg Se/kg decreased ($P < 0.05$) cell viability, promoted ($P < 0.05$) apoptosis, and increased medium LDH activity. In conclusion, serum from pigs fed a high-Se diet may have anti-cancer potential.
This work was partially supported by NSFC Projects 30628019, 30700585, and 30871844, and the Chang Jiang Scholars Program (XGL).

Key Words: selenium, lung cancer, pig, serum, cell culture

W236 Effect of sodium selenite and turmeric powder on Gompertz nonlinear function in broilers reared under heat stress. A. Zeinali*[1], H. Kermanshahi[1], H. Ziaie[2], H. Farhangfar[3], and A. Riasi[3], [1]*Ferdowsi University*, *Mashhad, Khorasan, Iran*, [2]*Agriculture and Natural Resources Research Center*, *Birjand, South Khorasan, Iran*, [3]*Birjand University*, *Birjand, Khorasan, Iran*.

An experiment was conducted to study the effect of organic and inorganic antioxidant on Gompertz nonlinear function in broilers reared under heat stress. So, 180 one-day old chickens (male and female) were used in a completely randomized block design with 6 treatments and 3 replicates. The experimental diets were (T1) control diet ; (T2) control diet + 5 g/kg turmeric powder; (T3) control diet + 10 g/kg turmeric powder; (T4) control diet + 0.3 mg/kg sodium selenite; (T5) control diet + 0.3 mg/kg sodium selenite + 5 g/kg turmeric powder; and (T6) control diet + 0.3 mg/kg sodium selenite + 10 g/kg turmeric powder. Broilers were subjected to heat stress (35°C) during the fifth and sixth weeks. The results showed that diets including 10 g/kg turmeric powder significantly increased final weight (Wf), weight at inflection time (Wt) and time at inflection time (t) ($P < 0.05$). However, the difference between 10 and 5 g/kg turmeric powder levels was not significant. The interaction between selenium and sex was significant on Wf in such a way that male chickens fed with selenium had higher Wf.

Key Words: selenium, turmeric powder, nonlinear model

W237 Modelling the fate of dietary phosphorus in the digestive tract of growing pigs: a way to optimize phytase efficacy in releasing dietary P. M. P. Letourneau-Montminy*[1], A. Narcy[2], M. Magnin[3], and C. Pomar[1], [1]*Agriculture and Agri-Food Canada*, *Sherbrooke, Qc, Canada*, [2]*INRA UR83*, *Nouzilly, France*, [3]*BNA Nutrition Animale*, *Chateau-Gontier, France*.

A mathematical model simulating the fate of all forms of dietary phosphorus (P) in the digestive tract of the growing pig was developed to provide ways to improve dietary P utilization. It was developed using in vitro and in vivo information. Three compartments are distinguished into the model: 1) the stomach in which dietary forms of P can be solubilised and phytic P (PP) hydrolyzed by phytases, 2) the proximal small intestine in which intense absorption occurs and 3) the distal small intestine in which P may form insoluble complexes with calcium that reduces its absorption. Flows between compartments of all forms of P are assumed to follow mass action laws parameterized with experimental data. The prediction capabilities of the model were assessed by comparing actual and simulated apparent total tract digestibility of P (ATTD), considering experiment effect, based on pig published data not used for model development. It revealed adequate prediction of P digestibility in diets supplemented or not with plant or microbial (Aspergillus niger) phytase (ATTDobserved = 5.53 + 0.87 x ATTDpredicted, n=281, nexp=66 R2=0.85, RSD=4.2% relMSPE=9.4%). Model sensitivity and behavior analysis showed that the hydrolysis of PP by phytases is largely dependent on PP solubility. Phytic P enters into the model in non-solubilised forms (PPns) and is then solubilised (PPs) according to the stomach pH. The equilibrium between PPns and PPs is also represented allowing PPns to solubilise after PPs has been hydrolysed by phytase. The simulation of a corn-soybean meal control diet supplemented with 1000 FTU/kg of A. niger phytase resulted in a 60% PP hydrolysis. This diet was used as control to study the effectiveness of phytase in releasing P from phytate. PPs hydrolysis is improved by increasing stomach mean retention time (74%) and by lowering its pH (66%). Based on the present simulation study, PP hydrolysis is mainly limited by the solubilisation of PPns. Further studies are needed to highlight and to quantify the impact of other factors that may interfere with PP solubility in the digestive tract of pigs.

Key Words: modelling, phytase, pigs

W238 Expression of borate transporter (NaBC1) mRNA by growing pigs is sensitive to dietary boron levels. S. F. Liao*, J. S. Monegue, M. D. Lindemann, G. L. Cromwell, and J. C. Matthews, *Department of Animal and Food Sciences, University of Kentucky*, *Lexington*.

Metabolic studies indicate that homeostatic control of elemental B in animals primarily involves the absorption and excretion of borate through gastrointestinal and renal epithelia, respectively. Recently a borate transporter, NaBC1 (SLC4A11), has been identified in the basolateral membranes of mammalian epithelial cells. A nutrient balance study was conducted to determine the effect of B supplementation on DM, N, Ca, and P digestibilities of growing barrows (initial BW=74.0±9.8 kg) commonly fed a corn-soybean meal diet without P supplementation for 12 d and then supplemented with either (n=8) 0 (Basal), 50, or 100 ppm B (prilled sodium borate pentahydrate) for 12 d (7-d adaptation, 5-d collection). Supplementation of B did not affect nutrient digestibilities. To determine (1) if pig jejunal (J) and ileal (I) epithelia, and kidney (K) express NaBC1 mRNA and (2) if expression is sensitive to dietary B concentration, total RNA was extracted from individual tissue homogenates prepared from all the pigs killed at the end of the balance study. The cDNA sequences of the RT-PCR products (130 base pairs each) generated from each tissue shared 100% identity to each other and to the putative pig NaBC1 sequence (GenBank no. XM_001924562). Subsequent real-time RT-PCR analysis quantified the relative amount of NaBC1 mRNA (NaBCl:18S) expressed. Compared to the Basal level, 50 ppm supplemental B tended ($P = 0.11$) to increase (248%) J, did not affect ($P = 0.83$) I, and decreased ($P = 0.02$) K NaBC1 mRNA contents, whereas 100 ppm supplemental B did not affect ($0.23 \leq P \leq 0.42$) the expression by any tissue. The tissue NaBC1 mRNA content did not differ ($P \geq 0.19$) between pigs fed B at 50 vs. 100 ppm. The finding that pig J, I, and K express NaBC1 mRNA is novel. Despite no effect on measured digestibilities, that 50 ppm supplemental B differentially altered NaBC1 mRNA content suggests that NaBC1 expression may be responsive to borate levels in digesta, blood, or both.

Key Words: borate transporter (NaBC1, SLC4A11), nutrient-gene interaction, pig

W239 Evaluating trace mineral level and form in diets fed gilts: effects on ovulation rate, embryonic survival and mineral composition of conceptus products. W. L. Pope[1], B. J. Middendorf[1], H. S. Cárdenas[1,2], D. C. Mahan[1], and K. A. Jacques*[3], [1]*OARDC, Department of Animal Sciences, The Ohio State University*, *Columbus,* [2]*College of Medicine, The Ohio State University*, *Columbus,* [3]*Alltech Inc.*, *Nicholasville, KY*.

Crossbred gilts (n=210) (Large White × Landrace) × PIC boar (line 280) were utilized to examine whether the previously observed increase in litter size after replacing inorganic trace elements with an organic source was due to improved ovulation rate, embryonic survival and/or fetal survival. At 45-kg body weight, gilts were randomly assigned to one of four dietary treatments; 1) industry levels of inorganic trace elements (Cu, 15; Fe, 120; Mn, 40; Zn, 120; Se, 0.3 ppm), 2) NRC levels of organic Cu, Fe, Mn, Zn (Bioplex) and Se (Sel-Plex) (Alltech Inc.), 3) industry levels of organic and 4) 1.5 times industry levels of organic trace elements. Due to space limitations of the barn, the design of this experiment was accomplished in 9 reps over a 2-year period. Within each replicate, the treatments were rotated so that differences due to pens or locations were randomized throughout the experiment. Gilts were individually penned and at about 130 kg were naturally mated at 12 and 24 h after onset of estrus. Boars had at least 3 days rest between matings. Gilts were slaughtered at day 30 of gestation. Resulting conception rate, ovulation rate, total embryos, total live embryos and embryonic survival were unaffected by treatment with overall means of 88.8, 16.9 (corpora lutea), 13.8, 13.6 and 80.3%, respectively. Macro and microelement content of embryonic and endometrial tissues collected at slaughter and of allantoic and amnionic fluids were analyzed in a subset (n=12) of gilts from each treatment group. Amounts of macro and microelements were altered ($P<0.05$) in numerous comparisons of endometrial or embryonic tissues and in allantoic or amniotic fluids of gilts fed organic versus inorganic trace elements. As the form or amount of trace minerals in the diet had no effect on ovulation rate, number of live embryos and embryonic survival, any improvement in litter size must be attributable to events occurring after 30 days of gestation.

Key Words: trace minerals, ovulation rate, fetal survival

W240 Cloning of porcine pancreatic α-amylase gene and characterization of the enzyme over-expressed in *Pichia pastoris*. T. Qin[1], H. Zhao[1], X. Xia[1], and X. G. Lei*[1,2], [1]*Int. Ctr. of Future Agriculture for Human Health, Sichuan Agri. Univ.*, *Chengdu, China*, [2]*Cornell University*, *Ithaca, NY*.

α-Amylase (α-1,4-glucan-4-glucanohydrolase, EC.3.2.1.1) catalyzes the hydrolysis of α-(1,4) glycosidic linkages in starch and various malto-oligosaccharides, and may be used to improve feed carbohydrate utilization by animals. The objective of this study was to develop an efficient expression system to produce porcine pancreatic α-amylase (PPA). The full-length cDNA encoding the PPA was isolated from porcine pancreas by RT-PCR and cloned into the pPICZαA (Invitrogen, Shanghai, China) expression vector. The pPICZαA-PPA plasmid was transformed into *Pichia pastoris* (X33) cells, and transformants were screened by SYBR-green quantitative real-time Q-PCR (ABI 7900HT, Applied Biosystems, Foster City, CA). After the transformants were induced by 0.5% methanol for 3 d, the extracellular PPA protein containing a his-tag appended to the C terminus was purified using Ni Sepharose High Performance affinity column (GE Healthcare, Piscataway, NJ). The purified recombinant PPA showed a molecular mass of approximately 58 kDa, an optimal temperature of 50°C, an optimal pH of 7.5, K_m of 65 mg/ml (soluble starch), and V_{max} of 1.7 mg/min, respectively. After an exposure to 50° for 30 min, the recombinant PPA lost nearly 50% activity. The recombinant enzyme was more sensitive to the inhibition by Cu^{2+} than Fe^{3+}, Ca^{2+}, or Zn^{2+}. In conclusion, we have cloned the PPA gene and produced a relative high level of the functional enzyme in *P. pastoris*.

Key Words: porcine, pancreatic, α-amylase, *Pichia pastoris*, gene expression

W241 Heterologous expression of a truncated bovine lactoferrin gene in *E. coli* to produce a novel antimicrobial peptide. L. H. Sun[1], Y. Liu*1,2, H. Zhao[1], M. Y. Xie[1], J. Xing[1], X. J. Xia[1], and X. G. Lei[1,2], [1]*Int. Ctr. of Future Agriculture for Human Health, Sichuan Agri. Univ.*, *Chengdu, China*, [2]*Cornell University*, *Ithaca, NY*.

Antibiotic resistance has become a major concern for the animal feed industry and human medicine worldwide. As a promising alternative of antibiotics, LfcinB is a peptide of 25 amino acids that originates from the N-terminus (Phe17 to Phe41) of bovine lactoferrin. Because LfcinB has a broad spectrum of potent antimicrobial activity, it is highly toxic to heterologous expression hosts like *E. coli* cells. The objective of this experiment was to develop an efficient expression system to produce an inactive or non-toxic precursor of LfcinB in *E. coli*. A DNA fragment encoding the N-terminal 121 amino acids of bovine lactoferrin that contained the LfcinB peptide was synthesized and inserted into an expression vector pET-30a(+) (Merck, Shanghai, China). The construct

was transformed into *E. coli* strain Rosetta (DE3) cells. As shown by the SDS-PAGE, a truncated bovine lactoferrin with a molecular mass of approximately 19.2 kDa was produced by the transformants, and the yield accounted for 30% of the total cell protein. We are currently investigating if LfcinB can be released from the overly-produced truncated bovine lactoferrin by pepsin at the acid pH in the stomach of animals. In summary, our approach in producing the LfcinB precursor may offer advantages of convenience and cost over other expression systems.
Supported by the 863 program (2007AA100602 and 2007AA100601-6) and by the Chang Jiang Scholars Program of the Chinese Ministry of Education (XGL).

Key Words: lactoferrin, lactoferricin, gene expression, antimicrobial peptide

W242 Cloning and expression of palustrin-OG1 in *E. coli*. Y. G. Xie*, Y. F. Liu, C. Luan, F. F. Han, and Y. Z. Wang, *Institute of Feed Science, Zhejiang University*, *Hangzhou, Zhejiang, China*.

Palustrin-OG1 is a novel antimicrobial peptide (AMP) isolated from the skin of the frog *Odorrana grahami*. It is a 31 amino acid peptide with antibacterial activities against a broad spectrum of microorganisms, especially against *S. aureus* ATCC 25923. With increasing resistance to existing antibiotics, it is imperative to develop new therapeutics such as AMPs. So far there have been no reports about its structure and antibacterial mechanism. In order to obtain enough amount of palustrin-OG1 for biological and structural studies, the gene encoding mature peptide of palustrin-OG1 was deduced from its amino acid sequence according to the codon bias of *E. coli* and synthesized with the method of gene splicing by overlapping extension PCR(SOE–PCR). Palustrin-OG1 gene was recombined to the expression vector pET32a(+) homologously to construct the recombinant expression plasmid pET32a(+)–OG1. The recombinant plasmid was then transferred into *E. coli* BL21 (DE3) and induced for 3h by IPTG with the final concentration of 1 m*M*. The soluble form fusion protein expressed in *E. coli* was up to 57.97mg/L. After ultrasonic disruption of cells, the soluble protein was purified by nickel column chromatography and desalted through Sephadex G25 column chromatography. Palustrin-OG1 was released from purified fusion protein after cleavage by enterokinase for 16h. The agar diffusion test showed the released palustrin-OG1 exerted activity against *S. aureus* ATCC25923. The integration strategy such as codon bias, homologous recombination and protease cleavage would provide an effective platform for biological and structural studies or production of AMPs as therapeutics.

Key Words: palustrin-OG1, fusion expression, *E. coli*

W243 Activated carbon does not reduce or prevent the effects of zearalenone in gilts. D. Srichana*[1], T. Srichana[2], W. Suttitham[1], P. Panja[1], A. Sumrit[3], and D. R. Ledoux[4], [1]*Department of Agricultural Technology, Faculty of Science & Technology, Thammasat University*, *Pathumtani, Thailand*, [2]*Faculty of Pharmaceutical Sciences, Prince of Songkla University*, *Songkla, Thailand*, [3]*Plant Pathology Research Group, Office of Plant Protection Research and Development, Department of Agriculture*, *Bangkok, Thailand*, [4]*Division of Animal Science, University of Missouri*.

The objective of this research was to produce activated carbon (AC) and evaluate its efficacy as an absorbent for zearalenone (ZEA) in swine diets. Three experiments (Exp.) were conducted to achieve this objective. In Exp. 1, 5 methods (M1 to M5) for producing AC were evaluated and included; M1), coconut shells (CS) treated with KOH (2:1) then heated at 400°C for 1 h and 800°C for 3 h; M2), CS treated with K_2CO_3 (1:1) then heated at 110oC over night and 800oC for 3 h; M3), CS treated with K_2CO_3 (2:1) then heated at 110°C over night and 800°C for 3 h; M4), CS heated at 400°C for 1 h then heated at 800°C for 3 h; and M5), CS heated at 110°C over night and then heated at 800°C for 3 h. Nitrogen gas was let in at 5 l/h during both heat treatments. Methylene blue indexes were not different among the 5 methods ($P > 0.05$), however ash content was different ($P < 0.05$) and ranged from 1.5% for M4 to 3.9% for M1. In Exp. 2, an in vitro procedure was used to evaluate the efficacy of the 5 ACs, from Exp. 1, to adsorb ZEA. The ZEA was analyzed using HPLC-fluorescence. ZEA adsorption by ACs produced by M3, M4 and M5 were not different ($P > 0.05$) and averaged 97%, whereas ZEA adsorption by ACs produced by M1 and M2 averaged 87 and 54%, respectively. Based on these results and production costs, the AC produced by M4 was chosen for evaluation in Exp. 3 which was conducted to evaluate the ability of M4 AC to ameliorate or prevent the effects of ZEA in 19 wk old gilts fed a diet contaminated with ZEA for 4 wks. The treatments were arranged as a 2 × 2 factorial in a CRD (4 replicates). The main factors were levels of AC (0 or 1% in diet) and concentrations of ZEA (0 or 1.165 ppm) in diets. Feed intake and FCR of the gilts were significantly higher ($P < 0.05$) in pigs fed diets containing 1% AC. Diets containing ZEA did not affect production performances, uterus weight and liver weight. The gilts fed diets containing ZEA had red swollen vulvas throughout the experimental period. However, no residues of ZEA or α-zearalenol were found in muscle, uterus or liver tissues of pigs fed ZEA. The data indicated that 1% AC, produced by M4, did not alleviate the effects of ZEA in gilts.

Key Words: zearalenone, activated carbon, gilt

W244 Gender effect on nutrient digestibility and reproductive organ sizes by zearalenone feeding with different levels of Calibrin-Z enterosorbent in young pigs. Z. B. Yang*[1], S. Z. Jiang[1], and F. Chi[2], [1]*Shandong Agricultural University*, *Tai-an, Shandong, PRC*, [2]*Amlan International*, *Chicago, IL*.

We previously reported addition of 1 ppm zearalenone (ZEA) reduced dietary protein (CP) and energy (GE) utilization in gilts and the reduced CP and GE were improved by addition of clay enterosorbent (CE). In present study, a total of 36 pigs (L × Y × D; 18 M, 18 F; 8.84 ± 0.21 kg) were used to study the genders' response to ZEA feeding. Pigs were divided into 6 treatments and fed diets contained 0 or 1 ppm ZEA with addition of different levels of CE (Calibrin-Z). Pigs were fed treatment diets (Table 1) individually in metabolic cages for 21 d. Vulva and testicle sizes were measured at 3-d intervals, and total feces were collected and pooled on 3-d bases for CP, GE, Ca, and P digestibility determination. Vulva sizes increased ($P < 0.01$) with ZEA feeding and the increased vulva sizes were reduced linearly as dietary CE increased. No treatment differences were observed with testicle size in male pigs. No treatment effect was obtained on ADG, ADFI and FE; however, the female pigs showed a poorer FE ($P = 0.01$) than the male pigs. There were differences ($P < 0.01$) on GE, Ca, and P digestibility between treatments but not on CP digestibility. Pigs fed Diet 3 showed lower Ca and P digestibility ($P < 0.01$) as compared with the pigs fed Diet 1. Additions of CE to ZEA contaminated diet improved ($P < 0.01$) GE, Ca, and P digestibility compared with the pigs fed ZEA alone (Diet 3). And the increased nutrient digestibility was improved as the dietary CE levels increased. A gender effect on CP, GE, Ca, and P digestibility ($P < 0.05$) was observed in the study with no interactions between treatments and sexes. For nutrient digestibility, a gender effect was observed with ZEA feeding (Diet 1 vs. Diet 3) where female pigs showed a decrease ($P < 0.01$) of CP digestibility, and male pigs showed decreases ($P < 0.01$) of Ca and P digestibility. The study showed that the reduced nutrient

digestibility by ZEA feeding maybe gender dependent in young pigs. Also, the increased vulva sizes and the reduced nutrient digestibility resulting from ZEA feeding can be ameliorated by Calibrin-Z.

Table 1. Treatments and Results

Treatment	ZEA, ppm	Calibrin-Z, %	Vulva Size, mm^2	DCP, %	DGE, %	DCa, %	DP, %
Diet 1	0	0	52^{c}	88.4	88.4^{c}	67.3^{a}	57.7^{a}
Diet 2	0	0.1	51^{c}	88.6	88.7^{c}	66.8^{ab}	55.8^{cd}
Diet 3	1	0	190^{a}	87.5	88.3^{c}	65.5^{c}	55.0^{d}
Diet 4	1	0.1	142^{ab}	88.2	88.9^{bc}	66.2^{bc}	55.4^{d}
Diet 5	1	0.2	124^{b}	88.3	89.3^{ab}	67.1^{ab}	56.4^{bc}
Diet 6	1	0.4	110^{b}	88.8	89.4^{a}	67.0^{ab}	56.9^{ab}

DCP - digestible CP; DGE - digestible energy; DCa - digestible Ca; DP - digestible P.

Key Words: gender, zearalenone, clay enterosorbent, digestibility, pigs

W245 Effects of dietary *Fusarium* mycotoxins on intestinal lymphocyte subset populations, cell proliferation and histological changes in avian lymphoid organs. C. K. Girish*, T. K. Smith, H. J. Boermans, P. Anil Kumar, and G. N. Girgis, *University of Guelph, Guelph, Ontario, Canada*.

An experiment was conducted to investigate the effects of dietary *Fusarium* mycotoxins on gut immunity, cell proliferation, and histology of avian lymphoid organs. The efficacy of a polymeric glucomannan mycotoxin adsorbent (GMA) was also determined. Seventy-two 1-d-old male turkey poults were fed corn, wheat, and soybean meal-based diets for 21 d. Diets included control grains, contaminated grains and contaminated grains + 0.2% GMA. The major contaminant was deoxynivalenol (DON, vomitoxin; 3.9 µg/g) with lesser amounts of zearalenone (0.67 to 0.75 µg/g) 15-acetyl-deoxynivalenol (0.34 µg/g) and HT-2 toxin (0.078 to 0.085 µg/g). The T and B-lymphocyte populations and crypt cellular proliferation in duodenum, jejunum, ileum and cecal tonsils were measured immunohistochemically on d 14 and 21. Histological changes were recorded after 14 and 21 d of feeding. Feeding contaminated grains significantly ($P = 0.004$) increased the percentage of B-lymphocytes in ileum on day 14, and reduced ($P = 0.04$) the percentages of $CD8^{+}$-lymphocytes in cecal tonsil on d 21. GMA supplementation prevented these effects. The feeding of contaminated diets also caused a reduction ($P = 0.03$) in ileal crypt proliferating cells and a significant (P=0.003) increase in spleen secondary follicle on d 21. In conclusion, feeding grains naturally contaminated with *Fusarium* mycotoxins results in adverse effects on gut immunity and mucosal cell proliferation. The feeding of GMA can prevent some of these effects.

Key Words: *Fusarium* mycotoxin, intestinal lymphocyte, immunohistochemistry, lymphoid organ, turkey

W246 Effects of purified zearalenone on serum metabolites and antioxidant status in young gilts. S. Z. Jiang[1], Z. B. Yang*[1], and F. Chi[2], [1]*Shandong Agricultural University, Tai-an, Shandong, PRC*, [2]*Amlan International, Chicago, IL*.

The study was designed to investigate the adverse effects of dietary zearalenone (ZEA) on oxidative stress and organ damage in young female pigs. A total of 20 gilts (L × Y × D; 10.36 ± 1.21 kg BW) were fed a commercial diet for 7 d adaptation and then divided into 4 groups. Diets were a corn-soy-fishmeal based with an addition of 0, 1, 2, or 3 ppm ZEA to the basal diet. Pigs were fed the test diets ad libitum for 18 d. All measurements and analyses were based on individual pig. Vulva length, width, and height were measured at 4-d intervals. Serum samples were collected for enzyme activities and antioxidant status analyses. Genital organs, liver, kidney and spleen were isolated, weighed, and the relative organ weights were calculated. Results showed that gilts fed different levels of ZEA had no effect on weight gain and feed intake. The vulva length, width and height were increased linearly as dietary ZEA concentrations increased ($P < 0.01$). Relative organ weights including genital organs, liver, and kidney weights were increased linearly as dietary ZEA increased ($P < 0.01$). Serum aspartate aminotransferase, alanine aminotransferase, alkaline phosphatase, γ-glutamate transferase, urea, and creatinine in the serum were all linearly increased as dietary ZEA increased in test diets ($P < 0.05$). Malondialdehyde concentrations in both serum and liver were also increased linearly by increased dietary ZEA ($P < 0.001$). Unlike the liver and kidney, relative spleen weight was decreased linearly as dietary ZEA concentrations increased ($P < 0.01$). Activities of total superoxide dismutase and glutathione peroxidase in the serum and liver ($P < 0.05$) were also reduced linearly as dietary ZEA increased. Results suggested that besides genital organs, the liver, kidney and spleen may also be target tissues in young gilts fed diets containing 1 to 3 ppm ZEA for 18 d. The reduced relative spleen weights suggested potential detrimental effect on pig immunity by feeding ZEA. Elevated key liver enzymes in the serum suggested a progressive liver damage by feeding ZEA, and the damage was probably mediated by the lower antioxidant enzymes in the liver and serum.

Table 1. Serum markers and relative organs weights of gilts fed diets with various levels of ZEA

	0 ppm-ZEA	1 ppm-ZEA	2 ppm-ZEA	3 ppm-ZEA
Aspartate AT, U/L	40.1^{b}	44.6^{b}	53.5^{ab}	66.9^{a}
Alanine AT, U/L	49.5^{c}	55.0^{bc}	62.5^{ab}	66.0^{a}
Alkaline phosphatase, U/L	221.0^{c}	245.6^{b}	264.7^{b}	298.4^{a}
γ-glutamate transferase, U/L	32.2^{c}	35.8^{bc}	38.0^{b}	48.7^{a}
Urea, mmol/L	2.8^{c}	3.8^{bc}	4.2^{b}	5.3^{a}
Creatinine, µmol/L	71.2^{c}	86.1^{bc}	89.7^{ab}	96.3^{a}
Genital organ, g/kg BW	$.33^{d}$	$.53^{c}$	$.74^{b}$	1.16^{a}
Liver, g/kg BW	30.2^{b}	33.4^{b}	36.7^{ab}	44.3^{a}
Spleen, g/kg BW	2.20^{a}	2.10^{ab}	1.90^{bc}	1.83^{c}

AT - aminotransferase.

Key Words: zearalenone, serum enzymes, oxidative stress

W247 A survey of free and conjugated deoxynivalenol in the 2008 Ontario corn crop. S.-T. Tran*[1], G. Stewart[2], and T. K. Smith[1], [1]*University of Guelph, Guelph, ON, Canada*, [2]*Ontario Ministry of Agriculture, Food and Rural Affaires, Guelph, ON, Canada*.

Deoxynivalenol (DON, vomitoxin), one of the most important mycotoxins produced by many *Fusarium* species, is found as a common contaminant of crops worldwide. DON can reduce production efficiency and cause serious economic losses to livestock and poultry producers. Recent studies have described the presence of conjugated forms of DON (glycosides and fatty acid). The aim of the current study was, therefore, to investigate the natural occurrence of free and conjugated DON in Canadian corn. Free and conjugated DON were determined by HPLC and ELISA kits (AgraQuant DON kit) in 86 corn samples collected from the 2008 Ontario crop. Free DON was found in all samples and concentrations determined by ELISA were similar to values determined

in most samples using HPLC. Conjugated DON, however, was not detected in 15 samples. Levels of DON ranged from 0.01 to 14.00 μg/g. Samples highly contaminated with DON did not necessarily show a high concentration of conjugated DON. The highest levels of free DON were found in corn samples from the south and south-west regions of Ontario while samples from eastern region were less contaminated with 8 of 13 samples found to contain 0.01 μg/g. Conjugated DON was found mainly in corn from the east-central region with 5 of 6 samples showing high levels of conjugated DON. Low levels of conjugated DON (<10%) were detected in the majority of corn samples from the south-west region (13 of 19 samples) and from the central region (23 of 36 samples). The reasons for the differences between regions could be due to climatic conditions or plant genetics. The current survey of free and conjugated DON in the 2008 Ontario corn crop emphasizes the potential challenges in understanding the hazard posed by DON contaminated feedstuffs. Although much research has been carried out since the original discovery of free and conjugated DON, the significance of these mycotoxins for animal health remains to be determined.

Key Words: deoxynivalenol, conjugated, corn

W248 Impact of ochratoxin A (OTA) and zearalenone (ZEA) on growth performance and pig physiology. U. Hofsteter* and I. Rodrigues, *Biomin Holding GmbH*, *Herzogenburg, Austria*.

The objective of this study was to evaluate the negative impact of OTA and ZEA on piglets and to investigate the effects of a mycotoxin deactivator. A total of 48 female crossbred weaning piglets were divided into 6 groups: negative control; positive control (2kg/mt); toxin group (500μg/kg OTA, 250μg/kg ZEA); trial group 1 (500μg/kg OTA, 250μg/kg ZEA, 0.5kg/mt); trial group 2 (500μg/kg OTA, 250μg/kg ZEA, 1kg/mt); trial group 3 (500μg/kg OTA, 250μg/kg ZEA, 2kg/mt). Data was analyzed using the General Linear Model Procedure of SAS in a completely randomized design. Comparison of the group averages was done using Duncan's Multiple Range Test. Uterus, ovaries, kidneys and liver were evaluated for histopathological changes. Significantly heavier ($P<0.05$) pigs compared to the toxin group resulted from the addition of the mycotoxin deactivator in the OTA and ZEA contaminated diets. The relative weight of the different organs tended to be lower (uterus and liver showed $P<0.1$, ovaries and kidneys were not significant) in pigs fed contaminated diets, but no incidence of vulvovaginitis was observed within the groups. Pigs fed the control and diets with 0.10% and 0.20% of the feed additive had normal uterine body and horn, which are characterized by thick endometrium and enlarged glands. The ovaries from pigs fed the contaminated diets exhibited only one young tertiary follicle with several atretic follicles, an indication of degeneration. Although relative kidney weights did not vary within the groups, renal lesions were microscopically observed in pigs fed OTA and ZEA. Respectively one pig from group 3 to 6 exhibited nephrotoxicosis, the primary toxic response to OTA, which is characterized by degenerative changes such as swollen, pale, vacuolated cells in the renal tubular epithelium. Livers from pigs fed the control diets had normal cells whereas those fed OTA and ZEA contaminated diets showed liver sinusoids with red blood cells, a sign of congestion. The combination of OTA and ZEA showed a negative impact on performance and physiological parameters which were overcome by the addition of the mycotoxin deactivator.

Key Words: ochratoxin A, zearalenone, physiology

W249 Adverse effects of feed-borne *Fusarium* mycotoxins on performance and serum chemistry of rabbits. M. A. Hewitt*, G. N. Girgis, C. K. Girish, and T. K. Smith, *University of Guelph*, *Guelph, Ontario, Canada*.

The effects of *Fusarium* mycotoxins on performance and metabolism of livestock and poultry have been described in the literature. There is a lack of information, however, regarding the effects of *Fusarium* mycotoxins on rabbits. An experiment was conducted to investigate the impact of feed-borne *Fusarium* mycotoxins on performance, hematology and serum chemistry of male New Zealand White rabbits. Rabbits were fed either a control diet or a diet containing corn and wheat naturally contaminated with *Fusarium* mycotoxins. The contaminated diet contained 5.0 μg/g deoxynivalenol (DON) and 0.24 μg/g 15-acetyl-DON. At the end of the 12 days experimental period, there were trends towards reduced body weight gain and feed efficiency in rabbits fed the contaminated diet. Serum urea concentrations were significantly higher ($P = 0.02$) in rabbits fed the contaminated diet compared to controls. Increased serum concentrations of urea in cattle and uric acid in poultry have been described to be a result of altered protein metabolism following ingestion of *Fusarium* mycotoxin-contaminated diets.

Key Words: rabbit, *Fusarium* mycotoxins, urea

W250 Enrichment of eggs of Japanese quail with α-tocopherol. R. H. Marques, R. A. Gravena, J. D. T. Silva, F. H. Hada, J. Roccon, J. Picarelli, S. A. Queiroz, and V. M. B. Moraes*, *São Paulo State University*, *SP - Brazil*.

The objective of this study was to evaluate the effect of diets supplemented with vitamin E on the concentration of α-tocopherol in egg yolks of Japanese quail. One hundred 92 70-d-old quail were randomly distributed into 4 treatment groups with 6 replicates of 8 birds in each pen. The birds were placed on 1 of 4 dietary treatments (0, 200, 400 and 600 IU vitamin E/kg feed) for 4 lay cycles. Three eggs were collected per treatment at 56 d. Levels of α-tocopherol in yolk determined by high performance liquid chromatography showed a linear relationship ($y = 0.223 + 0.0015x$, $R^2 = 0.9256$), with dietary vitamin E supplementation levels ($P < 0.05$). In treatments using diets supplemented with 600 IU vitamin E/kg feed, α-tocopherol reached a value of 479.05% above control values, suggesting that the nutritional value of eggs can be enhanced by the addition of vitamin E to diets.

Table 1. Effect of vitamin E in quail diet on concentration of α-tocopherol in egg yolk

Vitamin E	α-tocopherol concentration in yolk (mg/g)	% increase
Control	0.191	-
200 IU	0.579	203.14
400 IU	0.789	313.08
600 IU	1.106	479.05
Probability	0.001*	-
F values	273.52	-
CV[1] (%)	14.68	-

[1]Coefficient of variation, * significant ($P < 0.001$).

Key Words: egg yolk, quail, α-tocopherol

W251 Expression of kyphosis in young pigs is altered by carryover effects of sow vitamin D status. L. A. Rortvedt*, L. A. Zappitelli, J. L. Reichert, J. R. Booth, and T. D. Crenshaw, *University of Wisconsin*, *Madison*.

Kyphosis, or 'hump-backs', is an idiopathic disease that may affect 30% of pigs. The UW Swine Center had a flare-up and subsidence of kyphosis over 4 mo that affected ~20% of pigs. The incidence was consistent with unintentional omission of vitamin D (D) from all diets. This experiment was designed to determine if kyphosis was expressed in pigs produced by sows fed no supplemental D. Crossbred (LR × LW), multiparious sows (n = 8) were fed corn-SBM diets supplemented with either 280 (+D) or 0 (-D) IU vitamin D_3/kg diet from breeding through lactation. At weaning (4 wk), 6 pigs (3, +D; 3, -D) were scanned using DXA (GE Lunar Prodigy) to determine whole body bone mineral content (BMC, g/pig) then killed to assess femur properties. The other 75 pigs were weaned and randomly assigned by weight within sow groups to diets that supplied either 120% (HCaP) or 80% (LCaP) of required Ca and P. Pig diets had no added D. At 9 wk all pigs were fed HCaP diets until termination at 13 wk. Serum Ca and P were assessed at 4 and 9 wk. A subset of pigs were scanned and killed at 9 (n = 12) and 13 (n = 25) wk. Kyphosis was evident at 9 wk in 4 of 19 pigs from –D litters fed LCaP, but not in other groups. At 13 wk, 5 of 15 pigs in –D litters fed LCaP and 5 of 17 pigs from +D litters fed LCaP showed kyphosis. No pigs fed HCaP showed kyphosis regardless of sow D diets. Growth, BMC, and serum P were reduced ($P < 0.05$) in pigs fed LCaP compared with HCaP, but reductions were greater (interaction, $P < 0.05$) in pigs from sows fed -D diets. Evidence of sow diet effects were detected in BMC of pigs at 13 wk. In conclusion, kyphosis was induced in pigs fed diets without supplemental D and marginal Ca P. Evidence of kyphosis occurred at a younger age if pigs were produced by sows fed -D diets.

Table 1.

Vitamin D, IU/kg	280	280	0	0	
Ca P, % of required	120	80	120	80	SEM
ADG, kg/d [a, b]	0.649	0.480	0.547	0.428	0.034
9 wk serum Ca, mg/dL[a]	12.81	13.13	11.49	12.44	0.25
9 wk serum P, mg/dL [a, b, c]	11.02	5.39	9.31	5.37	0.19
DXA BMC, g [b, c]	1070	796	1128	642	49

a. +D vs -D, $P < 0.05$; b. HCaP vs. LCaP, $P < 0.05$; c. D × CaP, $P < 0.05$.

Key Words: skeletal, maternal imprint, DXA

W252 Incorporating whole grain sorghum in broiler rations. C. Marr*, C. M. Rude, M. A. Barrios, R. Rierson, and R. S. Beyer, *Kansas State University*, *Manhattan*.

Commercial poultry producers streamline feed production and lower costs by utilizing fewer ingredients in feed rations. This reduces opportunities to utilize nontraditional grains or by products when prices decline since storage bins and specialized handling equipment may require investment that is not used at full capacity. It may be possible to incorporate some ingredients into formulations to realize savings without changing the manufacturing process if the ingredients could be used without excessive processing. Because grain sorghum is sometimes priced competitively with corn, work was conducted to determine methods of incorporating whole sorghum directly into feed rations. A typical corn-soy broiler starter formula was adjusted to incorporate 15% grain sorghum, substituting mostly for the corn fraction. The cereal grains were ground and mixed into a mash control ration. The treatments included 0, 5, 10 and 15% whole sorghum, substituted on a 1:1 basis for the ground sorghum. Cobb 500 broiler chicks were placed in Petersime battery units, 6 per pen, 8 reps per treatment, with feed and water provided ad libitum. All feed was overlaid with a screen of 1-inch mesh to prevent the chicks from segregating the feed. The trial was conducted for 21 d, during which BW and FI were determined for day 7, 14, and 21. At each week, the data indicate that adding whole grain sorghum decreased BWG and FC compared to ground sorghum. At 5% added whole grain sorghum, the effects were smaller and were not significant at each period. The data suggest that whole sorghum particles could be difficult for new chicks to process since the digestive system is not fully functional compared to adult birds which possess a mature gizzard capable of grinding large feed particles. It was observed that the chicks were attracted to the dark sorghum berries which were consumed immediately if the feed was stirred. Because the birds appeared to consume all of the diet, it was assumed that selective feeding did not affect performance. Additional studies are required to determine if adding whole sorghum to pelleted rations during the grower phase will decrease selection and affect broiler performance.

Key Words: sorghum, whole grain, broiler

W253 Water consumption and performance of broilers receiving Mate (*Ilex paraguariensis*) infusions. A. M. C. Racanicci*[1], J. F. M. Menten[2], and J. Rabello[1], [1]*University of Brasília (UnB)*, *Brasília, DF, Brazil*, [2]*University of São Paulo (ESALQ)*, *Piracicaba, SP, Brazil*.

Aqueous extracts of mate are known to be an important source of phenolic compounds with a strong antioxidant capacity in chicken meat products. The objective of this study was to offer infusions of mate in substitution of water to broilers and evaluate performance and oxidative stability of cooked meat balls. One hundred male Cobb broilers were allotted in cages and distributed randomly to 4 treatments with 5 repetitions of 5 birds. From 11 to 21 d of age, birds were fed conventional corn-soybean meal diets ad libitum and received water (CON) or infusions prepared with hot water (90 °C) and 3 concentrations of mate 0.1, 0.5 or 1.0% as experimental treatments (MA0.1, MA0.5 and MA1.0). Birds received liquids in trough drinkers and the consumption was measured every two days. At 21 d of age, body weight (BW) and feed consumption were recorded to calculate individual weight gain (WG), feed intake (FI) and feed conversion ratio (FCR). Breast meat from 8 birds per treatment was used to prepare meat balls (30 g ± 0.5 g), cooked in boiling water for 8 m and stored in the dark in a cold room (4 °C) for 3 d. Progression of lipid oxidation in meat balls was evaluated by analyzing TBARS (thiobarbituric acid reactive substances; expressed in µmol of malondialdehyde (MDA) per kg of meat). Averages of BW and WG obtained from CON, MA0.1 and MA1.0 (966.8, 966.4, 984. g and 63.6, 63.2 and 61.6 g/d, respectively) were similar ($P > 0.05$), however, MA0.5 showed reduced values (907.2 g and 57.9 g/d, respectively) compared to CON and MA0.1. Averages of FI were not affected ($P > 0.05$) by treatments (86.2, 88.2, 83.6 and 84.4 g/d, respectively) but FCR was affected negatively ($P < 0.05$) by MA0.5, which showed the higher average (1.45) compared to CON and MA1.0 (1.36 and 1.37). The substitution of water by mate infusions did not affect ($P > 0.05$) liquid consumption, however, was effective to protect meat balls from lipid oxidation during storage. This effect can be demonstrated by lower TBARS ($P < 0.05$) in meat balls from MA0.1, MA0.5 and MA1.0 (36.63, 34.35 and 34.23 µmol MDA/kg of meat, respectively) compared to CON (48.88 µmol MDA/kg of meat).

Key Words: natural antioxidants, mate, liquid consumption

W254 Effect of fiber separation from ground corn flour on nutritional value of poultry diets. R. Srinivasan* and A. Corzo, *Mississippi State University*, *Mississippi State*.

In a previous demonstrational study, the Elusieve process, a combination of sieving and elutriation (air classification), was found to be effective in fiber separation from ground corn flour. Corn flour was sieved into

four size fractions and the three biggest size fractions were air classified (aspirated) individually to separate fiber from each of the three size fractions. The material remaining after fiber removal is called enhanced corn flour. Ground corn flour is a major ingredient in diets for swine and poultry, which do not digest fiber very well because they are non-ruminant animals. Fiber separation could increase the nutritional value of corn flour for broilers and could decrease the usage of expensive dietary ingredients such as oil/fat and enzymes. The objective of this study was to determine the effect of fiber separation on nutritional value of poultry diets by carrying out broiler feeding trials. Fiber separation increased starch content in corn flour by 3.0% points. The grow-out study encompassed the period between 0 to 21 d of age using Ross × Ross 308 males obtained from a commercial hatchery. Day-old chicks were randomly placed in each of 24 floor pens (15 birds/pen; 360 birds total). There were 2 different dietary treatments (regular corn diet and enhanced corn diet) with each treatment being replicated 12 times. Diets were formulated to be isocaloric, isonitrogenous, and similar in calcium, phosphorus and all limiting amino acids. Data were analyzed by the GLM procedure of SAS (2004) and treatment effects were separated using Tukey's multiple comparisons test option of SAS (2004) using an α of 0.05. The body weight gain of chicks was significantly higher (by 4.3%) and feed conversion ratio was significantly lower (by 3 points) when fed with enhanced corn diet compared with the regular corn diet. Thus, fiber separation from corn flour increases nutritional value of broiler diets.

Key Words: fiber, separation, elusieve

W255 The effect of using different levels of corn gluten meal in free range chickens diet. C. B.-V. Rabello*, A. F. da Silva, S. B. P. de Lima, H. Pandorfi, M. B. dos Santos, C. da Costa Lopes, and M. d. C. M. M. Ludke, *Universidade Federal Rural de Pernambuco*, *Recife, Pernambuco, Brasil*.

The objective of this work was evaluated the effect of inclusion of the corn gluten meal (CGM21) on performance and carcass yield of free range chickens. A total 240 free range chickens, females with 32 days-old, were distributed according with completely randomized design, five levels of inclusion of the CGM21 and 4 replicates. One reference diet based on corn and soybean meal was formulated and three test diets containing 7, 14 and 21% CGM21 (21% crude protein). The birds were housed in breeding system semi-intensive with access to the piquete containing pasture. Feed intake, weight gain and feed conversion were evaluated weekly. The Carcasses were evaluated (weight and yield) at 84 d, when eviscerated carcass (with head and feet), eviscerated carcass (without head + feet), thighs, drumsticks, wings, back, edible offal (liver, heart and gizzard), and abdominal fat were measured. The assay had two periods: grower phases (32 to 63 d of age) and finish phase (64 to 84 d of age). Data underwent regression analysis. In the growth phase the weight gain (WG), feed intake (FI) and feed conversion (FC) were not affected by increasing CGM21 inclusion in diets, but in the final (64 to 84 d of age) and total period (32 to 84 d of age) showed effect about the CA with better results when we included 10.0 and 9.8% of CGM21, respectively; the WG in the total period had quadratic effect with the better level of inclusion of CGM21 of 9.0%;. In the evaluation of carcass weights of carcass, breast, thigh, wing, back, neck, heart, gizzard and abdominal fat did not show significant effects. The liver and drumstick of birds had similar response, with higher weights when they were included: 11.65 and 9.63% of GM21, respectively. The yield of breast, wing, back, thigh, heart and gizzard were not affected, but the drumstick, liver and abdominal fat showed a quadratic effect with the highest level 13.7%, 8.5% and 10.8% of the inclusion of CGM21, respectively. The inclusion of gluten meal for free-range chickens can not exceed the level of 10% from at growth phase (63 days old), but can use around 21% in the initial phase (28 days old).

Key Words: growth performance, free-range chicken, carcass yield

W256 Effects of feeding low-density diets to Hy-Line W-36 laying hens on production performance. S. A. dePersio*[1], K. W. Koelkebeck[1], C. M. Parsons[1], P. L. Utterback[1], C. W. Utterback[1], N. O'Sullivan[2], K. Bregendahl[2], and J. Arango[2], [1]*University of Illinois*, *Urbana*, [2]*Hy-Line International*, *Dallas Center, IA*.

An experiment was conducted using 480 Hy-Line W-36 hens (18 wk of age) to determine whether feeding diets of different nutrient densities would affect egg production performance. At 18 wk of age hens were moved from a floor grow out facility to a caged layer building, weighed, and allotted to 6 replicate groups of 16 hens each (2 adjacent cages containing 8 hens per cage, 60.9 x 58.4 cm) per treatment diet in a completely randomized design so that mean body weight was similar for each treatment. Treatments consisted of 5 diets formulated to contain 85 (Diet 1), 90 (Diet 2), 95 (Diet 3), 100 (Diet 4), and 105 (Diet 5) % of the energy and nutrient recommendations stated in the 2009 Hy-Line W-36 management guide. Egg production performance was measured for 22 wk from 18 to 40 wk of age. At Week 14, egg production of hens fed Diet 1 (85% of control) dropped greatly to 57.6%. It was decided to switch these hens to the control diet (Diet 4). After this, egg production of Diet 1 hens began recovering and was stable by Week 17. Hens fed the control diet (Diet 4) came into production sooner than the other treatments, but by Week 5 all treatments had similar egg production. Overall average hen-day egg production for Diets 1 through 5 was 76.1, 80.6, 81.3, 84.2, and 82.1%, respectively. Hens fed Diets 1, 2, and 3 had lower ($P<0.05$) egg production than those fed the control diet. Hens fed Diets 2 and 4 consumed more ($P<0.05$) feed than those fed Diets 1 and 5. Feed efficiency was the greatest ($P<0.05$) for hens fed Diets 4 and 5. Egg weight was heavier for hens fed Diet 5 vs. Diets 1 and 2, while egg mass was greater for hens fed Diets 4 and 5 vs. Diets 1 and 2. The results of this study show that feeding Hy-Line W-36 hens diets formulated to contain lower nutrient density specifications (85% of control) than recommended may compromise early production performance.

Key Words: laying hens, low density diets, egg production

W257 Effect of prebiotic on performance and some blood parameters of partridge. H. Hashemipour, V. Khaksar, H. Kermanshahi, and A. Golian*, *Ferdowsi University of Mashhad*, *Khorasan Razavi, Iran*.

In modern poultry production, newly hatched chicks have no contact with maternal feces and so no maternal spectrum of antigens is present. In this situation, chicks can be affected by a number of pathogenic intestinal microorganisms, and fortifying diets with prebiotics can alleviate this problem. This experiment evaluates the effect on the performance, carcass characteristics and some blood parameters of the chukar partridge (*Alectoris chukar chukar*) of dietary supplementation with a prebiotic (Fermacto). Eighty day-old mixed sex chicks in a completely randomized design with two treatments (with or without 0.18% Fermacto) and four replicates of 10 birds each was used. The experimental period lasted 16 weeks in two phases of starter (0-8 weeks) and grower (9-16 weeks). Performance data recorded biweekly and carcass characteristics and some blood parameters were measured at the end of the experiment. Data revealed that the supplementation of Fermacto significantly ($P<0.05$) increased breast and gastrointestinal tract percentages, decreased the back-neck percentage, lowered blood triglyceride and total cholesterol and increased blood calcium levels in

the Fermacto-treated group. Under the conditions of this study, it was concluded that the dietary supplementation of 0.18% Fermacto might offer some beneficial effects in chukar partridges to improve their carcass quality and some blood parameters.

Key Words: prebiotics, performance, partridge

W258 Influence of diet quality on nutrient digestibility and productive performance of weanling pigs. J. D. Berrocoso*, C. H. Zúñiga, M. P. Serrano, L. Cámara, and G. G. Mateos, *Universidad Politécnica de Madrid*, *Madrid, Spain*.

The effect of ingredient composition of the diet on nutrient digestibility and growth performance was studied in piglets. There were 6 experimental prestarter diets (27-47 d of age) with similar NE and AA content. The positive control diet contained 40% cooked corn (HPC), 14% lactose (LAC), and 10% fish meal (FM). Two other experimental diets had the same composition than the control diet but the HPC was substituted by either raw corn (RC) or cooked rice (HPR). Two extra diets were similar to the positive control diet but contained only 7% LAC or 4% FM. Finally, there was a control negative diet with 40% RC, 7% LAC, and 4% FM. From 47 to 68 days age, half of the pens received a standard SBM-raw corn-lard diet and the other half a diet with similar nutrient profile that included 1.3% LAC, 5% FM, 20% HPC, 2% soy protein concentrate, and 1% soybean oil. Each treatment was replicated 6 times (6 pigs per box). Type of diet did not affect growth performance of pigs at any stage. Piglets fed the rice diet had lower incidence of diarrhea (DI) from 27 to 47 d of age than those fed the raw corn control diet ($P < 0.1$), with DI of pigs from the other treatments being intermediate. At 36 days of age, CP digestibility was not affected by dietary treatment but the CTTAD of GE, DM, and OM was lower ($P < 0.05$) for piglets fed raw corn than for piglets fed HPR with piglets fed HPC being intermediate. Also, an increase in the LAC content of the diet improved ($P < 0.05$) digestibility of these dietary components. Feeding program diet did not affect digestibility of any of the nutrients at 57 d of age. It is concluded that piglets weaned at 27 d of age performed similarly when fed diets containing raw corn and low levels of LAC an FM than when fed more complex diets but DI was reduced with the inclusion of cooked rice. Also, 47 d-old pigs (>11 kg BW) do not need to include any sophisticated ingredients in the diet, for optimal performance.

Key Words: cooked cereal, piglet nutrient digestibility, incidence of diarrhea

W259 Effects of different level of fish meal on growth performance, intestinal microbiology, and blood parameters of weaned pigs. H. F. Ji*, J. Wang, D. C. Shan, S. X. Wang, D. Y. Zhang, F. M. Wang, L. Hou, and Y. M. Wang, *Institute of Animal Husbandry and Veterinary Medicine, Beijing Academy of Agriculture and Forestry Sciences*, *Beijing, China*.

This study was undertaken to determine the effect of one commercial fish meal (CP, 65.5% DM) as protein sources on growth performance and blood parameters of weaned pigs. Sixty piglets (Large White × Landrace) weaned at 28 d of age (7.32 ± 0.86 kg BW), were assigned randomly to 4 treatments (n=15) in a completely randomized design. The 4 treatments included 1 basal diet (control) and 3 diets with different level of fish meal (2%, 5%, and 8% of diet). The experiment lasted thirty three days. Body weight and feed consumption of animals were determined on d 0 and 33 of the study to calculate ADG and G:F. The incidence of diarrhea in piglets was observed and recorded 3 times per day during the study. Fresh fecal samples were collected to evaluate shedding of *E. coli* and *Lactobacillus* and blood samples were collected from jugular vein to measure ω-3 fatty acid and C-reactive protein (CRP) at the end of the experiment. Utilization of fish meal improved ($P < 0.05$) overall ADG and G:F in comparison with the control. Along with the increase of fish meal in the diets, ADG and G:F were all increased significantly ($P < 0.05$). The incidence of diarrhea was significantly decreased ($P < 0.05$) by dietary fish meal inclusion during 0-10 d postweaning, while the diarrhea incidence was 0% when fish meal was included in the diet during 11-33 d postweaning. Fecal samples from pigs receiving diets containing fish meal had greater ($P < 0.05$) *Lactobacillus* counts than those from control pigs, and no difference existed in *E. coli* counts. The eicosapentaenoic acid (EPA, C20:5) and docosahexaenoic acid (DHA, C22:6) content of the blood increased ($P < 0.05$) with increasing fish meal in the diet. Piglets fed the diet containing 8% fish meal had the lowest ($P < 0.05$) CRP production. The current results indicated that fish meal as a protein sources in diets of young pigs enhanced growth performance by increasing ADG and G:F and decreasing the incidence of diarrhea, and improved intestinal microbes, ω-3 fatty acid level and physiological status.

Key Words: fish meal, weaned pig

W260 Energy value of cassava products and their use in weaning-growing pigs. E. Salcedo[1], L. Mestra[1], T. Rivero*[1], Y. Avellaneda[1], G. Afanador[1,2], and C. Ariza-Nieto[1], [1]*CORPOICA*, *Bogota, Colombia*, [2]*Universidad Nacional de Colombia*, *Bogota, Colombia*.

This study evaluated the digestible energy (DE) value of cassava meal, cassava meal extruded, and cassava foliage from 6 varieties of cassava harvested in 3 microregions of Colombia and evaluated their use in wean to finishing pigs. The DE was determined using the mobile nylon bag technique (MNBT). Samples, 1 g, ground through a 0.5-mm mesh, were enclosed in nylon bags (25 × 40 mm; 48 µm). Following pre-digestion (0.1 N HCl; pepsin 754.8 IU/1;4 h), eight bags of each feedstuff were inserted via a T-cannula placed in the duodenum. The material, remaining in the bags after passing through the digestive tract, was pooled within pig and feedstuff and used to estimate DE. The effect of cassava meal was evaluated in diets for weaning to growing pigs and its economic implication was estimated. Twenty (20) pigs with an average body weight of 15 kg were randomly assigned to one of the two treatments groups (with cassava, without cassava) in a phase feeding system approach; pre-starter (15-20 kg), starter (20-50 kg) and growth (50-70 kg). Pigs were individually weighed every other week until slaughter. Feed intake and feed conversion were record at the end of each phase. Data were analyzed as a completely randomized design using the GLM procedure of SAS. The digestible energy coefficient of cassava foliage was low (18.2%) compared to cassava meal (87.8%). The extrusion process increased the energy coefficient of the cassava meal (93.3%); therefore, the DE in pigs of cassava meal extruded was greater (3519 kcal/kg) compared to cassava meal (3309 kcal/kg). Cassava meal grown in Valley of Sinu river, Cordoba, Colombia showed the greatest energy value (3634 Kcal/Kg) and its inclusion at a rate of 25% in wean to growth pig diets showed that body weight gain, feed intake, and feed conversion were not significantly affected (P>0.05), The economic analysis showed that the inclusion of cassava meal significantly (P<0.05) reduced the cost of feed per kilogram of diet, because cassava meal price was 55% less than corn. Additionally, the cost per kilogram of pigs fed cassava meal was reduced (-$0.25) compared to pigs on the control group.

Key Words: cassava meal, digestible energy, pigs

W261 Effect of three feeding programs on body reserves gain of gestating sows. A. García-Rendón[1], J. López[2], A. G. Borbolla*[2], and E. Toledo[2], [1]*Granjas Covadonga*, *Estado de México, México*, [2]*Departamento de Producción Animal: Cerdos. Facultad de Medicina Veterinaria y Zootecnia. Universidad Nacional Autónoma de México*, *Coyoacán, D.F. México*.

An elevated number of pigs weaned/sow/year is essential to maintain pig farm productivity and efficiency. This is related to the amount and type of body reserves in the sow. During lactation, body reserves of sows are intensively mobilized for milk production, due to an insufficient feed consumption. Feeding programs during gestation therefore, must be designed to optimize protein deposition and avoid excessive fat accumulation. The objective of this study was to evaluate 3 different feeding programs on protein and fat gain of pregnant sows over 2 gestation cycles. Three hundred and 40 sows were assigned randomly to 3 treatments: Tr. 1: feed allowance based on visual body condition at mating. Tr. 2: Feed allowance based on body condition evaluated by weight and back fat using an ultrasound device. Tr. 3: Feed allowance according to the expected net maternal gain established by NRC (1998). Body condition was determined using Noblet (1990) formulas. Variables were analyzed with ANOVA, using a significance level of ($P < 0.05$). Initial and final weights ± SE in both gestation cycles were not different ($P > 0.05$) for the 3 feeding programs (Cycle 1. Tr.1:193.7 ± 3.05 and 253.8 ± 4.9 Kg, Tr.2:197.5 ± 3.6 and 257.4 ± 4.7 Kg, Tr. 3:198.0 ± 3.5 and 260.2 ± 4.8 Kg, respectively; Cycle 2. Tr.1: 211.4 ± 2.80 and 268.60 ± 2.7 Kg, Tr.2: 218.3 ± 3.6 and 271.1 ± 3.1 kg, Tr.3: 219.7 ± 2.9 and 275.6 ± 3.1 Kg, respectively). Accordingly, total weight gain during gestation was similar ($P > 0.05$) for all treatments in both cycles (Cycle 1. 60 ± 2.5 Kg; Cycle 2. 57.5 ± 1.5 Kg). As well on net maternal gain no differences ($P > 0.05$) were observed in any cycle (Cycle 1. 32.6 ± 2.0 Kg; Cycle 2. 30.4 ± 1.5 Kg). Differences ($P < 0.05$) over feed consumption and total body fat gain during the 2 gestation cycles are shown in Table 1. As for protein gain no differences ($P > 0.05$) were observed in both cycles (Cycle 1. 6.08 ± 0.5 Kg; Cycle 2. 5.1 ± 0.2 Kg). The use of a suitable feeding program during gestation, besides optimizing body reserves gain (fat and muscle), can improve sow output, and therefore increase its productivity, and longevity in the farm.

Table 1. Effect of feeding program on feed consumption and body composition of gestating sows.

	Gestation 1			Gestation 2		
	Treatment 1	Treatment 2	Treatment 3	Treatment 1	Treatment 2	Treatment 3
Total feed consumption, Kg	263.7 ± 1.3[a]	269.1 ± 3.4[b]	287.8 ± 1.2[c]	271.5 ± 0.3[d]	292.7 ± 3.1[e]	293.6 ± 1.4[e]
Body fat gain, Kg	6.4 ± 0.7[a]	9.1 ± 0.8[b]	8.5±0.9[a,b]	9.4 ± 0.5	9.9 ± 0.5	10.1 ± 0.5

[a,b,c,d,e]Means with different superscript letter differ (P < 0.05) for the same gestation.

Key Words: body reserves, feeding programs, gestating sows

W262 Effect of triticale on blood chemistry and performance of commercial growing turkeys. H. Zarghi, A. Golian*, and H. Aghel, *Ferdowsi University of Mashhad*, *Mashhad, Khorasan Razavi, Iran*.

A trial was conducted to study the performance of male broiler turkeys fed diets with triticale replaced for corn at the levels of 0, 25, 50, 75 and 100%. Each diet was fed to five groups of twelve male birds each. The diets were provided isocaloric and isonitrogenous for each period of 30- 53, 54-83, 84-94 and 95-116 d of age. Feed and water were fed ad-libitum. Similar weight gain, feed intake and feed conversion observed in birds fed control or diets contained up to 75% triticale replaced for corn. However, the average daily weight gain decreased, feed intake and feed conversion increased when 100% of corn was replaced with triticale during all periods (P<0.05). Although, carcass yield decreased in birds fed triticale contained diets, small intestine and large intestine weight and blood serum TG increased, whereas serum HDL and LDL decreased when measured at 116 d of age ($P < 0.05$). This study revealed that the turkey producers may substitute up to 75% of the corn with triticale in grower and finisher diets without adverse effect on performance.

Key Words: turkey performance, triticale, blood chemistry

W263 Influence of origin on in vitro protein and dry matter digestibility of soybean meal. S. Santos-Rosell, P. García-Rebollar, N. Núñez-Romero, M. P. Serrano, and G. G. Mateos*, *Universidad Politécnica de Madrid*, *Madrid, Spain*.

Previous works have demonstrated that the origin of the beans might affect the nutrient content and availability of soybean meals (SBM). In vitro procedures can be used to predict the *in vivo* ileal digestibility of SBM in broilers. The present research was conducted to determine the influence of origin (USA; Brazil, BRA; Argentine, ARG) on in vitro digestibility of N and DM of SBM. An adaptation of the Boisen and Fernandez (1995) method consisting on a two-step enzymatic hydrolysis simulating digestion in the stomach and small intestine followed by measurement of the remaining residues for the two digestion steps was used. The one-step method (stomach digestion) was an incubation of the SBM samples with pepsin at pH 2. The two-step method consisted in including a second multi-enzyme hydrolysis process (pancreatin at pH 7) to the pepsine digestion to simulate ileal digestibility. On DM bases, the BRA meals (n = 7) had higher CP content (55.9 vs. 54.3 and 53.1%; P < 0.001) than the USA (n = 8) and ARG (n = 7) meals. After the one-step enzymatic digestion (stomach), N digestibility was higher (67.7 vs. 65.8 and 64.9%, $P < 0.01$) for BRA meals than for USA and ARG meals. Also, DM digestibility (57.6 vs. 56.1 vs. 55.1; $P < 0.05$) was higher for BRA than for USA meals with the ARG meals being intermediate. When the two-step hydrolysis process (stomach and small intestine) was used, USA SBM had higher N digestibility (88.2 vs. 87.5 vs. 86.4; $P < 0.05$) than BRA meals and ARG meals were intermediate. Also, DM digestibility was higher (71.0 and 71.5 vs. 69.2; $P < 0.05$) for USA and ARG than for BRA meals. In conclusion, the in vitro hydrolysis methodology showed that the contribution of the small intestine to total digestion of N and DM is lower for BRA SBM than for USA and ARG meals and that those differences might be associated to different nutritional values for poultry of commercial available SBM differing in origin.

Key Words: soybean meal origin, in vitro digestibility, nutritional value

W264 Cloning of the porcine selenoprotein V gene and its RNA abundance in different tissues of young pigs fed three levels of dietary selenium concentrations. Q. S. Zhang[1], H. Zhao[1], J. C. Zhou[1], K. N. Wang[1], J. Y. Tang[1], X. J. Xia[1], and X. G. Lei*1,2, [1]*Int. Ctr. of Future Agriculture for Human Health, Sichuan Agri. Univ.*, *Chengdu, China*, [2]*Cornell University*, *Ithaca, NY*.

Porcine selenoprotein V (Sel V) gene sequence and regulation of its expression remain unknown. In this study, we cloned a 1,233 base pair cDNA coding for the porcine Sel V gene and determined responses of its mRNA abundance to dietary Se concentrations. A total of 24 male pigs (5-wk old, 9.2 ± 0.4 kg BW) with a Se-deficient (0.03 mg Se/kg) corn-soy basal diet (BD) supplemented with 0, 0.3 and 3.0 mg Se/kg as Se-enriched yeast for 16 wk. At the end, pigs were killed to collect blood and nine tissues for total RNA isolation to conduct quantitative real-time Q-PCR analysis. While dietary Se supplement (0.3 or 3 mg/kg) exerted no significant effect on final body weights of pigs, it increased ($P < 0.05$) GPX activities and Se concentrations in both blood and liver. Among all the tissues assayed, testis had the highest ($P < 0.05$) and thyroid had the second highest ($P < 0.05$) Sel V mRNA levels that were not significantly different among the three dietary Se concentrations. Compared with pigs fed 0.3 and 3 mg Se/kg, pigs fed BD exhibited a lower ($P < 0.05$) Sel V mRNA level in kidney, but higher ($P < 0.05$) Sel V mRNA levels in hypothalamus and muscle, respectively. Only kidney Sel V mRNA levels were different ($P < 0.05$) between pigs fed 0.3 and 3 mg Se/kg. In conclusion, effects of dietary Se concentrations on Sel V gene expression varied with tissues in pigs.
This work was partially supported by NSFC Projects 30628019, 30700585, and 30871844, and the Chang Jiang Scholars Program (XGL).

Key Words: Sel V, gene expression, selenoprotein, real-time RT-PCR, pig

W265 Phosphate status impacts bone integrity and stem cell proliferation in neonatal pigs. L. S. Alexander*, B. S. Seabolt, and C. H. Stahl, *North Carolina State University*, *Raleigh*.

Mesenchymal stem cells (MSC) are essential to postnatal bone growth and our previous research indicates that dietary phosphate (PO_4) level impacts proliferation of these cells in vivo. To determine the effect of early PO_4 nutrition on bone integrity and MSC activity, fifteen pigs (1.5 + 0.2 kg) between 24 and 36 hr old were divided into 3 dietary treatment groups. Over a 12 d period, pigs were either fed a PO_4 adequate diet or 1 of 2 diets that exceeded PO_4 requirements. Blood collected at d 6 and d 12 was analyzed for sera PO_4, Ca, and PTH concentrations. Remaining sera was pooled from each treatment group to determine the impact of sera on MSC proliferation in vitro. At the conclusion of the trial, tibias were collected for bone measures and MSC were isolated from bone marrow of individual animals. While sera PO_4 did not differ between treatment groups at either time point, a dose response was noted in sera Ca ($P < 0.05$) and PTH ($P < 0.05$) concentrations at d 6, with adequate animals having the lowest sera PTH concentrations and correspondingly higher circulating Ca when compared to the other groups. Although, the tibias of animals receiving the PO_4 adequate diet were larger ($P < 0.05$) and thicker ($P < 0.1$) than the bones of those animals receiving excess PO_4, ash percentage did not differ between groups. Proliferation of MSC treated for 24 hr in sera from each group was effected by PO_4 status ($P < 0.1$) of the animal and tended to be influenced by PO_4 status of the sera. Because circulating PO_4 did not differ between groups, the changes in bone measures, sera mineral and hormone concentrations, and MSC proliferation would suggest possible differences in PO_4 utilization. Additional research is needed to further clarify how PO_4 status affects MSC activity and the subsequent alterations in bone integrity.

Key Words: pig, phosphate, bone

W266 The effect of calcium and phosphorus supplementation on production traits of laying hens. T. D. Knezacek*, J. P. Dahiya, K. V. Schwean-Lardner, and H. L. Classen, *University of Saskatchewan*, *Saskatoon, Canada*.

Research in our laboratory found short term feeding of high calcium (Ca) levels could increase bone mineralization. Though not investigated, this response may benefit bird welfare by reducing cage layer fatigue and bone breakage. Consequently, research investigating the relationship between Ca and available phosphorus (AP) was completed to determine the effect of increasing levels of these minerals on laying hen performance. Rations were fed to 864 Lohmann LSL Lite hens in 4 phases from 19-31, 31-43, 43-55 and 55-67 wks of age. From 19-31 wks of age, all hens were fed the same diet (3.80% Ca, 0.45% AP). The remaining phases each had 12 dietary treatments consisting of 4 levels of Ca and 3 levels of AP (3.80-4.27% Ca, 0.40-0.50% AP; 3.80-4.74% Ca, 0.35-0.55% AP; and 3.80-5.20% Ca, 0.30-0.60% AP, respectively). Egg weight, specific gravity and feed intake were measured at 4 wk intervals. Overall, level of Ca and AP inclusion had no effect on hen-day egg production, egg quality, egg weight, egg specific gravity, feed intake, feed to egg mass ratio or bird mortality. Ca level affected hen body weight at 66 wks of age (P=0.0309), with birds fed the lowest Ca level being lighter (1.752 kg) than birds fed the highest Ca level (1.818 kg). Hens fed higher levels of AP had poorer feed efficiency (P=0.0180) due to reduced egg production later in the cycle and feed intake that was similar to lower levels of AP. Though not statistically significant, hens fed higher Ca levels had a greater incidence of fatty-liver hemorrhagic syndrome. There was also a trend for higher mortality due to cage layer fatigue in low Ca and low Ca-AP diets. There were no significant interactions between level of Ca and AP supplementation. In conclusion, Ca and AP supplementation in later-phase layer rations did not affect hen performance suggesting a variety of Ca:AP ratios will meet the requirements for egg production.

Key Words: calcium, phosphorus, egg production

W267 The effects of strain and dietary phosphorus level on large tom turkey performance. B. N. West*, K. G. S. Lilly, K. R. Beaman, L. K. Shires, S. A. Loop, and J. S. Moritz, *West Virginia University*, *Morgantown*.

There are several challenges associated with maintaining a competitive edge in commercial poultry production. Choosing the appropriate genetic strain of turkey can significantly impact feed conversion and carcass yield, thus profitability. In addition, environmental impacts of production agriculture (especially manure disposal) are becoming increasingly more scrutinized and consequently regulated. Dietary phosphorus levels can also significantly impact diet cost. The objective of this study was to determine differences between strain use and dietary phosphorus level in a research setting that mimics commercial production. This was a 2x2 factorial design utilizing two strains (Nicholas and Hybrid) and two levels of dietary phosphorus (high and low) in finishing diets (d-105 through d-138). All birds were reared at the newly renovated West

Virginia University turkey research facility and all diets were manufactured at a commercial feed mill. Male poults (1216) were randomly placed in one of 16 pens and randomly assigned one of four treatments. Live weight gain (LWG), feed intake, feed conversion ratio (FCR), and percent mortality were recorded from d-1 through d-138. Both strains had similar finishing weights and mortality percentages (P>0.05), but the Hybrid strain had a significantly better FCR (P<0.05). An enzyme linked to protein degradation, Lysine-Ketoglutarate Reductase (LKR), had greater expression in Nicholas than Hybrid toms (d-1 through d-136), thus supporting an inferior FCR in the Nicholas strain. Changes in dietary phosphorus in finishing diets did not affect performance or litter phosphorus content, thus indicating potential to decrease feed cost but not environmental impacts.

Key Words: turkey, phosphorus, genetic strain

W268 Impact of breeder mineral nutrition on chick development. L. F. Araujo*[1], C. S. S. Araujo[3], L. C. G. S. Barbosa[3], L. V. B. Pereira3,1, S. Hubbard[3], and M. T. Kidd[2], [1]*University of Sao Paulo*, *Pirassununga, SP, Brazil*, [2]*University of Arkansas*, *Fayetteville,* [3]*Mississippi State University*, *Mississippi State*.

The objective of this research was to investigate chick development measured as chick quality, and growth rates of chicks, from broiler breeders fed supplemental minerals. Breeders received a control diet (vitamin and mineral premix devoid of Se) or diets containing supplemental Se (0.3 mg/kg), Zn (30 mg/kg), Mn (40 mg/kg) from organic sources, and the combination of the three minerals. Organic minerals were supplied as crystalline metal glycinate (zinc and manganese) and selenium proteinate. All dietary treatments were supplied in mash form. Breeders were housed in a floor pen facility with 40 pens (8 replications/treatment). Each pen was equipped with 1 feeder, nipple drinkers and 1 nest. Each pen contained three females which were inseminated before eggs were collected. A total of 450 eggs (90 eggs per treatment) and 800 eggs (160 eggs per treatment) were obtained and set at 31 and 42 wks of age, respectively. Chick quality characteristics included dehydration, navel condition (open navel, small navel, and large navel), wet chicks, dried yolk, red hocks, and bone strength. Furthermore, as characteristics of growth rate, it was evaluated relation between chick length and body weight at process age, and eggs production in broiler breeders. At hatch, chicks were wing banded by treatment and chick quality was assessed. Ten chicks per treatment at d 1 were euthanized and their tibias were collected to evaluate bone strength. No significant differences were noted among treatments for dehydration, navel conditions, wet chicks, dried yolk and red hocks. However, progeny from breeders fed supplemental minerals showed bigger bone strength than birds from hens fed control treatment ($P < 0.05$). Furthermore, BW increased at process age according to chick length. Chicks from hens supplemented with Mn showed an increase on BW at process age and this improvement was related to chick length at hatch. Mineral supplementation resulted in an improvement at eggs production. Chick development is positively affected by breeder mineral nutrition.
FAPESP (Financial Support: 09/07178-4).

Key Words: bone strength, chick length, chick quality

W269 The effect of feeding corn distillers dried grain with solubles to sows in gestation and lactation on sow productivity. M. Roux*, S. Kitt, and R. Moser, *JBS United, INC.*, *Sheridan, IN*.

One thousand and twenty sows (340/treatment PIC Line C29) and their pigs were used to evaluate the effects of feeding corn distillers dried grains with solubles (DDGS) in gestation and lactation over multiple reproductive cycles on sow productivity. Sows were blocked by parity (avg. 2.1) and allotted to 1) non-DDGS corn-soybean meal (SBM) control diet or two levels of DDGS 2) 15%/7.5% and 3) 30%/15% in gestation/lactation, respectively. All gestation diets were formulated to contain 0.62% SID lysine and 3,340 kcal/kg ME. Lactation diets were formulated to contain 1.11% SID lysine and 3,460 kcal/kg ME. Treatments were initiated at an average of 47 days prior to farrow and continued through the subsequent gestation and lactation. At the end of the first lactation, sows fed the highest level of DDGS (30% in gestation/15% in lactation) had less back fat (BF), reduced ADFI, and greater weight loss ($P < 0.05$); but trended to have a reduced wean-to-estrus interval (WEI, $P < 0.08$) compared to sows fed the non-DDGS diet. There were no differences among treatments in litter response variables (total born, born alive, birth weight, wean weight, number weaned, pre-wean mortality, $P > 0.10$). Sows fed high DDGS in the subsequent gestation and lactation responded to dietary treatments in a similar fashion as in the previous lactation with respect to body weight loss, BF, ADFI, and return-to-estrus. There was no difference in subsequent litter performance (total born, born alive, birth weight, wean weight, number weaned, and pre-wean mortality, $P > 0.10$). At trial completion, DDGS samples were pooled by month and screened for mycotoxins. Average vomitoxin and zearalenone levels were 3.06 ppm ± 1.12 and 0.11 ppm ± 0.04, respectively. Overall, supplementation of DDGS in gestation and lactation diets with moderate mycotoxin levels had little impact upon reproductive and lactation performance.

Key Words: DDGS, sow, lactation

W270 The effect of feeding corn distillers dried grain with solubles to sows in gestation and lactation on sow productivity. M. Roux*, S. Kitt, and R. Moser, *JBS United, INC.*, *Sheridan, IN*.

One thousand and twenty sows (340/treatment PIC Line C29) and their pigs were used to evaluate the effects of feeding corn distillers dried grains with solubles (DDGS) in gestation and lactation over multiple reproductive cycles on sow productivity. Sows were blocked by parity (avg. 2.1) and allotted to 1) non-DDGS corn-soybean meal (SBM) control diet or two levels of DDGS 2) 15%/7.5% and 3) 30%/15% in gestation/lactation, respectively. All gestation diets were formulated to contain 0.62% SID lysine and 3,340 kcal/kg ME. Lactation diets were formulated to contain 1.11% SID lysine and 3,460 kcal/kg ME. Treatments were initiated at an average of 47 days prior to farrow and continued through the subsequent gestation and lactation. At the end of the first lactation, sows fed the highest level of DDGS (30% in gestation/15% in lactation) had less back fat (BF), reduced ADFI, and greater weight loss ($P < 0.05$); but trended to have a reduced wean-to-estrus interval (WEI, $P < 0.08$) compared to sows fed the non-DDGS diet. There were no differences among treatments in litter response variables (total born, born alive, birth weight, wean weight, number weaned, pre-wean mortality, $P > 0.10$). Sows fed high DDGS in the subsequent gestation and lactation responded to dietary treatments in a similar fashion as in the previous lactation with respect to body weight loss, BF, ADFI, and return-to-estrus. There was no difference in subsequent litter performance (total born, born alive, birth weight, wean weight, number weaned, and pre-wean mortality, $P > 0.10$). At trial completion, DDGS samples were pooled by month and screened for mycotoxins. Average vomitoxin and zearalenone levels were 3.06 ppm ± 1.12 and 0.11 ppm ± 0.04, respectively. Overall, supplementation of DDGS in gestation and lactation diets with moderate mycotoxin levels had little impact upon reproductive and lactation performance.

Key Words: DDGS, sow, lactation

W271 Amino acid transporter mRNA abundance in porcine mammary tissue during pregnancy and lactation. R. Manjarin*[1], J. P. Steibel[1], V. Zamora[2], N. Am-in[3], R. Kirkwood[1], C. Ernst[1], P. Weber[1], N. P. Taylor[1], and N. L. Trottier[1], [1]*Michigan State University*, *East Lansing,*[2]*Colegio de Postgraduados*, *Montecillo, Estado de Mexico, Mexico*, [3]*Chulalongkorn University*, *Bangkok, Thailand*.

The objective of this study was to test the hypothesis that mRNA abundance of genes encoding for mammary synthesized milk proteins α-lactalbumin and β-casein is positively correlated with mRNA abundance of specific amino acid transporter genes during late pregnancy and lactation. Four sows (parity 5) were selected one week before farrowing and fed a corn-soybean meal-based diet for lactation. Mammary tissue was collected by biopsy 4 d prior to farrowing (−4 d), and on d 5 (early) and 17 (peak) of lactation. Gene expression of amino acid transporters $b^{0,+}$AT (SLC7A9), y^+LAT1 (SLC7A7), y^+LAT2 (SLC7A6), $ATB^{0,+}$ (SLC6A14), CAT-1 (SLC7A1) and CAT-2b (SLC7A2), and of mammary synthesized milk proteins β-casein (CSN2) and α-lactalbumin (LALBA) was assessed by measuring mRNA abundance using relative quantitative PCR. Coefficient of variability (R^2) and mixed model analysis were used for data analysis. Compared to early lactation, CAT-1 mRNA abundance was lower ($P < 0.05$) on −4 d and higher ($P < 0.05$) on peak lactation. For $ATB^{0,+}$ and y^+LAT2, mRNA abundance was lower ($P < 0.001$ and $P < 0.01$, respectively) on −4 d compared to early lactation, and did not differ at peak lactation. Transcript abundance of transporters CAT-2b, y^+LAT1 and $b^{0,+}$AT did not differ between −4 d and early lactation or between peak and early lactation. For β-casein, mRNA abundance was lower ($P < 0.01$) on −4 d compared to early lactation, and tended to be higher ($P = 0.06$) at peak lactation. Compared to early lactation, α-lactalbumin mRNA abundance was lower ($P < 0.0001$) on −4 d, but did not differ at peak lactation. CAT-1, y^+LAT2 and $ATB^{0,+}$ mRNA abundance was positively correlated with mRNA abundance of β-casein ($P < 0.001$; $R^2 = 0.65$, 0.60 and 0.63, respectively) and with mRNA abundance of α-lactalbumin ($P < 0.001$; $R^2 = 0.53$, 0.79 and 0.79, respectively). In conclusion, gene expression of amino acid transporters CAT-1, $ATB^{0,+}$ and y^+LAT2 is upregulated during lactation in porcine mammary gland and positively correlated to expression of genes encoding for the mammary synthesized milk proteins β-casein and α-lactalbumin.

Key Words: amino acid, transporter, sow

Physiology and Endocrinology: Endocrinology and Metabolism

W272 Effects of lactation and pregnancy status on concentrations of insulin and IGF-1, and correlations with metabolic indicators in Holstein dairy cattle. I. M. Thompson*[1], R. L. A. Cerri[1], I. H. Kim[2], A. D. Ealy[1], P. J. Hansen[1], C. R. Staples[1], and W. W. Thatcher[1], [1]*University of Florida*, *Gainesville,*[2]*Chungbuk National University*, *Cheongju, South Korea*.

Objectives were to develop and characterize an experimental platform to evaluate lactation and pregnancy effects for subsequent transcriptome analyses in dairy cattle. Pregnant heifers (n=34) were assigned randomly after calving to a lactating group (L, n=17) and a non-lactating group (NL, n=17). The L was fed a TMR (1.65Mcal NEL/kg, 16.5% CP). The NL was fed a maintenance ration (1.45 Mcal NEL/kg, 12.2% CP). Blood was collected thrice weekly for 8 wk and analyzed for insulin, IGF-1, NEFA, BHBA, glucose, and BUN. Cows were pre-synchronized and enrolled in a timed (T)-AI protocol, but only 10 in the L and 12 in the NL were TAI. On d 17 after GnRH/TAI, cows were slaughtered and reproductive tissues collected. Analysis of variance for main effects, and simple and partial correlations were performed. Mean plasma concentrations of insulin postpartum did not differ between NL and L (1.28 vs. 1.24 ng/mL), but a Pregnancy × Lactation interaction ($P < 0.01$) was detected, because of increased insulin concentrations in lactating pregnant compared with non-lactating pregnant. Concentration of IGF-1 was lower ($P < 0.01$) for L compared with NL (135.2 vs. 203.4 ng/mL), and also different ($P = 0.01$) between cyclic and pregnant (144.5 vs. 194.1 ng/mL). Insulin was not correlated ($P > 0.10$) with any of the metabolites measured in both simple and partial correlations. Concentrations of IGF-1 had a +0.25 correlation ($P < 0.01$) with glucose, but this correlation was not significant when adjusted for lactation. A negative correlation ($P < 0.01$) between IGF-1 and NEFA (r = –0.33), and BUN (r = –0.25) was detected. Among metabolites, the highest correlation was between BHBA and BUN ($P < 0.01$; r = +0.586). In conclusion, lactation\diet and pregnancy status altered concentrations of IGF-1 in plasma, but insulin was not affected. Concentrations of IGF-1 in plasma were better predictors of metabolite concentrations than insulin.

Key Words: lactation, pregnancy, IGF-1

W273 Comparison of body condition score, body weight and milk yield and composition of Holstein and crossbred dairy cows. L. G. D. Mendonca*, C. C. Abade, E. M. da Silva, and R. C. Chebel, *Department of Veterinary Population Medicine, University of Minnesota*, *Saint Paul*.

Objectives were to compare body condition score (BCS) and body weight (BW) changes and milk yield and composition between Holstein and crossbred cows. Cows (Holstein = 45 and crossbred = 46) were enrolled in the study 45 d before expected calving date. Cows received a BCS and were weighed at 45 and 15 d before expected calving date, immediately after calving (0 days in milk, DIM), and at 28 and 56 DIM. Milk yield and composition during the first 3 mo postpartum were recorded and yield of energy corrected milk (ECM) was calculated. Holstein cows had smaller ($P < 0.01$) BCS than crossbred cows throughout the study (3.1 ± 0.1 vs. 3.4 ± 0.1) but there was no interaction between breed and study day ($P = 0.42$). Body weight was not affected by breed ($P = 0.63$) or by the interaction between breed and study day ($P = 0.16$). Average milk yield was ($P = 0.03$) greater for Holstein cows (38.9 ± 1.1 vs. 34.8 ± 1.5 Kg/d) and the interaction between breed and mo of lactation affected ($P < 0.01$) milk yield because milk yield of Holstein cows was only greater ($P < 0.01$) on the third mo of lactation (44.4 ± 1.3 vs. 37.6 ± 1.6 Kg/d). Milk fat concentration was not (P = 0.43) different between breeds (4.1 ± 0.1%), but Holstein cows had greater ($P < 0.01$) fat yield (1.5 ± 0.1 vs. 1.3 ± 0.1 Kg/d). Holstein cows had ($P < 0.01$) smaller milk protein concentration (3.1 ± 0.1 vs. 3.4 ± 0.1%) and protein yield was ($P < 0.01$) affected by the interaction between breed and study day because on the third mo of lactation Holstein cows had ($P < 0.01$) greater protein yield (1.3 ± 0.1 vs. 1.0 ± 0.1 Kg/d). Average ECM yield on the first 3 mo postpartum was greater ($P < 0.01$) for Holstein than crossbred cows (40.0 ± 1.0 vs. 35.6 ± 1.3 Kg/d) and there was a tendency ($P = 0.07$) for the interaction between breed and mo of lactation to affect ECM yield because Holstein cows had ($P < 0.01$) greater ECM yield on the third mo (42.5 ± 1.2 vs. 35.6 ± 1.6 Kg/d). Linear somatic cell count was not ($P = 0.33$) affected by breed. Although Holstein cows produced more milk in the first 3 mo of lactation, this does not appear to be in detriment of BCS or body weight.

Key Words: crossbred cow, milk yield, body condition score

W274 Association between peripartum cortisol, haptoglobin, non-esterifed fatty acid and milk yield in Holstein cows. J. M. Huzzey*[1], T. R. Overton[1], D. V. Nydam[1], and R. J. Grant[2], [1]*Cornell University*, *Ithaca, NY*, [2]*W.H. Miner Agricultural Research Institute*, *Chazy, NY*.

The objective of this study was to evaluate the relationship between peripartum indicators of stress, inflammation and energy status with milk yield. Blood and fecal samples from 414 Holstein dairy cows were collected weekly beginning 3 weeks before until 1 week after calving. Plasma was analyzed for cortisol, haptoglobin (Hp) and non-esterified fatty acid (NEFA) and fecal samples were analyzed for cortisol metabolites (11,17-dioxoandrostanes). A range of cut-points were evaluated for each metabolite and their relationship to milk yield [305 mature equivalent (305ME) predicted from the second test day (averaging 63 DIM)] was assessed using mixed models. Fecal cortisol metabolites (FCM) were not associated with 305ME in primiparous (PP) cows. Multiparous (MP) cows with FCM > 250 ng steroid/g fecal DM during wk −3 or −2 relative to calving had on average a 966 kg lower 305ME ($P \leq 0.05$) relative to cows below this cutpoint. Projected 305ME was 1162 kg lower among MP cows with FCM > 70 ng steroid/g fecal DM during wk +1 (P = 0.001). There was no association between plasma cortisol and milk yield at any period relative to calving for either MP or PP cows. Projected 305ME tended to be 1322 kg lower (P = 0.07) in PP cows with Hp > 1.1 g/L during wk −3. MP cows with Hp > 1.1 g/L during wk −2, −1 or +1 had on average a 1496 kg lower projected 305ME ($P \leq 0.05$). There was no association between prepartum NEFA and 305ME in PP cows, however, PP cows with NEFA > 600 mEq/L during wk +1 had a 851 kg greater projected 305ME (P = 0.02). MP cows with NEFA > 500 mEq/L during wk −3, −2, or −1 had on average a 1371 kg lower projected 305ME ($P \leq 0.01$). During wk +1, MP cows with NEFA > 600 mEq/L had a 517 kg lower projected 305ME (P = 0.05). High concentrations of these metabolites before or after calving, particularly among MP cows, may suggest that opportunities exist to improve milk yield.

Key Words: milk yield, haptoglobin, cortisol

W275 Relationship between IGF-I polymorphism and metabolic and endocrine profiles of dairy cows on grazing conditions during the transition period. G. Ruprechter*[1], A. Meikle[1], P. Nicolini[1], and

M. Carriquiry[2], [1]*School of Veterinary Sciences, UDELAR*, *Montevideo, Uruguay*, [2]*School of Agronomy, UDELAR*, *Montevideo, Uruguay*.

Primiparous Holstein cows (n=42) of a Uruguayan commercial farm, blocked by calving date, were used to evaluate the effect of a IGF-I polymorphism (C/T position 512) located in the promoter region of the gene (variant A/B), on metabolic and endocrine profiles during the transition period. Cows were distributed as follows: AA (n=15), AB (n=15) and BB (n=12). Cows grazed a mixture of ryegrass (*Lolium multiflorum*) and alfalfa (*Medicago sativa*) and were supplemented with a ration including corn silage, high moisture corn grain, and sunflower meal (12, 5 and 2 kg DM, respectively). The diet offered had 17% crude protein and 1.7 Mcal/kg DM of net energy of lactation. Blood samples and BCS data (scale 1-5) collected at −7, 30, and 60 days of lactation. Genotyping of IGF–I was performed using PCR–RFLP. Nonesterified fatty acids (NEFA) and β-hydroxybutyrate (BHB) concentrations were determined spectrophotometrically and IGF-I and insulin concentrations by RIA. Means from repeated measure analyses were considered to differ when $P < 0.05$. There were no differences in BCS among IGF–I genotypes. However, plasma levels of NEFA, BHB, and insulin were affected ($P < 0.04$) by IGF–I genotype. Concentrations of NEFA and BHB were greater in AA than BB cows, being levels intermediate in heterozygous cows (0.44, 0.41, and 0.33 ± 0.03 mmol/L and 0.30, 0.26, and 0.23±0.02 mmol/L for NEFA and BHB of AA, AB, and BB cows, respectively). Insulin concentrations were less in AA than BB cows, and intermediate in AB cows (2.77, 3.21, and 3.98 ± 0.33 μUI/mL, for AA, AB, and BB, respectively). The IGF-I genotype did not affect ($P = 0.39$) differentially circulating IGF-I in blood (86.4, 97.7, and 94.6 ± 7.3 ng/mL, for AA, AB, and BB, respectively). There was no interaction ($P > 0.12$) between IGF-I genotype and day of lactation for any of the variables studied. Although plasma concentrations of IGF-I were not affected by IGF-I genotype, energy status of BB genotype cows appeared to be improved during early lactation.

Key Words: SNP, energy balance, dairy cattle

W276 Effects of intravenous glucose infusion and nutritional balance on serum concentrations of NEFA, glucose, insulin, and progesterone in non-lactating dairy cows. F. Vieira*[1], C. Lopes[1], B. Cappellozza[1], A. Scarpa[1], R. Cooke[2], and J. L. Vasconcelos[1], [1]*FMVZ - UNESP*, *Botucatu, SP, Brazil*, [2]*Oregon State University*, *Burns*.

The objective of this study was to evaluate serum concentrations of non-esterified fatty acids, glucose, insulin, and progesterone in non-lactating dairy cows according to nutritional balance and glucose infusion. Ten non-lactating, ovariectomized Gir × Holstein cows were stratified by body weight (BW) and body condition score (BCS) on d −28 of the study, and randomly assigned to: 1) negative nutrient balance (NB) and 2) positive nutrient balance (PB). All cows were inserted with an intravaginal progesterone releasing device on d −14, which remained in cows until the end of the study. Cow BW and BCS were assessed again on d 0. On d 0, cows within nutritional treatment were randomly assigned to receive, in a crossover design containing 2 periods of 24 h each: 1) intravenous glucose infusion (GLUC; 0.5 g of glucose/kg of BW, over a 3 h period), or 2) intravenous saline infusion (SAL; 0.9% solution over a 3 h period). Prior to the beginning of each period, all cows were fasted for 12 h. Blood samples were collected, relative to the beginning of the infusion, at −12 and −11.5 (beginning of fasting), and at −0.5, 0, 0.5, 1, 2, 3, 4, 5, and 6 h. Following the last blood collection of period 1, cows received (PB) or not (NB) concentrate and returned to respective pastures. Changes in BCS and BW were greater in NB cows compared to PB cows (−0.60 and −0.25 ± 0.090 for BCS, respectively; −22.4 and 1.2 ± 6.58 kg for BW, respectively). Cows receiving GLUC had greater glucose concentrations from 0.5 to 3 h relative to infusion compared to SAL cows. Insulin concentrations were greater in PB cows assigned to GLUC compared to SAL cohorts at 0.5 and 3 h following infusion, whereas NB cows assigned to GLUC had greater insulin concentrations compared to SAL cohorts at 0.5, 1, 2, and 3 h. Progesterone concentrations were greater in PB cows assigned to GLUC at 2, 3, and 4 h following infusion compared to SAL cohorts. In conclusion, the effects of glucose infusion on serum concentrations of insulin and progesterone in non-lactating dairy cows were dependent on cow nutritional status.

Key Words: glucose infusion, insulin, progesterone

Physiology and Endocrinology: Hormonal Regulation of the Estrous Cycle in Dairy Cattle

W277 Effects of treatments with hCG or GnRH on serum progesterone (P4) and conception rates (CR) in lactating dairy cows submitted to timed artificial insemination (AI) or embryo transfer (ET). P. Justolin*[1], P. Morelli[1], M. Reis[1], O. Sá Filho[1], F. Aragon[2], M. Veras[2], S. Soriano[3], and J. L. Vasconcelos[1], [1]*FMVZ - UNESP*, *Botucatu, SP, Brazil*, [2]*Pioneiros Veterinary Clinic*, *Carambei, PR, Brazil*, [3]*Colorado Dairies*, *Araras, SP, Brazil*.

The effects of treatments with GnRH or hCG 7 d after induced ovulation on P4 and CR in lactating Holstein cows submitted to AI or ET were evaluated. A total of 993 protocols for synchronization of ovulation, performed in 684 lactating Holstein cows (169.8±4.4 DPP; 37.9±0.3 Kg milk/day), were initially used in this study. Synchronization protocols consisted in CIDR insert + GnRH on d −10, CIDR withdrawal + PGF2α on d −3, and estradiol cypionate on d −2. On d −2, cows were assigned to receive either AI on d 0 or ET on d 7. On d 7, ovaries of all cows were evaluated by ultrasonography (US), and only cows with presence of CL remained in the study (834 protocols performed in 661 cows). Within each breeding-technique (BT) group, cows were assigned to receive either (1) no treatments (Control), (2) GnRH on d 7 (GnRH), or (3) hCG (2,500 IU) on d 7 (hCG). Blood samples were collected from a subgroup of 179 cows on d14 for P4 analysis (P4d14). Pregnancy was evaluated by US on d 31 ± 3. The P4d14 was greater in gonadotropin-treated than in Control cows ($P < 0.01$), but did not differ ($P > 0.1$) between GnRH and hCG groups (Control: 4.86±0.36; GnRH: 6.22±0.35; hCG: 6.88±0.36 ng/mL). The CR was greater ($P < 0.05$) in ET than in AI cows (45.2% [168/372] vs. 31.6% [146/462]), in primiparous than in multiparous (42.7% [141/330] vs. 34.3% [173/504]). There was an interaction ($P < 0.05$) between BT and treatment on CR, in manner that treatments affected the CR at ET (Control: 38.1% [48/126]; GnRH: 52.4% [65/124]; hCG: 45.1% [55/122]; $P < 0.05$), but not at AI (Control: 30.1% [47/156]; GnRH: 32.2% [50/155]; hCG: 32.4% [49/151]; $P > 0.1$). Rectal temperature on d 7 negatively affected CR (y = EXP[16.7 - 0.4 • ×] / 1 + EXP[16.7 - 0.4 • ×]; $P < 0.01$). Thus, treatments with GnRH or hCG on d 7 increased P4d14 and improved CR of cows submitted to ET, but not to AI, and rectal temperature on d 7 negatively affected CR regardless of BT or treatment.

Key Words: embryo transfer, lactating cows, conception rate

W278 Effect of the treatment with GnRH seven days after embryo transfer (ET) on reproductive performance in lactating dairy cows. P. Morelli*[1], P. Justolin[1], M. Reis[1], O. Sá Filho[1], F. Aragon[2], M. Veras[2], S. Soriano[3], and J. L. Vasconcelos[1], [1]*FMVZ - UNESP*, *Botucatu, SP, Brazil*, [2]*Pioneiros Veterinary Clinic*, *Carambei, PR, Brazil*, [3]*Colorado Dairies*, *Araras, SP, Brazil*.

The effects of treatments with GnRH 7 d after ET on conception rate (CR) in lactating Holstein cows were evaluated. A total of 350 lactating Holstein cows (192.9 ± 7.6 DPP; 35.1 ± 0.8 Kg milk/day), were initially submitted to a synchronization of ovulation protocol consisting of CIDR insert + GnRH on d −10, CIDR withdrawal + PGF2α on d −3, and estradiol cypionate on d −2. On d 7, ovaries of all cows were evaluated by ultrasonography (US), and those cows with presence of luteal tissue (n = 285) received one fresh embryo into the uterine horn ipsilateral to the CL and an i.m. injection of 100 µg of gonadorelin (GnRH). On d14, cows were randomly assigned to receive (G7+14; n = 147) or not (G7; n = 138) an additional treatment with GnRH. Rectal temperature was measured in all cows immediately after morning milking of d 7 (RTd7) and d 14 (RTd14). Pregnancy was evaluated by US on d 31 ± 3 (US1) and 62 ± 3 (US2). The CR was calculated by dividing the number of pregnant cows by the number of cows receiving an embryo on d 7. The CR-31d was not affected by treatment (G7: 48.5% [67/138]; G7+14: 42.9% [63/147]; $P > 0.1$), but tended to be positively affected by milk production (y = EXP[-0.01 + 0.8 • ×] / 1 + EXP[-0.01 + 0.8 • ×]; $P = 0.06$). The CR-62d was not affected by treatment (G7: 39.8% [55/138]; G7+14: 37.4% [55/147]; $P > 0.1$), but was positively affected by milk production (y = EXP[-1.2 + 0.02 • ×] / 1 + EXP[-1.2 + 0.02 • ×]; $P = 0.04$) and tended to be negatively affected by RTd14 (y = EXP[23.1 - 0.6 •×] / 1 + EXP[23.1 - 0.6 • ×]; $P = 0.05$). In summary, treatment with GnRH 7 d after ET did not improve reproductive performance of dairy cows that received a previous GnRH treatment concurrently with ET.

Key Words: embryo transfer, lactating dairy cows, conception rate

W279 Effect of moment of induced ovulation and progesterone (P4) for resynchronization on fertility of Holstein cows in a 5-d timed AI program. R. S. Bisinotto*, E. S. Ribeiro, L. T. Martins, R. S. Marsola, L. F. Greco, C. A. Risco, W. W. Thatcher, and J. E. P. Santos, *University of Florida*, *Gainesville*.

The effects of the interval from GnRH to insemination (AI) at first AI and supplemental P4 for resynchronization on pregnancy per AI (P/AI) were evaluated. In study 1, cows received 2 injections of prostaglandin (PGF) at 46 and 60 d in milk (DIM). The timed AI protocols began with an injection of GnRH at 72 DIM, and an injection of PGF 5 and 6 d later. Cows were randomly assigned to receive the final GnRH either 56 h after the first PGF of the protocol and AI 16 h later (5d-OVS56, n=634) or GnRH and AI 72 h after the first PGF (5d-COS72, n=593). The proportion of cows in estrus on the day of AI was greater (P=0.003) for the 5d-COS72 than 5d-OVS56 (40.6 vs. 32.4%). P/AI did not differ between treatments on d 32 (5d-OVS56=46.4 vs. 5d-COS72=45.5%) or 60 after AI (5d-OVS56=40.7 vs. 5d-COS72=38.6%). In study 2, nonpregnant cows on d 32 after the first AI received either an intravaginal P4 insert (RCIDR, n=341) or no P4 (RCON, n=334) from the GnRH to the first PGF of the resynchronization (d 0 GnRH, d 5 and 6 PGF, d 7.5 GnRH, 16 h timed AI). Ovaries were scanned (n=340) at the first PGF and final GnRH to detect premature ovulation. Blood was sampled (n=398) at AI and 7 d later for analysis of P4. Synchronization to the protocol was considered when cows had no premature ovulation and when concentrations of P4 at AI and 7 d later were, respectively, <1.0 ng/mL and >2.26 ng/mL. P/AI was greater ($P < 0.05$) for RCIDR than RCON on d 32 (RCON=43.1 vs. RCIDR=51.3%) and d 60 after AI (RCON=37.8 vs. RCIDR=45.5%). Only 5.6% (19/340) of the cows ovulated prematurely, and it tended ($P = 0.09$) to be greater for RCON than RCIDR cows (RCON=7.5 vs. RCIDR=3.6%). Concentrations of P4 on the day of AI and 7 d later (RCON = 0.25 and 2.88; RCIDR = 0.32 and 2.72 ng/mL) did not differ between treatments. Synchronization to treatments did not differ and were 57.8% for RCON and 61.4% for RCIDR. Results indicate that administration of the final GnRH simultaneously with AI does not impair fertility of cows subjected to a 5-d timed AI protocol and that supplementation with P4 during resynchronization improves P/AI.

Key Words: dairy cow, progesterone, timed AI

W280 Evaluation of a mechanistic, dynamic, metabolic model of regulation of reproductive processes in dairy cattle. P. Celi[2], I. Lean[2], H. Raadsma[2], A. Rabiee[2], and J. P. McNamara*[1], [1]*Washington State University*, *Pullman,* [2]*University of Sydney*, *Camden, NSW, Australia*.

The objective was to conduct and initial evaluation of a conceptual research model which describes functional control at the metabolic level, of reproductive processes in dairy cattle; and is suitable for evaluation of data, concepts and hypotheses regarding underlying genetic, nutritional and physiological control of reproduction. This research model used an existing, extensively evaluated model of bovine metabolism (Molly, UC Davis), including glucose, amino acids and fatty acids by muscle, adipose, visceral and mammary tissues. Equations for pulses of LH release, FSH, follicular growth, estrogen and progesterone concentrations in cycling and pregnant animals, ovulation, fetal growth and early embryonic mortality were developed from literature values. The model links glucose with LH release; glucose and IGF1 with follicular growth; and also describes effects of feed intake, metabolic rate and milk production on liver metabolism of estrogen and progesterone. This initial evaluation was a standard evaluation of behavior and sensitivity—did the variables respond in a similar fashion and rate to those in the literature that were not used for the model construction. The statistical standard compared the model output to observed data, and adequacy was decided if the output was within one least significant difference (LSD) based on $P <$ 0.05. Hormonal concentrations during cycling and pregnancy simulated literature values within 1 LSD. Increased metabolic rate (a function of milk production or feed intake) increased degradation of estrogen and progesterone, shortening length of estrus and decreasing progesterone in early pregnancy. The behavior was in the proper direction and magnitude for these variables within 1 LSD ($P < 0.05$) of published values. The model can be useful to frame specific hypotheses on control of reproductive processes by genetic and nutritional mechanisms: and to form a framework of more specific models at cellular and molecular levels of the processes of reproduction in the dairy cow.

Key Words: reproduction, nutrition, research model

W281 Effects of different ovulatory stimulus (GnRH vs. estradiol cypionate) on follicular dynamics of a progesterone-based timed AI protocol in Holstein cows. R. M. Ferreira, H. Ayres*, L. U. Gimenes, and P. S. Baruselli, *Department of Animal Reproduction, University of São Paulo*, *São Paulo, SP, Brazil*.

The aim of this study was to evaluate the effects of estradiol cypionate (EC) at progesterone (P4) device removal, GnRH 56h later or both on follicular dynamics in Holstein cows. At random stages of the estrous cycle (D0), 57 Holstein cows received 2mg estradiol benzoate (Estrogin , Farmavet, Brazil) and one P4 device (CIDR , Pfizer, Brazil). On D8, device was removed and all animals received 25mg dinoprost (Lutalyse, Pfizer, Brazil) plus 400 IU eCG (Folligon , Intervet, Brazil). On the same day (D8), cows were randomly allocated to one of three treatments, as follows: 1) ECP (1 mg; n=18) at P4 device removal; 2) GnRH (0.1mg gonadorelin; n=19) 56h after P4 device removal, and 3) ECP at P4 device removal and GnRH 56h later (n=20). Ultrasound examinations were performed at D0, D8, and every 12 h from P4 removal to disappearance of the ovulatory follicle, or 96 h after P4 withdrawal, whichever occurred first. The diameter of the ovulatory follicles (ØOF), time to ovulation after P4 removal (TOV), ovulation rate (OR) and number of ovulations (Nov) were also evaluated. Statistical analyses were performed with logistic regression by PROC GLIMMIX of SAS. The treatments affected the average TOV (EC=70.8^{a} vs. GnRH=77.3^{b} vs. EC+GnRH=65.3h^{a}; $P < 0.01$) and the ØOF (EC=13.0^{b} vs. GnRH=14.8^{a} vs. EC+GnRH 14.1mm^{ab}; $P = 0.02$). No differences were found on OR [EC=83.3% vs. GnRH=85.0% vs. EC+GnRH=90.0%; $P = 0.71$] and Nov (EC=1.1 vs. GnRH=1.3 vs. ECP+GnRH=1.3, $P = 0.20$). Also, analyses of contrast showed that cows receiving EC had an earlier TOV than cows treated with GnRH ($P < 0.01$). These data suggest that EC+GnRH can be used as an ovulatory stimulus, and its administration at P4 device removal induces ovulation about 70h later. Thus, if TAI is done 56h after P4 device removal, the ovulation will occur around 16–12 h after TAI, an adequate moment to achieve satisfactory pregnancy per AI.
We acknowledge Pfizer and Fazenda Campestre.

Key Words: estradiol cypionate, GnRH, Follicular dynamics

W282 Dose of equine chorionic gonadotropin necessary to cause multiple ovulation and increase in progesterone concentration following a synchronization protocol in lactating dairy cows. A. C. Denicol*[1], F. A. Rivera[1], L. G. D. Mendonca[2], C. D. Narciso[1], G. Lopes Jr.[1], R. G. S. Bruno[1], and R. C. Chebel[1,2], [1]*Veterinary Medicine Teaching and Research Center, University of California*, *Tulare,* [2]*Department of Veterinary Population Medicine, University of Minnesota*, *Saint Paul*.

Objective was to establish a minimum dose of equine chorionic gonadotropin (eCG) capable of inducing multiple ovulation and accessory corpora lutea (CL) and increasing concentrations of progesterone (P4) in lactating dairy cows. Forty-eight lactating Holstein cows were randomly assigned to one of three treatments at the beginning of a timed AI (TAI) protocol: control (n = 10), eCG6 (n = 19) and eCG8 (n = 19). The TAI protocol consisted of GnRH (100 µg i.m.), 7 d later prostaglandin (PG) F2α (25 mg i.m.), and 72 h later GnRH (100 µg i.m.) and TAI. Cows in the eCG6 and eCG8 treatments received 600 and 800 IU of eCG i.m., respectively, 48 h after the first GnRH. Blood was sampled and ovaries were scanned at the time of each injection of the TAI protocol, 48 h after the first GnRH injection, and 7 d after TAI. Concentrations of estradiol on the day of PGF2α injection was not (3.6 0.1 pg/mL; $P = 0.70$) affected by treatment, but the number of follicles > 10 mm on the day of the second GnRH was ($P = 0.03$) greater for eCG8 cows (control = 1.8 ± 0.2, eCG6 = 1.6 ± 0.2, eCG8 = 2.2 ± 0.2). Although the proportion of cows with a CL 7 d after TAI was not ($P = 0.19$) different (control = 100, eCG6 = 73.7, eCG8 = 84.2%), eCG8 cows tended ($P = 0.14$) to be more likely to have an accessory CL (control = 10.0, eCG6 = 15.8, eCG8 = 36.8%). Twelve cows (control = 2, eCG6 = 4, eCG8 = 6) failed to synchronize their estrous cycles and were removed from further analysis. The cumulative CL volume of eCG8 cows was ($P < 0.01$) larger than control and eCG6 cows (control = 7.5 ± 2.0, eCG6 = 5.0 ± 1.2, eCG8 = 10.9 ± 1.5 cm3), and eCG8 cows had ($P < 0.01$) greater P4 concentration 7 d after AI (control = 1.5 ± 0.5, eCG6 = 1.3 ± 0.3, eCG8 = 3.0 ± 0.4 ng/mL). We conclude from this experiment that a dose of 800 IU of eCG is capable of inducing accessory CL and increasing P4 concentration in lactating dairy cows following a TAI protocol.

Key Words: lactating dairy cow, equine chorionic gonadotropin, progesterone

W283 Effect of presynchronization with GnRH or hCG 7 d before resynchronization of ovulation initiated 25 d after a previous timed AI on fertility of lactating dairy cows. J. O. Giordano*, J. N. Guenther, G. Lopes Jr., M. M. Herlihy, A. B. Nascimento, M. C. Wiltbank, and P. M. Fricke, *University of Wisconsin*, *Madison*.

To determine the effect of presynchronization on fertility to resynchronization of ovulation (Resynch), lactating cows on a commercial dairy initiated Resynch 25 d after a prior TAI using GnRH and cloprostenol (PGF) as follows: (d 0, 200 µg GnRH; d 7, 750 µg PGF; 56 h, 100 µg

GnRH; 16 h, TAI). At the prior TAI, cows were randomly assigned to one of three treatments to receive: 2,000 IU hCG (Chorulon) 7 d before initiation of Resynch (HGPG, n=346); 200 µg GnRH 7 d before initiation of Resynch (GGPG, n=361); or no presynchronization (C, n=375). Cows diagnosed not pregnant at 32 d after prior TAI received the PGF injection of the Resynch and continued the protocols. Pregnancy was diagnosed at 32 and 53 d after Resynch TAI to determine pregnancies per AI (P/AI). Based on logistical regression analysis, treatment tended ($P = 0.07$) to affect P/AI 32 d after TAI [HGPG = 33.0% (114/346); GGPG = 30.8% (111/361); C = 25.3% (95/375)]. Based on statistical contrasts, HGPG cows had more ($P = 0.02$) P/AI than C cows, whereas P/AI for GGPG vs. C cows tended ($P = 0.10$) to differ and HGPG vs. GGPG cows did not ($P = 0.53$) differ. Pregnancy loss from 32 to 53 d after Resynch TAI was not affected by parity and did not differ ($P = 0.29$) among treatments [HGPG = 6.3% (7/112); GGPG = 9.9% (11/111); C = 4.3% (4/93)]. Treatment did not affect ($P = 0.13$) P/AI at 53 d after TAI when all treatments were included in the model; however, when analyzed separately, HGPG cows tended to have more ($P = 0.08$) P/AI 53 d after Resynch TAI than C cows [30.5% (105/344) vs. 23.9% (89/373)]. Based on a subset of cows, ovulation to the last GnRH injection of Resynch did not differ among treatments [HGPG = 89.3% (176/197); GGPG = 89.8% (168/187); C = 89.9% (177/197)]. We conclude that presynchronization with hCG or GnRH 7 d before initiation of Resynch did not affect synchronization rate, but that hCG increased fertility whereas GnRH tended to increase fertility compared to Ovsynch initiated 25 d after a prior TAI.
Supported by Hatch project WIS01171

Key Words: hCG, resynchronization, fertility

W284 Milk estradiol and pedometer activity during estrus in dairy cows. N. Kendall, D. Scholey, and G. Mann*, *University of Nottingham*, *School of Biosciences, Division of Animal Sciences, Sutton Bonington Campus, Loughborough, LE12 12RD, UK*.

While it is well established that elevated concentrations of estradiol are responsible for the induction of estrus, the relationship between concentration of estradiol and intensity of estrus is less clear. In this study we have used pedometer activity to quantitatively measure estrous activity at insemination and related this to peak concentrations of milk estradiol during the previous 24h period to determine if estrus intensity is affected by estradiol concentration. The study was carried out in 37 lactating, naturally cycling Holstein Friesian cows maintained under a commercial herd management regimen. Cows were milked by robot and a milk sample taken and pedometer activity data collected at each milking. Cows were inseminated on the basis of observed estrus and/or elevated pedometer activity and daily milk progesterone measurements undertaken to confirm that cows were at the correct stage of the cycle when insemination took place and pedometer and milk estradiol measurements were made. Validated measurements were obtained from a total of 61 estrus periods during which peak pedometer activity was 310 ± 19 steps per hour (range 89 - 776 steps per hour) and peak milk estradiol concentration 4.6 ± 0.2 pg/ml (range 1.8 - 9.1 pg/mL). There was no association between peak concentration of milk estradiol and peak pedometer activity ($P = 0.59$). Furthermore, comparison of successful and unsuccessful inseminations revealed no differences in either milk estradiol (4.3 ± 0.4 vs. 4.8 ± 0.3 pg/mL) or pedometer activity (290 ± 40 vs. 318 ± 22) in cows conceiving or failing to conceive. However, in cows (n = 26) in which measurements were made during successive estrous periods, there were significant ($P < 0.01$) associations in both milk estradiol ($R^2 = 0.28$) and pedometer activity ($R^2 = 0.25$) between previous and subsequent estrous periods. These results demonstrated that while both estradiol concentrations and pedometer activity at estrus appear to exhibit some repeatability within cows, the peak concentration of estradiol in milk was not correlated with estrus intensity.
This work was funded by Defra, the Milk Development Council and Intervet under the Link Sustainable Livestock Programme.

Key Words: cow, estrus, estradiol

W285 Effect of treatment with human chorionic gonadotropin (hCG) and/or intravaginal progesterone (CIDR) on day 5 after AI on fertility in lactating dairy cows. A. B. Nascimento*, J. N. Guenther, F. P. Dalla Costa, M. M. Herlihy, A. Keskin, G. Lopes Jr., and M. C. Wiltbank, *University of Wisconsin*, *Madison*.

Secretion of progesterone (P4) from the corpus luteum (CL) is essential for pregnancy in cattle. Our previous research indicates that lactating dairy cows synchronized with Double-Ovsynch, have much lower P4 after ovulation than heifers (P4 < 50% of heifer, P4 from Day 6 to 13 after AI) in spite of ovulating a similar size follicle. Treatment of these cows on Day 5 after AI with both hCG (to induce an accessory CL) and a CIDR can increase P4 to heifer concentrations. Our primary hypothesis is that supplementation with P4 after AI (hCG and/or CIDR) will increase % of dairy cows pregnant to timed AI. Further, we hypothesized that CIDR treatment until Day 22 after AI would synchronize estrus in non-pregnant cows (~Day 25), produce a more optimal time to begin Ovsynch (Day 7 of new cycle), and increase % pregnant at second timed AI. Lactating Holstein cows (n=794) were synchronized with Double-Ovsynch (First Ovsynch: GnRH-7d-$PGF_2\propto$-3d-GnRH)-7d-(Breeding Ovsynch: GnRH-7d-$PGF_2\propto$-56h-GnRH-16h-AI). On Day 5 after AI cows were randomly assigned to receive no treatment (Control), CIDR, 2,000 IU hCG or CIDR+hCG. The CIDR was removed on Day 22 after AI and pregnancy diagnosis was performed by ultrasound on Day 32 after AI, with resynch initiated on Day 32. A high % of cows were pregnant to first AI (379/794 = 47.7%) with no treatment effects ($P = 0.82$; Control: 98/197 = 49.7%; CIDR: 95/195 = 48.7%; hCG: 95/201 = 47.3%; CIDR+hCG: 91/201 = 45.3%). Non pregnant cows after first AI (n=313) were evaluated for % pregnant to second AI to test the second hypothesis. There were also no differences ($P = 0.66$) on % pregnant to second AI (Control: 26/78 = 33.3%; CIDR: 28/72 = 38.9%; hCG: 24/76 = 31.6%; CIDR+hCG: 26/87 = 29.9%). In conclusion, the results from first AI did not support our primary hypothesis but indicate no impact of P4 supplementation in lactating dairy cows synchronized with Double-Ovsynch in spite of the low circulating P4 in these cows.

Key Words: progesterone, CIDR, hCG

W286 A comparison of conception rates between new and re-used Eazi-Breed CIDRs. R. Giles*[1], G. Seidel[2], C. McConnel[2], and K. McSweeney[1], [1]*Bovine Reproductive Specialists*, *Loveland, CO,* [2]*Colorado State University*, *Fort Collins*.

Intravaginal progesterone (CIDR) inserts can help acyclic dairy cows return to normal cyclicity and successful ovulation for timed AI. However, CIDRs are relatively expensive and the cost per pregnancy would be decreased if CIDRs could be effectively used again. The objective of this study was to determine whether Eazi-Breed CIDRs used within an OvSynch program could be re-used efficaciously in cows diagnosed as acyclic. The study was conducted on 3 dairies (A, B, C) in northern Colorado from January 2009 through January 2010. Enrolled cows were limited to lactations 1-4 and times bred 1-4. Lactating dairy cows (dairies A, N = 631; B, N = 349; and C, N = 378) were scanned ultrasonographically prior to the start of an OvSynch program and diagnosed as being cystic (follicle greater than 25 mm and absence

of corpus luteum (CL)), or without a CL. All cows received 100 μg of GnRH im, and were scanned 7 days later. Cows observed as being persistently cystic or without a CL (acyclic) for two weeks in a row were enrolled into a CIDR sync program. This program involved CIDR (1.38 g progesterone) insertion and im administration of 100 μg GnRH on day 0, CIDR removal and im administration of 25 mg PGF2α on day 7, im administration of 100 μg GnRH 56 h following CIDR removal, and AI 16-18 h later. Cows with odd numbered ear tags received re-used CIDRs and even numbered cows received new CIDRs. Pregnancy status was determined on day 32-39 by ultrasonography. Conception rates (day 32-39) with new CIDRs were slightly higher in both categories (Cystic: new-37/106 (34.9%), re-used-35/114 (30.7%); Acyclic: new-194/559 (34.7%), re-used-184/579 (31.8%)). None of these differences was significant (P>0.1) nor was there a significant difference for all re-used (31.6% pregnant) vs. all new CIDRs (34.7% pregnant; one-tail chi-squared; Fisher-Yates correction). No treatment × dairy effect was noted, although overall pregnancy rates were lower ($P < 0.05$) at dairy C (29.4%) than dairies A (35.0%) or B (37.2%).

Key Words: CIDR, acyclic, OvSynch

W287 Progesterone concentration required for establishment of pregnancy following embryo transfer in lactating Holstein cows. A. G. Kenyon*[1], L. G. D. Mendonca[3], G. Lopes Jr.[1], J. R. Lima[1], J. E. P. Santos[2], and R. C. Chebel[1,3], [1]*Veterinary Medicine Teaching and Research Center, University of California Davis*, *Tulare,* [2]*Department of Animal Sciences, University of Florida*, *Gainesville,* [3]*Department of Veterinary Population Medicine, University of Minnesota*, *Saint Paul*.

Objectives were to determine minimal progesterone (P4) concentration from estrous cycle d 4 to 28 necessary for establishment of pregnancy following embryo transfer (ET) in lactating Holstein cows. Cows at 30 ± 3 DIM were synchronized (d −35 PGF2α, d −28 CIDR, d −21 PGF2α and CIDR removal, d −9 GnRH, d −2 PGF2α, d 0 GnRH) and on d 0 were randomly assigned to the low progesterone (LP4, n = 28) or control (n = 55) treatments. Cows in the LP4 received 2 injections of PGF2α, on d 4 and 5, and a CIDR insert starting on d 5, which was replaced every 7 d until d 28. Blood was sampled on d −9, −2, 0, 4, 7, 14, 21, and 28 and ovaries were examined with ultrasound on d −9, −2, and 7. On d 7, all LP4 cows and control cows bearing a corpus luteum (CL) received ET. Pregnancy was diagnosed on d 28 and 67 d after ET. Proportion of cows ovulating to the GnRH on d −9 (50.6%; P=0.76) and that had luteolysis after PGF2α on d −2 (78.1%; P = 0.99) were not different between treatments. Progesterone concentrations on d −9 (6.10 ± 0.34 ng/mL; P=0.52), d −2 (0.47 ± 0.05 ng/mL; $P = 0.87$), and d 0 (1.54 ± 0.14 ng/mL; $P = 0.97$) were not different between treatments. Total CL volume on d 7 was ($P < 0.01$) smaller for LP4 cows (1.9 ± 0.6 vs. 6.1 ± 0.4 cm3). Proportions of cows pregnant at 28 (27.3 vs. 0%; $P < 0.01$) and 67 (13.0 vs. 0%; $P = 0.05$) d after ET were greater for control cows. Average P4 from d 4 to 28 was greater for control cows (3.7 ± 0.2 vs. 1.7 ± 0.3 ng/mL; $P < 0.01$), but there was ($P > 0.01$) an interaction between treatment and day as in d 4 (1.6 ± 0.2 ng/mL; $P = 0.40$) and 7 (2.4 ± 0.1 ng/mL; $P = 0.17$) there were no differences, but on day 14 (5.5 ± 0.4 vs. 2.0 ± 0.5 ng/mL; $P < 0.01$), 21 (3.5 ± 0.6 vs. 1.8 ± 0.7 ng/mL; $P = 0.06$), and 28 (5.4 ± 0.6 vs. 1.6 ± 0.8 ng/mL; $P < 0.01$) control cows had greater P4. Average P4 < 1.8 ng/mL from d 4 to 28 and P4 concentration < 2.5 ng/mL on d 14 were not conducive to establishment of pregnancy.

Key Words: progesterone, Holstein cow, embryo survival

W288 A comparison between sexed and conventional semen and some reproduction items in Iranian Holstein dairy herds. A. A. Naserian*[1], F. Karavan[2], and A. Razavi[3], [1]*Ferdowsi University of Mashhad*, *Mashhad, Iran*, [2]*Nemoneh dairy farm*, *Gorgan, Iran*, [3]*Karaj Islamic Azad University*, *Karaj, Iran*.

The aim of this study was a comparison between sexed and conventional semen and some reproduction items in Iranian Holstein dairy farms in northeast of Iran. Data were collected from computerized management software of every herd from January 2006 through December 2008. All herds, 5–10 percentage of heifers were bred with sexed semen. The female calves were bred at age 14–15 mo with 126–130 Cm height. The diets were balanced to meet or exceed the minimum nutritional requirements of heifers for a gain 0.75–0.8 Kg/d (NRC 2001). The data were analyzed with ANOVA by using the general linear model of SAS 2003. The means were comparison by the Tukey method. The results have been shown in the Table 1.Therefore, sexed semen in a new tool for producing more female calves in commercial dairy herds.

Table 1. Reproduction items amongst sexed and conventional semen heifers

Item	sexed	conventional	SEM	P-value
Age of breeding (month)	14.97	15.23	0.138	0.543
Times of AI	1.61	1.41	0.021	0.283
Birth difficulty (score)	1a	1.94b	0.016	0.001
Heifer height at breeding (cm)	125.12	126.33	1.718	0.261
Female calves (%)	85.81a	48.12b	0.981	0.001
Pregnancy length (month)	8.88	9.16	0.134	0.110

Key Words: sexed semen, conventional semen, reproduction items

W289 Dose reduction of fluorogestone acetate through partition of sponges in a program of estrus synchronization. J. L. Cordero[1], T. Sánchez[1], P. Molina[1], R. Nieto[1], J. Peralta[2], M. Cárdenas[3], O. Mejía[4], J. Nuñez[4], E. García*[5], and J. L. Figueroa[1], [1]*Programa de Ganadería, Colegio de Postgraduados*, *Texcoco, México*, [2]*ICAP, Medicina Veterinaria y Zootecnia*, *UAEH, Hidalgo, México*, [3]*INNSZ*, *México City*, [4]*CEIEPO UNAM*, *Tres Marías, México*, [5]*CUCSUR, UADG*, *Autlán Jalisco, México*.

The objective of the experiment was to determine the effect of dose reduction in sponges impregnated with fluorogestone acetate (FGA) through the partition of the same, in the main reproductive variables of Dorset ewes. Forty-four ewes were randomly assigned in four groups: Complete sponge control group, 40 mg of FGA (n=11); half sponge group, theoretically with 20 mg of FGA (n=11); one-quarter sponge group theoretically with 10 mg of FGA (n=11), and one-eighth sponge group theoretically with 5 mg FGA (n=11). Sponges remained inserted for 12 days, and 10 days after insertion all groups received a dose of 15 mg of prostaglandin (PGF2α). There was a 100% of estrous onset for groups with 40, 20 and 10 mg of FGA, but not for the 5 mg group with 81% ($P \leq 0.05$). There were no differences ($P \geq 0.05$) among treatments for gestation rate (40 and 10 mg of FGA= 100%, 20 mg of FGA= 82%, and 5 mg of FGA= 60%). Concerning to LH secretion, differences existed only in amplitude among 5 mg of FGA group (65 ± 6.40 ng mL^{-1}), compared with 40, 20 and 10 mg of FGA groups (41± 9.21; 38 ±7.94, and 23 ± 4.68 ng mL^{-1}, respectively). Under the present experimental conditions we conclude that doses of 40, 20 and 10 mg of FGA can effectively synchronize estrus in the breeding season however, 5 mg of FGA resulted in alterations in LH secretion.

Key Words: progesterone, luteinizing hormone, Dorset ewes.

W290 Neuroendocrine regulation of rearing behavior in the native Thai hen. O. Chaiyachet[1], D. Chokchaloemwong[1], N. Prakobsaeng[1], N. Sartsoongnoen[2], S. Kosonsiriluk[3], I. Rozenboim[4], M. E. El Halawani[3], T. E. Porter[5], and Y. Chaiseha*[1], [1]*Suranaree University of Technology*, *Nakhon Ratchasima, Thailand*, [2]*Nakhon Ratchasima Rajabhat University*, *Nakhon Ratchasima, Thailand*, [3]*University of Minnesota*, *St. Paul*, [4]*The Hebrew University of Jerusalem*, *Rehovot, Israel*, [5]*University of Maryland*, *College Park*.

Prolactin (PRL) circulating levels change during the avian reproductive cycle and vasoactive intestinal peptide (VIP) is the avian PRL releasing factor. This study investigated the changes in the VIP/PRL system of hens rearing their young as compared to hens deprived of rearing their chicks. The numbers of VIP-immunoreactive (VIP-ir) neurons in the nucleus infundibuli hypothalami (IN) and nucleus inferioris hypothalami (IH) of native Thai hens rearing chicks (R) were compared with those of non-rearing chicks (NR; n=4). Plasma PRL levels were determined by enzyme-linked immunosorbent assay. The numbers of VIP-ir neurons in the IN-IH on the day of hatch, and on days 4 (RD4), 7 (RD7), 10 (RD10), and 14 (RD14) of rearing were 59.4±5.9, 53.9±3.4, 30.3±1.0, 12.9±1.1, and 13.8±0.8 cells, respectively. When hens were not allowed to rear chicks, the number of VIP-ir neurons decreased as compared to their respective hens rearing chicks ($P<0.05$, NRD4=28.7±4.1; NRD7=15.3±6.6; NRD10=11.1±3.6; NRD14=14.8±2.5 cells). During the rearing period (week 1-5; n=6), PRL levels of R hens were compared (RW1 vs NRW1; 34.2±1.8 vs 27.4±1.7; $P<0.05$, RW2 vs NRW2; 37.8±7.8 vs 26.4±5.2; $P<0.05$, RW3 vs NRW3; 41.1±8.6 vs 18.5±1.5; $P<0.05$, RW4 vs NRW4; 36.3±9.6 vs 31.3±5.3, RW5 vs NRW5; 39.2±5.0 vs 27.9±4.3 ng/ml). These results indicate, for the first time, a role for the VIP/PRL system in the rearing behavior in gallinaceous avian species. It is concluded that the VIP/PRL system is not only a key regulator of incubation behavior as it is well established but it may also be involved in the regulation of rearing behavior in native Thai chicken.
Supported by The Royal Golden Jubilee Ph.D. Program; #PHD/0230/2548(YC/OC).

Key Words: birds, rearing behavior, PRL

W291 Cloning and characterization of chicken 5-hydroxytryptamine (5-HT) receptors 1A and 1B. C. F. Wong*, A. H. Y. Kwok, J. C. W. Ho, Y. Wang, and F. C. Leung, *The University of Hong Kong*, *Hong Kong, HKSAR, China*.

The aim of this study is to clone and characterize 5-hydroxytryptamine (5-HT; serotonin) receptors, HTR1A and HTR1B, from chicken. 5-HT is a monoamine neurotransmitter derived from tryptophan and is believed to be involved in a broad range of biological activity including mitogenesis of smooth muscle cells, psychological disorders like schizophrenia, anxiety and depression, and neuroendocrine functions like regulation of ACTH, glutamate and dopamine release, via interaction with a large family of G protein-coupled receptors. However, these receptors were not well studied in avian species. In this study, the full-length genes were cloned from chicken by PCR. HTR1A gene encodes a putative 413-amino acid protein, which shares 80%, 80% and 78% identity with human, chimpanzee and mouse homologues, respectively. Similarly, HTR1B gene encodes a putative 379-amino acid protein, which shares 82%, 82% and 86% identity with human, chimpanzee and mouse homologues respectively. Using a pGL3-CRE luciferase reporter system, activation of both HTR1A and HTR1B by 5-HT were found to inhibit forskolin-stimulated luciferase activity in CHO cells, suggesting that both HTR1A and HTR1B are functionally coupled to Gi protein(s). Further characterization of HTR1A and HTR1B will shed light on the study of biological functions of 5-HT in chickens.

Key Words: chicken, 5-hydroxytryptamine, 5-hydroxytryptamine receptor

W292 Ergovaline and other ergopeptine alkaloids inhibit vesicular glutamate transporter (VGLUT)-mediated activity of bovine synaptic vesicles. Y. Xue*[1], J. R. Strickland[2], J. A. Boling[1], and J. C. Matthews[1], [1]*University of Kentucky*, *Lexington,* [2]*USDA-ARS, Forage-Animal Production Research Unit*, *Lexington, KY*.

L-Glutamate (Glu) is the major excitatory neurotransmitter responsible for the glutamatergic neurotransmission in the vertebrate central nervous system, including the gastrointestinal tract (GIT) of cattle. The vesicular Glu transporters VGLUT1 and VGLUT2 concentrate (50 m*M*) Glu (K_m = 1 to 4 m*M*) into synaptic vesicles (SV) for subsequent release into the synaptic cleft of glutamatergic neurons. To test the hypothesis that ergopeptine alkaloids inhibit VGLUT activity of bovine cerebral SV, a SV Glu uptake (vacuolar H^+ ATPase-dependent) model was developed. The effect of ergopeptine alkaloids on VGLUT activity was tested on SV isolated from cerebral tissue of Angus-cross steers that were naive to ergot alkaloids. Data were analyzed by ANOVA using GLM. Immunoblot analysis (n = 8) validated the presence of VGLUT1, VGLUT2, synaptophysin 1, and vacuolar H^+ ATPase proteins in purified SV. Functional analysis of the mean (n = 3, ± SE) SV VGLUT activity (50 μ*M*) was ATP- and vacuolar H^+ ATPase-dependent, and saturatable (apparent K_m = 1.53 ± 0.18 m*M*). IC_{50} experiments (n =3) revealed that VGLUT Glu uptake (50 μ*M*) was inhibited ($P \leq 0.048$) by ergopeptine alkaloids: bromocriptine (2.83 ± 0.59 μ*M*) < ergotamine (20.5 ± 2.77 μ*M*) < ergocornine (114 ± 23.1 μ*M*) < ergovaline (137 ± 6.55 μ*M*). Subsequent ergovaline K_i experiments (n = 3; Glu = 0.05, 0.10, 0.50, 1, 2, 4, 5 m*M*) demonstrated no change ($P = 0.332$) in apparent K_m. However, the V_{max} of Glu uptake was decreased ($P = 0.016$) when evaluated in the presence of 50, 100, and 200 μ*M* ergovaline, suggesting that ergovaline inhibits SV VGLUT activity through a non-competitive mechanism. The findings of this study suggest cattle with fescue toxicosis may have a reduced glutamatergic neurotransmission capacity. Thus GIT functions, including feed intake and digestion, may be impaired in cattle consuming ergopeptine alkaloids.

Key Words: bovine, ergot alkaloids, fescue toxicosis, glutamate transport, glutamatergic neurotransmission

W293 Comparison of the somatotropic axis of two precocial free-ranging ice seal species: harp (*Phoca groenlandica*) and hooded (*Cystophora cristata*). C. E. Anderson*[1], J. P. Richmond[1], J. M. Burns[2], and S. A. Zinn[1], [1]*University of Connecticut*, *Storrs,* [2]*University of Alaska-Anchorage*, *Anchorage*.

To determine if components of the somatotropic axis in marine mammals are associated with differing life history and maternal investment strategies, blood samples and morphometrics were collected from 35 free-ranging North Atlantic ice seals [hooded seals (*Cystophora cristata*), n = 15; and harp seals (*Phoca groenlandica*), n = 20] ranging in age from newborn to adult. For each species, animals were categorized as nursing, late nursing, weaned, and adult based on size, umbilical status, and pelage. Within a species, there were 5 individuals per category except there were no hooded seal pups categorized as late nursing due

to the 4 –d lactation. Radioimmunoassays were used to quantify serum IGF-1 and GH, using bovine and human antisera, respectively. Data were analyzed with the Proc Mixed function of SAS and included species and age as independent variables. On average hooded seals gained 24 ± 11 kg BW (6 kg/d) and 3.4 ± 0.2 cm of blubber during the 4-d nursing period ($P < 0.01$), without an increase in length (99.6 ± 3 cm; $P = 0.92$). During the 12-d lactation harp seal pups increased BW 34 ± 1.5 kg (8 to 42 kg; 2.8 kg/d), standard length 25 ± 3 cm (76 to 101 cm), and blubber depth 3.8 ± 0.2 cm ($P < 0.01$). Concentrations of GH were similar in hooded seal neonates and late nursing pups (7.5 and 6.24 ± 2.0 ng/mL; $P = 0.66$), but declined in harp seals for these periods ($P = 0.01$; 18.9 to 5.6 ± 2.0 ng/mL). Average IGF-1 was similar in neonates of both species (250 ± 44 ng/mL; $P = 0.52$) and increased in both harp and hooded seals during nursing (434 and 345 ± 44 ng/mL; $P = 0.01$). Coinciding with the post-weaning fast, harp seal IGF-1 rapidly declined from 434 to 120 ± 44 ng/mL, whereas GH increased from 5.6 to 12.4 ± 2.0 ng/mL ($P < 0.01$). Adult hooded seals were larger (293 ± 22 vs. 109 ± 22 kg) with greater IGF-1 (289 vs. 108 ± 32 ng/mL; $P < 0.01$) than adult harp seals, but there were no differences in GH (5.2 ± 1.2 ng/mL; $P > 0.10$). Concentrations of IGF-1 and GH reflect nutrient intake and growth rate during nursing and the post weaning fast in these precocial pinnipeds.

Key Words: pinnipeds, insulin-like growth factor-1, growth hormone

W294 Effects of age and sex on hematologic and serum biochemical values of broiler chickens. A. Viveros*[1], A. Brenes[2], I. Arroyo[1], M. Bascuñana[1], A. Angosto[1], and M. L. Fermin[1], [1]*Facultad de Veterinaria, UCM*, *Madrid, Spain*, [2]*Instituto del FRIO-ICTAN, CSIC*, *Madrid, Spain*.

Due to lack of reference values for avian blood profiles, hematological and serum biochemical reference values may provide valuable information about the health status of broiler chickens. An experiment was conducted to study the effects of age and sex on hematological and serum biochemical values for 7 weeks of age. A total of 120, 1-d-old male and female broiler chickens (Cobb strain), were randomly assigned to 20 cages (6 chicks per cage). Blood samples were collected weekly by cardiac puncture and analyzed for red blood cell count (RBC), hemoglobin content (Hb), packed cell volume (PCV), mean corpuscular volume (MCV), mean corpuscular hemoglobin (MCH), mean corpuscular hemoglobin concentration (MCHC), and white blood cell count (WBC), heterophil (He), basophil (Ba), eosinophil (Eo), lymphocyte (Ly), monocyte (Mo) and thrombocyte counts. Serum biochemical analysis included total protein, albumin, glucose, triglycerides, cholesterol, bile acids, uric acid, amylase, CPK, LDH, AST, calcium, phosphorus, and sodium. This study showed that age affects the hematological and serum biochemical values of the male and female broiler chicks. With increasing of age, the erythrocytic parameters (except MCV and MCH) and leukocytic parameters (except lymphocyte) were increased ($P < 0.001$), but MCV, MCH and absolute count of lymphocyte were decreased ($P < 0.001$). Regarding serum biochemical values, glucose, total protein, albumin, triglycerides, cholesterol, bile acids, CPK, LDH, AST, and phosphorus concentrations were increased ($P < 0.001$) and uric acid and amylase levels were decreased ($P < 0.001$) during breeding period. In comparison to male broilers, female broilers had higher ($P < 0.05$) RBC, Hb, and PCV levels ($P < 0.05$), and lower ($P < 0.001$) MCV, MCH, and heterophil values. Likewise, compared to male broilers, female broilers had higher ($P < 0.01$) levels of total protein, albumin, triglycerides, amylase, CPK, and AST, and lower ($P < 0.05$) levels of bile acids and uric acid. In conclusion, this study provided new information about age and sex-related changes of hematological and serum biochemical values in broiler chickens.

Key Words: chickens, hematological values, serum biochemical parameters

W295 Serum metabolite response of hens submitted to a second molt using soy hulls. H. Mazzuco*, L. S. Lopes, A. Coldebella, and V. S. Avila, *EMBRAPA Swine & Poultry*, *Concordia, SC, Brazil*.

In our previous study, similar physiological responses were observed for some blood metabolites of hens submitted to alternative and conventional molting methods. The present research was conducted to assess selected blood serum metabolites in laying hens induced to a second molt at the end of their 2nd laying cycle. 450 Hy-Line W-36 hens housed two per cage (759 cm2/bird) were molted at 142 wks of age and assigned to 5 treatments in a randomized complete block design (9 replicates/10 hens). The treatments were: Full-fed (FF), Conventional molt (CM, 10 d fasting) and alternative molt diets consisting of 95%, 85% or 75% of soy-hulls. Hens consumed the molting diets (except CM group) during 10 d and then were all fed cracked corn for 8 d followed by a pullet developer diet for 10 d. The serum metabolites evaluated were total calcium (TCa), ionized calcium (iCa), glucose (GLU), cholesterol (CHO), tryglicerides (TGL), high-density lipoproteins (HDL) and low-density lipoproteins (LDL). Samples of blood (5 mL) were taken from each hen and processed using a commercial kit on days 10 and 28 of molt, when birds were 143 and 146 wk-old, respectively. All data were subjected to ANOVA considering the effects of day of molt, treatment and interactions. Significant treatment × day of molt effects were observed in CHO ($P < 0.05$), HDL and LDL profiles ($P < 0.05$ and $P < 0.01$, respectively). CHO were higher for CM hens at 10 d of molt but not at 28 d, when FF hens showed higher levels. Lower levels of HDL were found in FF hens at 28 d of molt compared to the molted hens and at 10 d of molt, LDL levels were higher for FF. Treatment effect ($P < 0.01$) was observed for TCa and TGL. Highest levels of TCa and TGL at both days of molt were observed on FF hens. Day of molt influenced GLU and iCa ($P < 0.0001$) and higher levels at 28 d than 10 d were observed for both variables. During a second molt, changes in the circulating levels of blood metabolites reflected the dietary effects and for some, followed related patterns observed on hens in their first molt.

Key Words: blood calcium, serum lipoproteins, third cycle

W296 Pulmonary vascular pressure profiles in broilers selected for susceptibility to pulmonary hypertension syndrome: Age and gender comparisons. R. F. Wideman*, M. L. Eanes, K. R. Hamal, R. Klintworth, and N. B. Anthony, *University of Arkansas*, *Fayetteville*.

Broilers that are susceptible to pulmonary hypertension syndrome (PHS, ascites) have an elevated pulmonary arterial pressure (PAP) when compared with PHS-resistant broilers. Two distinctly different syndromes, pulmonary arterial hypertension (PAH) and pulmonary venous hypertension (PVH), both are associated with increases in PAP. Pulmonary arterial hypertension occurs when the right ventricle must elevate the PAP to overcome increased resistance to flow through restrictive pulmonary arterioles upstream from the pulmonary capillaries. In contrast, PVH is commonly caused by increased downstream (post-capillary) resistance. The sites of resistance to pulmonary blood flow are deduced by making contemporaneous measurements of the PAP and the wedge pressure (WP), and calculating the trans-pulmonary pressure gradient (TPG = PAP-WP). We obtained PAP, WP and TPG values from 8,12,16,20 and 24 wk old anesthetized male and female broilers from a PHS-susceptible line (IACUC Protocol #08036). Pressures were

recorded as a catheter inserted into a wing vein was advanced to the right atrium, right ventricle, main trunk of the pulmonary artery, and onward until the WP was obtained. Gender and age interactions were evaluated using the SigmaStat ANOVA package. To further characterize the relationship between PAP, WP and TPG the data also were pooled into three cohorts to compare vascular pressures in birds having the lowest PAP values (n = 52; range: 12 to 22.9 mmHg), intermediate PAP values (n = 63; range: 23 to 32.9 mmHg), and highest PAP values (n = 62; range: 33 to 62 mmHg). Within each of the age, gender and PAP cohort comparisons, broilers with elevated PAP consistently exhibited the hemodynamic characteristics of PAH (elevated PAP and TPG combined with a normal WP) but not PVH (elevated PAP and WP combined with a normal or reduced TPG). Susceptibility to PHS can be attributed primarily to pulmonary arterial hypertension associated with increased pre-capillary (arteriole) resistance.

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Key Words: broiler, pulmonary hypertension, ascites

W297 Regulatory effects of individual essential amino acids on casein synthesis rates in bovine mammary tissue slices. J. A. D. R. N. Appuhamy*, T. R. Wiles, and M. D. Hanigan, *Department of Dairy Science, Virginia Polytechnic Institute and State University*, *Blacksburg*.

In mammalian cells, amino acids are able to stimulate protein synthesis by phosphorylating mammalian target of rapamycin (mTOR) and ribosomal protein S6 (rpS6), and dephosphorylating eukaryotic elongation factor 2 (eEF2). Little work has explored the effects of these signals on milk protein synthesis in bovine mammary glands. The objective of this study was to investigate the effects of individual essential amino acid (EAA) deficiencies on cellular signals and protein synthesis rates in mammary tissue slices. Slices were prepared from the rear quarter of four lactating cows immediately after slaughter and incubated in serum free DMEM/F12 media containing all EAA (+EAA); media deprived of Arg, His, Ile, Leu, Lys, Met, Phe, Thr, Trp, or Val; or media deprived of all EAA (-EAA). After 1 h, 2D5-Phe was dosed into media and incubations continued for another 30 min. Cell lysates were subjected to Western immunoblotting analysis to determine total and phosphorylated mTOR (Ser2448), rpS6 (Ser235/236), and eEF2 (Thr56) and GC-MS analysis to determine 2D5-Phe enrichment (proportional to protein synthesis rates) in protein precipitated at pH=4.6 (enriched for casein). The –EAA treatment caused the phosphorylation state (PS) of mTOR and rpS6 to decrease by 46 and 76%, respectively, PS of eEF2 to increase by 136%, and protein synthesis to decrease by 46%. Phosphorylation of mTOR was positively correlated (r=0.80) with Phe enrichment. Deprivation of Leu resulted in the greatest reduction of PS for mTOR (46%) and rpS6 (51%) whereas Met deprivation was associated with the greatest PS increase for eEF2 (64%). The greatest reductions in protein synthesis were associated with Ile (58%), Leu (47%), and Met (45%) deprivations. Essential amino acids, in particular Leu and Met had substantial regulatory effects on protein synthesis efficiency in bovine mammary tissues, and a significant proportion of the signaling appeared to be mediated by mTOR.

Key Words: essential amino acid deprivation, casein synthesis rate, mTOR

W298 In vivo effects of insulin and dietary protein level on signaling proteins for protein synthesis in the mammary glands of lactating dairy cows. W. A. D. Nayananjalie*[1], A. G. Rius[1], D. Kirovski[2], J. A. D. R. N. Appuhamy[1], J. Escobar[1], and M. D. Hanigan[1], [1]*Virginia Polytechnic Institute and State University*, *Blacksburg,* [2]*University of Belgrade*, *Serbia*.

Insulin and amino acids have been found to significantly enhance muscle protein synthesis by signaling through mammalian target of rapamycin (mTOR) and in turn ribosomal protein S6 (rpS6), eukaryotic initiation factor 4E binding protein 1 (4EBP1), and eukaryotic elongation factor 2 (eEF2). Insulin also stimulates mTOR through Akt. Increased phosphorylation (PhS) of Akt, mTOR, rpS6 and 4EBP1 and decreased PhS of eEF2 stimulates protein synthesis. We hypothesized that insulin and amino acid supply would also cause a change in the PhS of these proteins to promote protein synthesis in bovine mammary glands. The effects of infused insulin and varying dietary protein on total and phosphorylated forms of Akt, mTOR, rpS6, 4EBP1, and eEF2 in mammary tissues of lactating dairy cows were examined. Cows were fed two levels of dietary crude proteins (17.5 or 14.0% of dietary DM) and infused with two levels of insulin (0 or 1 μg/kg BW) under euglycemic conditions in a 2 × 2 factorial design. At the end of each treatment period mammary tissue biopsies were harvested. Tissue homogenates were subjected to Western immunoblotting analysis for total and phosphorylated forms of Akt (Ser473), mTOR (Ser2448), rpS6 (Ser235/236), 4EBP1 (Thr37/46), and eEF2 (Thr56). Increasing dietary protein level increased ($P = 0.02$) PhS of Akt. Neither dietary protein nor insulin had significant effects on PhS or total mTOR expression. However, increased dietary protein and insulin infusion significantly increased both the PhS ($P < 0.01$) and total 4EBP1 ($P = 0.03$) expression. Total rpS6 expression ($P = 0.02$) but not PhS was increased when insulin was infused. Increased dietary protein was associated with greater total eEF2 ($P = 0.04$) expression. Increased rpS6 expression and increased PhS of 4EBP1 should stimulate protein synthesis, but the lack of change in mTOR PhS would not be stimulatory.

Key Words: insulin, dietary protein, signaling protein

W299 A novel multiplex real-time PCR assay for bovine liver pyruvate carboxylase 5′ UTR variants during the transition to lactation. H. M. White*, S. L. Koser, and S. S. Donkin, *Purdue University*, *West Lafayette, IN*.

Pyruvate carboxylase (PC; EC 6.4.1.1) is a key enzyme in glucose and energy metabolism. The bovine PC gene contains three promoter sequences (P3, P2, and P1 from 5′ to 3′) and is regulated by physiological changes such as the onset of calving and feed restriction. Expression of P1 is glucogenic and lipogenic tissue specific and codes for 5′ UTR A, B, C, and F whereas P2 and P3 are expressed in several tissues and code for 5′ UTR E and D, respectively. The objective of this study was to develop a multiplex real-time RT-PCR assay for bovine PC 5′ UTR variants and to characterize their expression during the transition to lactation. The multiplex assay was designed to quantify the PC coding region, 5′ UTR D, E, and F mRNA, as proxy measures for their relative promoter activities. Combined expression of 5′ UTR A, B, and C mRNA was determined by difference. Liver biopsy samples were collected from eight multiparous Holstein cows at −28, +1, and +28 days relative to calving (DRTC). Expression of PC mRNA was increased ($P < 0.05$) by 6-fold at +1 DRTC compared to precalving levels. Expression of variants from P1 was greater ($P < 0.05$) than variants from P2 or P3. Expression of 5′ UTR F from P1 was decreased ($P < 0.05$) and the combined expression of 5′ UTR A, B, and C from P1 increased ($P < 0.05$) at +1 DRTC. There was no effect ($P \geq 0.05$) of DRTC on 5′ UTR D or E mRNA expression. Increased expression of PC mRNA at calving is due to an increase in activity of PC promoter 1 and a lack of change in activity of PC promoters 2 and 3. These data suggests that the onset of calving leads to activation of factors specific to targets on bovine PC promoter 1.

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Key Words: pyruvate carboxylase, multiplex qPCR, transition cow

W300 Embryo quality characteristics from superovulated cows receiving a blend of bioactive peptides and oligosaccharides to support immune function (Grade One). G. H. L. Marquezini[1], V. R. G. Mercadante[1], M. M. Ward*[2], A. R. Spell[3], J. A. Carter[3], N. D. Paton[4], and G. C. Lamb[1], [1]*University of Florida*, *Marianna, FL*, [2]*Provimi North America, Inc.*, *Brookville, OH*, [3]*Advanced Reproductive Associates*, *Daphne, AL*, [4]*Provimi Holding, BV*, *Rotterdam, Netherlands*.

We determined whether supplementation of a blend of bioactive peptides and oligosaccharides to support immune function (Nutrition Horizons Grade One; Brookville, OH; US Patent no. 6,962,718) would alter quality, stage, and fertilization rate of embryos recovered after superovulation. Angus and Brangus cows were superovulated using follicle stimulating hormone as NIH-FSH-P1 and were stratified by breed before random assignment to treatment: 1) donors received 6 Grade One capsules (13 g/capsule) containing a blend of bioactive peptides and oligosaccharides (NHG1; n = 35); or 2) donors received 6 placebo capsules (13 g/capsule; Control; n = 37). Superovulation was initiated with a CIDR on d 0, 8 injections of FSH at 12 h intervals initiated on d 4, plus two injections of PGF 12 h apart on d 7. At 0 and 12 h after detected estrus cows received an AI. Boluses were inserted into the esophagus utilizing a balling gun. Cows received two boluses at CIDR insertion (d 0), at the first (d 4), and third (d 5) injection of FSH. Embryos were collected 7 d after first detected estrus and were recovered by nonsurgical embryo collection procedure and embryos were classified by stage and quality. Data was analyzed with PROC MIXED using flush as the experimental unit. Total ova (14.1 ± 1.8) and transferable embryos (5.2 ± 1.1) per flush for NHG1 and Control, did not differ. Mean number of grade 1 (2.5 ± 0.8) and 2 (2.7 ± 0.5) and no differences existed between treatments for degenerate (1.9 ± 0.4) or unfertilized ova (7.0 ± 1.4). However, the percentage of grade 1 embryos collected compared to recovered transferable embryos was greater ($P = 0.062$) for NHG1 (39.4%) than Control (23.4%). In addition, the percentage of grade 2 embryos collected compared to recovered transferable embryos was greater ($P < 0.05$) for Control (76.6%) than NHG1 (59.9%). We conclude that the number of transferable embryos collected per flush did not differ between treatments; however, the quality of transferable embryos was improved after embryo donor cows received NHG1 prior to embryo collection.

Key Words: embryo transfer, superovulation, immune function

W301 Evaluation of a distinct white Angus crossbred phenotype in southern Florida. P. G. M. A. Martins*[1], R. Cassiolato[1], F. Frigoni[1], M. M. Salin[1], D. B. Araujo[1], M. Meneghetti[1], G. C. Lamb[1], D. G. Riley[2], B. H. Carter[2], T. H. Friend[2], and J. D. Arthington[1], [1]*University of Florida, Range Cattle Research and Education Center*, *Ona,* [2]*Texas A&M University, Department of Animal Science*, *College Station*.

A distinct beef phenotype has emerged from offspring of Angus × Brahman × Charolais cows being mated to Simbrah bulls. A proportion of these female offspring, when mated to black Angus bulls, produced offspring with white hair coats. This phenotype persists in a majority of these heifers through a second cross with black Angus bulls resulting in white Angus crossbred calves with 75% black Angus genetics. The white hair coat of these offspring is thought to be derived from the dilution gene effects from the Charolais and Simmental breeds. The objectives of these initial studies were to compare body temperature and grazing behavior among these white and black phenotypes. In the first study, vaginal temperatures were assessed over 2 consecutive yr (n = 5 black and white phenotypes/yr). Temperatures were recorded over 5 consecutive summer days using an automated temperature logger (5.9 × 16.3 mm) placed in an intravaginal device. During the assessment period, heifers grazed a single pasture with no access to shade. In the second experiment, voluntary forage DMI was assessed in a fully shaded facility using weaned, yearling heifers (n = 9 black and 6 white) over a 42-d evaluation period. Heifers were provided free choice access to ground hay with grain supplement provided at 0.5% BW. Grazing behavior was evaluated in a subset of these heifers (n = 5 black and 5 white) by observing time spent in and out of shade and standing or lying over 10 individual 12-h observation periods (twice weekly; 5 wk). Average peak vaginal temperatures were 1.1 °C greater ($P < 0.001$) in black vs. white heifers (40.5 and 39.4 °C). There were no differences ($P = 0.15$) in voluntary forage intake when heifers were evaluated under full shade (1.49 vs. 1.27% BW for black and white heifers, respectively; SEM = 0.115); however, pasture observations during the summer daylight hours revealed that black heifers spent 7.4% more ($P < 0.01$) time in the shade compared to white heifers. These results suggest that Angus (50 to 75% black Angus) crossbred heifers with a white hair coat have a reduced non-shaded peak body temperature compared to black Angus cohorts. This reduction in body temperature may result in greater grazing times during the summer months in southern Florida.

Key Words: Angus, coat color, grazing

W302 The relationship of pulmonary arterial pressure with feed efficiency, performance, temperament, and feeding behavior in growing beef cattle. T. D. Maddock*, G. H. L. Marquezini, V. R. G. Mercadante, and G. C. Lamb, *University of Florida*, *Marianna*.

We examined whether pulmonary arterial pressure (PAP) has a relationship with feed efficiency, performance, temperament, or feeding behavior in growing beef cattle. Calves (n = 213; bulls, n = 107; heifers, n = 106; Angus and Angus-cross, n = 118; Charolais, n = 38; Zebu and Zebu-cross, n = 57; initial BW = 317 (SD = 39) kg) were placed in a feed intake facility and after 21 d of adaptation, daily DMI was recorded for 70 d. Diets (NEm = 1.34 Mcal/kg; NEg = 0.77 Mcal/kg; CP = 117 g/kg) were offered ad libitum. Ultrasound 12th rib LM area and fat depth (BF) and PAP (mg Hg) were measured on d 0 and 70. Chute score and exit velocity were measured on d 0, 35, and 70. Residual feed intake (RFI) was calculated by regressing ADG and mid-metabolic BW on daily DMI. Animals were classified as high, average, or low PAP (> 0.5 SD, ± 0.05 SD, and < 0.5 SD from the mean, respectively; mean PAP = 37.0, 32.6, 28.2, respectively). Least squares procedures using PROC MIXED of SAS were used to examine the effect of PAP group on other variables. Pearson correlation coefficients among traits were determined using the CORR procedure of SAS. There was no association between PAP and RFI, DMI, ADG, or G:F, but PAP was positively correlated to initial BF (r = 0.29, $P < 0.001$) and final BF (r = 0.19, $P = 0.009$) and was negatively correlated with chute score (r = –0.18, $P = 0.01$). Cattle with high PAP had lower RFI than those with average ($P = 0.03$) and low ($P = 0.04$) PAP. Cattle with low PAP had lower DMI, ADG, and G:F than cattle with average ($P = 0.008$, $P = 0.005$, $P = 0.05$, respectively) and high PAP ($P = 0.005$, $P < 0.001$, $P = 0.005$, respectively). Cattle with high and average PAP had a greater number of daily feeding events (consumed > 100 g DM) than low PAP cattle ($P = 0.02$, $P = 0.002$, respectively). There was no effect of PAP group on other feeding behavior traits, including daily feeding duration or eating rate (g DM/min). There was not a strong association between

PAP and performance traits, but calves with low PAP had lower intake, performance and subsequently lower feed efficiency.

Key Words: beef cattle, feed efficiency, pulmonary arterial pressure

W303 Technical and economic performance of a beef cattle production system: A case study in Bahia State, Brazil. F. A. Barbosa*[1], D. S. Graça[2], V. J. Andrade[2], I. M. Cezar[3], and R. C. Souza[2], [1]*University of Brasília (UnB)*, *Brasilia,DF, Brazil*, [2]*School of Veterinary Medicine, Federal University of Minas Gerais (UFMG)*, *Belo Horizonte, MG, Brazil*, [3]*Anhanguera-Uniderp University*, *Campo Grande, MS, Brazil*.

A case study on the transition from beef cattle breeding, rearing and fattening system to a cow-calf production system was assessed in the State of Bahia, Brazil, including production and economic performance over a four year period (January 2000 to December 2004). Production and economic data were collected using control software (Congado) and analyzed by electronic spreadsheets (Microsoft Excel). The system was developed exclusively on a grazing system of 2,926 hectares with a base herd comprised of Zebu (Tabapuã breed) and crossbred *Bos taurus* × *Bos indicus* cattle. During the rainy season the herd was fed mineral supplement based on a specific formulation for each animal category. Introduction of technologies related to pasture, feeding supplementation, breeding program, animal health practices, associated with technical-administrative management improved the animal performance indexes. Mean stocking rates ranged from 0.9, 1.3, 1.5, 1.4 to 1.5 heads/ha in 2000, 2001, 2002, 2003 and 2004, respectively. Annual mean rates of pregnancy, birth and weaning were 88.8%, 85.1% and 82.6%, respectively. As result of introduction crossbreeding, the mean weights at weaning and at slaughtering of males achieved 228.87 and 485.16 kg, respectively, with mean age at slaughtering of 24.6 months. Total accumulated cost was US 1,799,623.57. The total income of US 1,734,569.69 was not enough to pay the opportunity cost, resulting in a negative return on invested capital (RIC). The activity yielded total operating profit of US 484,194.82 during the five years evaluated. Mean RICs were 10.78% and 1.29% on operating and total profit, respectively. Estate valuation changed the return on the invested capital accumulated from the business to 9.75%. The implantation of a series of technologies improved animal performance indexes in the semi-intensive complete cycle system. The economic results indicated that the activity paid all operating costs but could not totally pay the opportunity cost.

Key Words: animal performance indexes, cost, profitability

W304 Economic efficiency and productivity of life-cycle beef cattle production systems in Bahia State, Brazil. F. A. Barbosa*[1], D. S. Graça[2], V. J. Andrade[2], I. M. Cezar[3], and R. C. Souza[2], [1]*University of Brasília (UnB)*, *Brasília, DF, Brazil*, [2]*School of Veterinary Medicine, Federal University of Minas Gerais (UFMG)*, *Belo Horizonte, MG, Brazil*, [3]*Anhanguera-Uniderp University*, *Campo Grande, MS, Brazil*.

Economic efficiency and productivity of three life-cycle cattle production systems were simulated using four different calving rates (CR): SCC - 87%; −4CR- 83%; −2CR - 85%; +2CR - 89%. This evaluation used case study data and simulated the effect of variation in calving rates on economic returns. Production and economic data were collected using control software (Congado) and analyzed by electronic spreadsheets (Microsoft Excel). The base system (SCC) was developed on grazing system of 2,926 hectares composed of Zebu cattle (Tabapuã breed) and crossbred *Bos taurus* × *Bos indicus* cattle (n=3453). Data were collected from this herd from January of 2000 to December of 2002. During the rainy season the herd was fed mineral supplement based on a specific formulation for each animal category. Systems −4 CR, −2CR and +2CR were simulated based on adjusted calving rates fluctuations according to energy requirement and herd composition during a three year periods. Liveweight sold were 149, 146, 144 and 141 kg/ha/year for −4CR, −2CR, SCC and +2CR, respectively. Accumulated profit were US 329,490.77; 311,271.28; 306,842.04 and 297,082.63 for −4CR, −2CR, SCC and +2CR, respectively. Returns over accumulated invested capital were 7.8, 7.4, 7.3 and 7.0% for −4CR, −2CR, SCC and +2CR, respectively. Calving rate fluctuation modified the economic efficiency and productivity of simulated production systems. Economic efficiency and productivity results decreased as calving rate increased.

Key Words: calving rate, cost, profitability

W305 Economic viability of breed Nelore and crossbreed F1 Nelore × Brahman produced in feedlot. R. A. Mandarino*, F. A. Barbosa, I. S. Silva, J. M. S. Diogo, and L. A. Chaves, *University of Brasília (UnB)*, *Brasília, DF, Brazil*.

The experiment evaluates the costs of production and economic viability of the feedlot, divided into two genetic groups and subjected to three diets. The experiment was conducted from August to November 2009, lasting 96 days. We used 42 bulls with an average age of 23 months, and 21 breed Nellore (NEL) and 21 crossbreed NellorexBrahman (NBR). Each genetic group was divided into three diets, with 7 animals each: SIL - corn silage and concentrate (corn grain, soybean meal, soybean hulls, urea and mineral supplement) at a ratio of 25:75 (in dry matter), PEL - exclusive diet of pellets; GRN - diet with whole grain corn and pellets. The experiment was conducted in a completely randomized in a 2 × 3 factorial, divided as follows: NELSIL, NELPEL, NELGRN, NBRSIL, NBRPEL and NBRGRN. The feeding costs were calculated using the daily offered quantity for each treatment and divided by the respective number of bulls. The labor costs and depreciation were divided by the bulls. The total operating cost (TOC) was calculated by summing the costs for food, labor costs (US 10.20 / beef) and depreciation (US 3.80/beef). The net margin per kg of carcass was obtained by difference between total revenue/kg and TOC/kg. The average initial body weights (IP) were: 350.7, 350.6, 355.8, 379.2, 375.7 and 376.1 kg for NELSIL, NELPEL, NELGRN, NBRSIL, NBRPEL and NBRGRN respectively. Mean weight (PF) were: 500, 464.4, 479.6, 510.7, 571.8 and 501.5 kg for NELSIL, NELPEL, NELGRN, NBRSIL, NBRPEL and NBRGRN respectively. TOC for Nellore in the period were US 215.0, 182.1, 195.4, 165.2, 180.3 and 222.6 to NBRSIL, NBRPEL, NBRGRN, NELGRN, NELPEL and NELSIL, respectively. The total operating cost per kg carcass were US 2.20, 2.06, 1.96, 1.64, 1.86 and 1.90 to NBRSIL, NBRPEL, NBRGRN, NELGRN, NELPEL and NELSIL, respectively. The net margin per kg of carcass were US 0.52, 0.65, 0.76, 1.08, 0.86 and 0.82 for NBRSIL, NBRPEL, NBRGRN, NELGRN, NELPEL and NELSIL, respectively. All treatments were economically viable, and the NEL with numerically higher net margin than the NBR, and diet GRN exceeding PEL and SIL.

Key Words: beef cattle, costs, genetic group

W306 Monitoring diet quality and body condition in beef cows grazing Arizona rangeland. D. R. Tolleson* and D. W. Schafer, *The University of Arizona*, *Tucson*.

Nutrition is the highest input cost in beef production. Monitoring the nutritional status of range cows is difficult. Near infrared spectroscopy (NIRS) of feces has been used to predict diet quality in cattle. When fecal NIRS is coupled with decision support software such as the Nutritional

Balance Analyzer (NutbalPro); nutritional status and animal performance can be monitored. Few reports on the applicability of these two methods exist for the southwestern US. Approximately 120 Hereford and 90 CGC composite (50% Red Angus, 25% Tarentaise, 25% Charolais) cows grazing in a single herd were used in a study to determine the ability of fecal NIRS/NutbalPro to project body condition score (BCS, 1 = thin, 9 = fat) under commercial scale rangeland conditions in central Arizona. Cattle were rotated across the 31,000 ha allotment at 10 to 20 day intervals. Fecal samples were collected in the pasture ~ monthly at the midpoint of each grazing period. A sample consisted of ~100g feces each from 5 to 10 animals of each breed. Samples were frozen and later analyzed by NIRS for prediction of diet crude protein (CP) and digestible organic matter (DOM). Fecal sampling occurred from November 2007 to October 2009. Cattle BCS was recorded for 10 to 30 individuals from each breed type at the time of fecal sampling beginning in November 2008. Along with fecal NIRS predicted diet quality, animal breed type and reproductive status characteristics, and environmental conditions were input to the NutbalPro software for each fecal sampling/BCS date (November 2008 to October 2009). Diet quality varied from a minimum of 5.24% CP and 56.89% DOM in January 2009 to a maximum of 14.61% CP and 62.87% DOM in August of 2008. Diet quality was related to observed seasonal changes and precipitation events. Projected BCS averaged 0.2 ± 0.06 score different than observed BCS (R^2 = 0.75, SE = 0.19, $P < 0.01$). The greatest difference in projected versus observed BCS occurred during periods of lowest diet quality. Body condition was predicted accurately enough to be useful in monitoring the nutrition of range beef cows under the conditions of this study.

Key Words: beef cattle, rangeland, near infrared spectroscopy

W307 Influence of residual feed intake, breed of sire and dam on the performance and carcass characteristics of early weaned steers during the feedlot phase. C. O. Trejo*, D. B. Faulkner, J. M. Dahlquist, and T. G. Nash, *University of Illinois*, *Urbana*.

Improving feed efficiency through management practices has become of more importance to the beef industry. The objectives were: (1) evaluate the effect of breed of sire and dam on the performance and carcass characteristics of early weaned steers (EW) during the feedlot phase; and (2) evaluate the effect of residual feed intake (RFI), breed of sire and dam on meat tenderness of EW. One hundred and fifty eight Angus (A), Simmental (S), Angus-Simmental, and Simmental-Angus steers were used across two different years. Animals were early weaned at 56 d of age. Animals were allotted to pens by weight and fed a common diet. Forty five steers classified in the high (H) RFI group and 113 steers in the low (L) RFI group. No differences were detected for initial weight (IW), adjusted final weight (AFW), and average daily gain (ADG). Steers in the H RFI group were 12% less efficient ($P < 0.0001$) than steers in the L RFI group. RFI differed ($P < 0.0001$) between H and L RFI groups. High RFI steers ate 1.5 kg more of expected feed intake. For carcass characteristics, only kidney, pelvic, and heart fat % (KPH) differed ($P = 0.0051$) between RFI groups. Meat tenderness did not differ between the RFI groups. Breed of sire had no effect on the performance characteristics. Breed of dam differed for IW ($P < 0.0001$), AFW ($P = 0.0014$), and RFI ($P = 0.0433$). For RFI, steers from S dams ate 0.5 kg/d less of expected feed intake. Steers from A sires had 0.33 cm ($P < 0.0001$) more of carcass back fat (BF) than steers from S sires. Progeny of A sires reported higher ($P = 0.0002$) marbling score (MS) than the progeny of S sires. Breed of dam had an effect in carcass characteristics. Steers from S dams had heavier HCW ($P = 0.0014$). Similar to breed of sire effects, BF ($P = 0.0003$) and MS ($P < 0.0001$) was higher in carcasses of steers from A dams. Breed of sire and dam interaction was significant only for MS. Pure bred A steers had the highest MS ($P < 0.05$). Identifying steers with L RFI potential and understanding the contribution of cross breeding can help improve feed efficiency without negative affecting carcass traits.

Key Words: residual feed intake, breed of dam, breed of sire

W308 Supplemental corn dry distillers grains plus soluble on performance of steers grazing native range. M. F. Martínez-Pérez, D. Calderón-Mendoza, F. Loya-Holguin, A. Soto-Gaspar de Alba, C. Murdock, A. M. Encinias, and S. A. Soto-Navarro*, *New Mexico State University*, *Las Cruces*.

Medium- to high-quality rangeland forage is low in available energy in relation to its rumen degradable protein content. To complement forage quality, energy and phosphorus are usually supplemented to cattle grazing medium to high-quality forage. Supplementation with feedstuffs rich in digestible fiber (energy) and phosphorus, such as corn distiller grains plus solubles (DDGS), could alleviate the deficiencies of growing forage. We hypothesized that supplementation of DDGS to cattle grazing native range during the summer season will alleviate nutritional deficiencies, and will improve cattle grazing performance. To evaluate effects of DDGS supplementation level on performance of steers grazing native range during the forage growing season, 72 (206 ± 23.6 kg; 2008) and 60 (230 ± 11.3 kg; 2009) English crossbred steer calves were used in a grazing experiment. The grazing period lasted 56 and 58 d and started on August 11 and 20 for 2008 and 2009, respectively. Steers were blocked by BW into light, medium, and heavy. Each block was divided into 4 grazing groups. Each grazing group (6 steers in 2008 and 5 in 2009) was assigned to 1 of 4 DDGS supplementation levels: 1) 0% supplementation (no supplement), 2) 0.2%, 3) 0.4% and 4) 0.6% of BW. Total amount of supplementation per paddock for 7 d was calculated and divided by 3 to determine amount of DDGS to be fed as it was offered 3 times weekly. Supplement intake (0, 0.42, 0.82, and 1.25 ± 0.03 kg/d, for 0, 0.2, 0.4, and 0.6% of BW, respectively), and ADG (0.64, 0.75, 0.80, 0.86 ± 0.03 kg/d for 0, 0.2, 0.4, and 0.6% BW, respectively) increased linearly ($P < 0.01$) with increasing DDGS supplementation level. Levels of DDGS supplementation did not affect ($P = 0.43$) supplement conversion (4.18, 6.72, and 6.03 ±1.26 kg as-fed supplement/kg of increased BW gain for 0.2, 0.4, and 0.6% BW, respectively). Supplemental DDGS improved performance of steers grazing native range during summer in the Southern Plains.

Key Words: DDGS, grazing native range, steers

W309 Predicted mineral intake utilizing both water and forage analysis varies by source and location of livestock water in Eastern Montana. J. T. Mulliniks*[1], J. Muscha[2], S. I. Lodge-Ivey[1], and M. K. Petersen[2], [1]*New Mexico State University*, *Las Cruces,* [2]*USDA-ARS, Fort Keogh Livestock and Range Research Laboratory*, *Miles City, MT*.

Livestock water can play an important role in contributing to mineral intake of cows grazing rangelands. Mineral analysis of both forage and water is needed to accurately assess mineral intake compared to animal requirements. Therefore, 93 pasture and water source combinations were sampled in May 2009 with the objective to predict total mineral intake (forage intake and water consumption) on a DM basis at the 22,257 ha USDA-ARS Fort Keogh Livestock and Range Research Laboratory in Miles City, MT. Mineral intake was predicted of a lactating beef cow with an estimated water and forage intake of 43.15 L/d (25.4 kg/d) and 2.4% of BW, respectively. Mineral content from hand plucked forage samples were analyzed from 43 pastures representing 3 geographical locations: north (N), southeast (SE), and southwest (SW). All drinking water locations from each pasture were sampled for mineral analysis

(Midwest Labs Inc.) from four sources: springs, pumped ground water, reservoirs, and flowing surface water. Location, source and the location by source interactions were evaluated and analyzed as a 3 × 4 factorial arrangement of treatments. Predicted intake of chloride, copper, dietary anion-cation difference (DACD), phosphorus, and potassium was affected ($P < 0.05$) by geographical location. Differences ($P < 0.05$) in mineral consumption due to water source were found in 5 analyzed minerals (Ca, Cl, DACD, Fe, and Mg). Location by source interactions ($P < 0.05$) were found for fluoride, sodium, and sulfur. Predicted fluoride and sulfur intake concentrations were at or above the maximum tolerable concentrations in the ground water sources in most pasture locations. Copper and zinc were below requirements for a lactating beef cow; whereas, most minerals were found at safe intake concentrations and met a lactating cow requirements. These results suggest that developing a mineral supplement to meet grazing livestock′s requirement should take into account both forage and water mineral content.

Key Words: beef cow, mineral intake, water analysis

W310 The environmental impact of corn-fed vs. grass-fed beef finishing systems. J. L. Capper*[1] and R. A. Cady[2], [1]*Department of Animal Sciences, Washington State University*, *Pullman,* [2]*Elanco Animal Health*, *Greenfield, IN*.

System productivity fundamentally influences the environmental impact of animal agriculture. A partial life cycle assessment model was used to quantify the effect of finishing beef steers in a corn-fed (conventional) or grass-fed system on resource use and methane output. The model was based on nutrient requirements and metabolism of Angus x Hereford steers grown from 254 kg at weaning to 635 kg at slaughter. Corn or grass-based diets were formulated according to NRC with growth rates based on ad libitum intake at age-appropriate bodyweights. Inputs included feed composition and quantity, crop and pasture yields, energy and fertilizer use for cropping, and fossil fuel use for transport. Steers finished on pasture have an added energy requirement for grazing activity, thus increasing daily maintenance requirements (Table 1). Grass-based diets promote greater ruminal acetic acid production, increasing daily enteric methane production. The reduced growth rate of grass-fed steers increases finishing period length, each additional day increasing both total energy requirements and methane emissions. The differential in energy yield per acre between pasture and corn increases the land use for grass-fed beef. Energy use, methane emissions and land area per kg of beef are considerably increased in grass-fed vs. corn-fed beef production systems. The results demonstrate that the popular perception of grass-fed beef as being more sustainable than corn-fed beef does not align with true sustainability when producing an equivalent amount of food from each system.

Table 1. Comparison of energy inputs, methane output and cropland required to finish beef steers in corn-fed or grass-fed systems

	Corn-fed	Grass-fed
Start weight (kg)	254	254
Finished weight (kg)	635	635
Growth rate (kg/d)	1.61	0.87
Finishing period length (d)	237	438
Daily maintenance energy (MJ)	26	33
Daily growth energy (MJ)	30	15
Total energy use (MJ)	47,123	118,308
Total methane emissions (kg)	53	149
Energy MJ/kg beef	133	333
Methane kg/kg beef	0.15	0.42
Total land required (ha)	0.21	2.70

Key Words: beef production, environmental impact, methane

W311 Assessment of thermal signatures of nose-clip weaned calves using digital infrared thermography. H. T. Boland*[1,2], S. Bowers[2], and S. T. Willard[2,3], [1]*Mississippi State University, Prairie Research Unit*, *Prairie,* [2]*Mississippi State University, Department of Animal and Dairy Sciences*, *Mississippi State,* [3]*Mississippi State University, Department of Biochemistry and Molecular Biology*, *Mississippi State*.

Anti-suckling nose-clips (NC) are used for two-stage, low-stress weaning. Different NC types are available including adjustable size NC (ADJ) and "one-size fits all," non-adjustable NC (ONE). A study was conducted in which beef calves (n=24, BW=242 ± 6 kg) were randomly assigned to be weaned with ADJ, ONE, or weaned conventionally by abrupt remote separation (CTRL). Digital infrared thermal imaging (DITI) is a non-invasive diagnostic tool for evaluating surface temperature gradients. The objective of this study was to investigate the use of DITI to determine whether temperature differences exist between calves weaned by different methods. Imaging was conducted using a FLIR P60 thermal camera and images were analyzed using ThermaCAM Researcher Pro (version 2.7). The lateral (LAT, inside the nostril) and anterior (ANT) surface temperature maximum of the nose, and eye temperature were recorded. The NC were placed on calves (d −5) and worn for 5 d prior to separation from dams (d 0). Images were taken at initial placement of NC and after removal on d 0. Blood was also collected on d −5 and 0, and serum analyzed for cortisol. Ambient temperature (AMB) ranged from 21.3 to 29.0°C at the time of imaging. Both LAT and ANT were positively correlated to one another ($r = 0.80$, $P < 0.01$) and to AMB ($r = 0.56$ and 0.55, respectively; $P < 0.01$). Cortisol and ANT tended to be positively correlated ($r = 0.24$, $P = 0.10$). Eye temperature (indicative of core body temperature) did not differ ($P > 0.10$) between treatments or days. There were no differences ($P > 0.10$) between CTRL, ONE or ADJ treatments in mean LAT (35.6, 34.6, or 35.0°C, respectively) or ANT (34.4, 33.9, 34.1°C, respectively). From d −5 to 0, ANT increased ($P < 0.01$) within all treatments; however, AMB ($P < 0.01$) also increased which may have impacted surface temperature. In ADJ and ONE calves the LAT increased ($P < 0.01$) from d −5 to 0, but not in CTRL calves ($P > 0.10$) which may be explained by minor inflammation that developed within the nostril of calves wearing NC. This suggests that DITI may be useful in evaluating effects of NC on nasal tissue. Effect of breathing on nostril imaging needs further examination.

Key Words: thermography, nose-clips, weaning

W312 Selenium incorporation and depletion in beef heifers grazing pastures with very high selenium levels grown in saline soils. S. O. Juchem*[1,2], S. E. Benes[2], P. H. Robinson[1], P. Vasquez[2], M. Brito[2], G. Getachew[1], and P. Chilibroste[3], [1]*University of California*, *Davis*, [2]*California State University*, *Fresno*, [3]*Facultad de Agronomía*, *Paysandú, Uruguay*.

Salinization of soils in parts of the westside of the San Joaquin Valley (CA, USA) has led to cultivation of salt tolerant forages such as 'Jose' tall wheatgrass (TWG) (*Thinopyrum ponticum* var. 'Jose') and creeping wildrye (CWR) (*Leymus triticoides* var. 'Rio'). Our objective was to measure tissue selenium (Se) concentrations and performance of beef heifers grazing TWG and CWR forages containing very high levels of Se (>3 mg/kg DM). Twenty 6 m old Angus heifers were allocated to two grazing areas, where each ~9 ha TWG or CWR area was divided into 2 subplots, with each subdivided into 4 paddocks that were rotationally grazed at 14 d intervals for 165 d. Blood was sampled at −25, 20, 45, 70, 91, 134 and 165 d of grazing, and muscle and liver biopsies were at −25, 91 and 165 d. Body weight (BW) was recorded before grazing and at 20, 45, 70, 91, 134 and 165 of grazing. At the end of grazing, heifers were moved to a feedlot and fed a ration that contained low levels of

Se (<0.25 ppm). Samples of liver, blood and recording of BW were at 23, 81, 136 and 208 d after grazing, whereas muscle was sampled at 81, 136 and 208 d. An additional blood sample was collected at 41 d. TWG had a higher level of metabolizable energy (6.7 vs. 6.0 MJ/kg DM) and Se (4.0 vs. 2.8 mg/kg DM), but lower CP level (7.9 vs. 9.0% DM) than CWR. BW gain was similar for TWG and CWR heifers (0.27 vs. 0.36 kg/d). Se accumulation in blood occurred quickly, increasing more than 3 fold by 20 d of grazing in TWG heifers (0.094 vs. 0.410 ppm Se), and CWR heifers had lower blood Se during the entire grazing period. Se accumulation in liver and muscle had similar patterns as in blood, but at slower rates. Se concentrations decreased after grazing (P<0.01), but rates of Se mobilization from blood, liver and muscle differed. By 81 d post grazing, concentrations of Se were reduced by 77% in liver, 49% in blood but only 31% in muscle. Results suggest that TWG and CWR production using saline drain water can be a viable alternative for salinized soils. In addition, muscle Se depletion occurs slowly enough to allow slaughter of beef cattle with enriched levels of Se in beef.

Key Words: salinity, selenosis

W313 Influence of shading of feedlot pens on performance of growing bull-calves during winter in northwest Mexico. R. Barajas*[1], B. J. Cervantes[1,2], M. Verdugo[1], M. A. Espino[1,3], E. A. Velazquez[1], J. A. Romo[1], and L. R. Flores[1], [1]*FMVZ-Universidad Autonoma de Sinaloa*, *Culiacan, Sinaloa, Mexico*, [2]*Ganadera Los Migueles SA de CV*, *Culiacan, Sinaloa, Mexico*, [3]*Técnología de Máxima Producción, S.A. de C.V.*, *Culiacan, Sinaloa, Mexico*.

The objective of this study was to determine the influence of shading in feedlot pens on feedlot performance of growing bull-calves during winter in northwest Mexico. Sixty bull-calves (BW = 225 ± 1.2 kg) were used in a 105-d feedlot experiment. In accordance to a randomized complete block design, bull-calves were blocked by initial-BW (light and heavy), and in groups of five were assigned to receive one of two allotment schedules which consisted the treatments: a) Six 6 × 12 m pens with no shade (control), and b) Six 6 × 12 m pens provided with 6 × 4 m of metallic-sheets ceiling (shade). Experimental data were analyzed by ANOVA for a randomized complete block design. Final BW was improved ($P = 0.05$) for calves allowed shade compared with controls (399 vs. 380 kg). ADG was increased ($P = 0.04$) 12% in shaded animals (1.655 vs. 1.477 kg/d for shaded and control, respectively). Dry matter intake was not affected ($P > 0.80$) by treatment (8.319 vs. 8.322 kg/d). Feed to gain ratio was increased ($P < 0.01$) in 11% for shaded bull-calves (5.015 vs. 5.619 kg of DM/kg of BW gain, for shade and control, respectively). Retained net energy for maintenance from the diet, was 12% higher ($P = 0.07$) in shaded bull-calves (1.957 vs. 1.747 Mcal/kg of DM for shade and control, respectively). Animals in control no shade treatment expenses 8% more NEm ($P = 0.06$) that expected (observed/expected NEm ratio = 0.92). It is concluded that use of shading on feedlot pens improves performance of growing bull-calves in northwest Mexico during the winter season.

Key Words: bull-calves, feedlot performance, shade

W314 Preliminary evaluation of grandsire marbling potential and ultrasound use on backgrounding and finishing performance, and carcass merit. C. J. Mueller*[1,2], T. DelCurto[1,2], R. R. Mills[1], C. P. Sullivan[1,2], and G. L. Tschida[1,2], [1]*Oregon State University*, *Corvallis*, [2]*Eastern Oregon Agricultural Research Center*, *Union*.

Forty-one crossbred calves (285 ± 32 kg) were backgrounded and finished to determine the impact of grandsire marbling potential and ultrasound use on predicting carcass merit. Dams were sired by either a high marbling EPD Angus bull (HIGH; Marbling EPD: +0.44, Acc: 0.23) or a low marbling EPD Angus bull (LOW; Marbling EPD: +0.02, Acc: 0.30) as evaluated by the American Angus Association, then bred to a common sire. Weaned calves were backgrounded on a barley-based diet in a common pen for 60 d. Calves were ultrasonographed for marbling (UMARB), muscle depth (UMD), and backfat (UBF) at the beginning (d0) and end of the backgrounding period (d60), and again at 72 d into the feedlot phase (d135). Gain and carcass data were evaluated as a 2 × 2 factorial design with grandsire and sex as main effects and calf age as a covariate. Correlations between ultrasound measurements and carcass data were used to determine the relevancy of ultrasound timing to carcass merit. Daily gain was similar ($P > 0.10$) between grandsire groups during both phases. Heavier carcass weights, increased backfat, and larger ribeye area (REA; $P < 0.05$) were evident in HIGH calves. No differences ($P > 0.10$) were detected for KPH, marbling score or yield grade between LOW and HIGH calves. A strong ($r > 0.50$) positive relationship between UBF, carcass backfat, and yield grade at d60 and d135 ($P < 0.05$) emerged across grandsires. Final marbling score had a weak positive relationship with UMARB at d0 and d60 ($P < 0.05$), but a strong positive relationship at d135 ($P < 0.05$). HIGH calves had stronger positive relationships between UMARB and final marbling score during both the backgrounding and finishing phases as compared to LOW calves. Though this data set is limited, it indicates that grandsire marbling potential may impact carcass merit through factors other than marbling, and use of ultrasound during the backgrounding phase to predict final carcass merit may be limited and dependent on marbling predisposition.

Key Words: marbling, ultrasound, beef cattle

W315 Growth and carcass merit of purebred Jersey steer calves finished on grain-based diets at two different energy levels. C. J. Mueller*[1,2], G. L. Tschida[1,2], and V. B. Cannon[1], [1]*Oregon State University*, *Corvallis*, [2]*Eastern Oregon Agricultural Research Center*, *Union*.

Twenty purebred Jersey steers were used to evaluate lifetime growth and carcass development while finished on different caloric-dense diets. Steers were grouped by weight (GRP = LIGHT, HEAVY) then randomly assigned to either a 70% (F70) or an 85% (F85) concentrate finishing diet. Data were analyzed as a 2 × 2 factorial design with GRP and finishing diet as main effects. Daily rations were distributed by pen during the growing phase and individually during the finishing phase. Growth data from the growing phase (168 d) were analyzed as LIGHT (77 ± 8 kg) versus HEAVY (97 ± 8 kg) only, since finishing treatments were yet to be applied. Growing phase ADG was not different ($P > 0.10$) between LIGHT (0.89 kg/d) and HEAVY (0.97 kg/d), respectively. LIGHT calves tended ($P < 0.10$) to consumer less feed per day versus HEAVY calves. During the finishing phase ADG for F85 steers (0.91 kg/d) was greater ($P < 0.05$) than F70 steers (0.82 kg/d). Intake was not different ($P > 0.10$) between F70 (7.77 kg) and F85 steers (7.65 kg), whereas G:F was lower ($P < 0.05$) for F70 steers (0.11 kg/kg) compared to F85 steers (0.12 kg/kg). Ultrasonography was used to track carcass changes and showed no differences ($P > 0.10$) in backfat accretion (+4.22 mm vs. +4.20 mm), muscle depth (+13.03 mm vs. +14.57 mm) or marbling score (+166 units vs. +177 units) for F70 and F85 steers, respectively. Ultrasound indicated that changes in muscle depth plateaued around 14 mo of age, while fat deposition continued to increase. Actual carcass data showed no differences ($P > 0.10$) in backfat (0.61 cm vs. 0.58 cm) or KPH (2.48% vs. 2.58%) between F70 and F85 steers, respectively. Ribeye area for F85 steers (23.98 cm^2) was greater ($P < 0.05$) than F70 steers (21.39 cm^2), whereas marbling score tended to be greater ($P < 0.10$) for F85

steers (640, modest) versus F70 steers (590, small). Calculated yield grade (2.97 and 2.77) and retail yield (49.93% and 49.58%) were not different ($P > 0.10$) between F70 and F85 steers, respectively. Jersey steers have the ability to produce highly marbled carcasses, but carcass quality must be valued against low growth efficiency.

Key Words: carcass, growth, Jersey steers

W316 Stocking rate and botanical composition effects on the physical characteristics of the streamside zones of pastures. D. A. Bear*[1], J. R. Russell[1], D. G. Morrical[1], M. Tufekcioglu[1], T. M. Isenhart[1], and J. L. Kovar[2], [1]*Iowa State University*, *Ames,* [2]*USDA-ARS National Laboratory for Agriculture and the Environment*, *Ames, IA*.

Grazing management that allow cattle to congregate near pasture streams may increase sediment, phosphorus, and pathogen loading of the streams by removing vegetation and depositing manure near the streams. To assess stocking rate and pasture characteristics effects on the risk of pollution of pasture streams, forage sward height (SH), bare and manure-covered soil, and forage species were measured within 15.2 m of the stream along each bank at up to 30 locations separated by 30.5 m in 13 pastures on 12 beef cow-calf farms in southern Iowa bimonthly from May through November for 3 yr. Stream bank erosion measurements were collected during spring, summer, and fall seasons by 1.6 × 76.2 cm fiberglass pins inserted perpendicular to the bank at 1 m intervals from the base to the top of each bank at 10 transects located at 32 m intervals along the stream. Cattle stocking records were maintained year-round by farm operators. The REG procedure of SAS analyzed bare and manure-covered ground proportions and erosion by stocking rates. Bare ground was weakly related ($r^2 = 0.15$) to annual stocking rate per stream m (cow-d/m), whereas manure-covered ground was more highly related ($r^2 = 0.35$) to period cow-d/m. In stepwise multiple regressions, forage SH decreased as tall fescue, legumes, bluegrass, and period stocking rate of cow-d/m increased ($r^2 = 0.56$). Proportions of bare soil increased as proportion of reed canarygrass decreased and legumes increased ($r^2 = 0.35$). Proportions of manure-covered ground increased as the cow-d/m per sampling period and the proportions of tall fescue and bluegrass in the vegetation increased, and decreased as proportions of broadleaf weeds and sedge increased ($r^2 = 0.47$). Annual stream bank erosion rates were not correlated ($r^2 = 0.001$) to annual cow-d/m or cow-d/ha. Erosion occurred primarily during the spring season, indicative of the freeze-thaw cycle and hydrological effects. Grazing management that alter temporal/spatial distribution of cattle may decrease nonpoint source pollution risks of pasture streams by maintaining forage SH and decreasing manure deposition within the streamside zones of pastures.

Key Words: hydrology, management, riparian areas

W317 Incidence of bovine Enterovirus, Coronavirus, and group A rotavirus, and concentration of total coliforms in Midwestern pasture streams. D. A. Bear*, Y. I. Cho, J. R. Russell, S. M. Ensley, and K. J. Yoon, *Iowa State University*, *Ames*.

The occurrence of bovine enteric pathogens and total coliform (TC) contamination in streams of 13 Midwestern cow/calf pastures was studied during the 2007-2009 grazing seasons. Water samples (n = 1274) were collected biweekly at upstream (UP) and downstream (DOWN) locations on each stream. Incidence of bovine Enterovirus (BEV), Coronavirus (BCV), and group A Rotavirus (BRV), and concentrations of TC were evaluated. Cattle presence in pastures on the day of sampling, and 2, 3, 4, 5, 6, and 7 d prior were evaluated for association of virus detection and TC. Cattle presence in pastures were analyzed for BEV, BCV, and BRV incidence by the FREQ procedure of SAS, Proc GLM analyzed TC differences by farm and UP and DOWN sites, and Proc REG regressed TC by stocking densities. Mean incidences of BEV, BCV, and BRV in all samples were 3.91, 1.12, and 0.49%, respectively, over the three grazing seasons. There were no differences ($P > 0.10$) for BEV, BCV, and BRV incidences between farms or samples collected from UP or DOWN locations. Incidence of BEV in combined samples were related ($P < 0.05$) to cattle presence in pastures on the day of sampling and 3 and 4 d prior to sampling, and tended ($P < 0.10$) to be related to cattle presence in pastures 2, 5 and 6 d prior to sampling. BCV or BRV incidences were not related ($P > 0.10$) to cattle presence in pastures at any time throughout the grazing seasons. In UP samples, BEV tended ($P < 0.10$) to be related to cattle presence in pastures on the day, and 2 and 4 d prior to sampling. Whereas, in DOWN samples, cattle presence in pastures on the day of sampling only tended ($P < 0.10$) to be related to BEV incidence. Mean TC were 1269 and 1417 colony-forming units (CFU)/100ml, respectively, for UP and DOWN samples. Differences ($P = 0.02$) were observed between farms, but not between sites on farms ($P = 0.31$), for concentrations of TC and were not related to cattle stocking rates of pastures. Preliminary results indicate that while BEV incidence may be related to cattle presence, but BCV and BRV incidences and TC were not related to cattle presence in pastures.

Key Words: enteric viruses, nonpoint source pollution, water quality

W318 Borax and Octabor treatment of stored swine manure: Reduction in hydrogen sulfide emissions and phytotoxicity to agronomic crops. M. Yokoyama*[1], S. Hengemuehle[1], D. Penner[1], J. Michael[1], C. Spence[2], T. Whitehead[2], R. von Bernuth[1], D. Rozeboom[1], and M. Cotta[2], [1]*Michigan State University*, *East Lansing,* [2]*USDA, Agricultural Research Service*, *Peoria, IL*.

Gaseous emissions from stored manure have become environmental and health issues for humans and animals as the livestock industry becomes more specialized and concentrated. Of particular concern is hydrogen sulfide, which is being targeted for regulatory control in concentrated animal farm operations. There are few technologies to control hydrogen sulfide emissions which are cost effective, safe for farmers and animals, and environmentally sustainable. Borax treatment (1%) is effective in reducing hydrogen sulfide emissions from stored swine manure. The objective of this study was to treat stored swine manure with lower amounts to reduce hydrogen sulfide emissions and determine the phytotoxicity of the treated manure as a fertilizer for crops. Ten treatments (0.1, 0.25, 0.5, 1.0% borax and 0.05, 0.1, 0.125, 0.25 and 0.5% Octabor and negative control, 0.0%) were evaluated in plastic carboys (19 L) with swine manure and monitored for hydrogen sulfide emissions for 30 d. 16S and PCR was used to quantify total bacteria and sulfate reducing bacteria. Treated manures were used as fertilizer for growing corn, wheat, soybean, alfalfa and dry beans for 42 d in a greenhouse. Hydrogen sulfide emissions decreased (25-50%) with borax and Octabor treatment and the decrease was dose dependent. Significant interactions ($P \leq 0.05$) between plant injury vs. plant boron content, plant boron content vs dry wt yield, and plant injury vs. dry wt yield was observed. The ranking of crop tolerance to borax and Octabor treated swine manure was: alfalfa, corn, wheat, soybean, dry beans. Borax and Octabor were bioavailable for plants with no soil accumulation. A significant reduction in total bacteria ($P \leq 0.01$) and sulfate reducing bacteria ($P \leq 0.05$) was observed for higher treatments. Borax and Octabor treatment (0.1-0.25%) of stored swine manure was tolerated by crops without injurious effects.
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Key Words: borax, octabor, swine manure, hydrogen sulfide

W319 Effect of dietary adipic acid and dried distillers grains plus solubles in combination with post-excretion amendment with sodium bisulfite on nitrogen loss from stored laying hen excreta. T. J. Applegate*[1], C. Romero[2], M. E. B. Abdalllh[3], R. Angel[4], and W. Powers[5], [1]*Purdue University*, *W Lafayette, IN,* [2]*Universidad Politecnica de Madrid*, *Madrid, Spain*, [3]*University of Khartoum*, *Khartoum, Sudan*, [4]*University of Maryland*, *College Park,* [5]*Michigan State University*, *E Lansing*.

Effects of dietary adipic acid (AA; 0 or 1%) or dried distillers grains plus solubles (DDGS; 0 or 20%) was determined on laying hen (Hyline W36) performance and egg characteristics from 26 to 34 wk of age (2 × 2 factorial arrangement of diets; 36 cages/diet; 2 hens/cage). All data were analyzed as a factorial experiment utilizing PROC MIXED procedure of SAS. Egg production, feed intake, and egg specific gravity were unaffected by diet. Hens fed diets with 20% DDGS produced 1.4% heavier eggs ($P < 0.02$), but was unaffected by AA. Egg shell percentage was reduced by 2.4 or 1.8% with either dietary AA or DDGS, respectively ($P < 0.02$). To determine the influence of diet and manure amendment on N loss during storage, excreta was collected during 2, 2-d collections by pooling 6 pens/diet (n=6 pools/collection), mixing and dividing into 2 equal portions for 14-d storage experiments with or without 8.8 kg/ 100 m2 of PLT (sodium bisulfite). Initial excreta pH was reduced by 0.2 pH units when hens were fed 1% AA or 20% DDGS ($P < 0.05$). The effect of feeding hens AA on manure pH was maintained for 7 d, but was lost by 14 d of storage; whereas the effect of feeding 20% DDGS on manure pH was maintained for 14 d of storage ($P < 0.01$). These dietary influences on manure pH during storage however were unrelated to N loss. While diet supplementation with adipic acid had no influence on manure N loss during storage, manure from hens fed 20% DDGS lost 32% more N during the first 7 d of storage vs. manure from hens eating no DDGS ($P < 0.02$). Surface amendment of manure with PLT resulted in a 41% reduction in manure N loss during the first 7 d of storage and a 14.7% reduction from 7 to 14 d of storage ($P < 0.05$). In conclusion, manure amendment with PLT resulted in a 26% reduction in N loss during manure storage for 14 d. Conversely, feeding hens diets containing 20% DDGS resulted in a 16.5% greater manure N loss during the same time period.

Key Words: sodium bisulfite, dry distillers grains plus solubles, nitrogen loss

W320 Evaluation of a silvopastoral system with *Alnus acuminata* on pasture productivity, milk production and economic returns in a high tropical ecosystem. A. Conde*[1], R. Hernandez[1], L. L. Betancourt[1], D. A. Castañeda[1], J. A. Umaña[1], T. Carvajal[2], and L. Sanchez[3], [1]*Universidad de La Salle*, *Bogotá, Colombia*, [2]*Universidad UDCA*, *Bogotá, Colombia*, [3]*CORPOICA*, *Bogotá, Colombia*.

The effect of introducing alders *Alnus acuminata* in pastures with a spatial distribution of 10 × 5 m was assessed in terms of on forage yield and quality, milk production and composition and economic efficiency. The study was carried out in a farm located in Usme Colombia (74°06′ W, 4°28′ N), with an elevation of 2650 m.a.s.l, ambient temperature between 6 to 12 °C and mean rainfall of 900 mm/yr. When the study began, the alders were five years old, with an average height of 2.5 m and a mean shade diameter of 3.5 m. A total of 12 Holstein cows in the third year of lactation were distributed randomly into two pasture treatments: T1-trees in the pasture and T2- pasture without trees, in a simple crossover design. All paddocks in the rotation were grazed every 60 d. Dry matter (DM) yield and botanical composition of grazed pastures were estimated using the double sampling and dry weight rank method, respectively. Milk production was recorded daily and fat, protein and lactose were analyzed weekly. The two pastures treatments were composed of *Pennisetum clandestinum* H. (68%), *Holcus lanatus* L. (8%), *Trifolium pratense* L. (6%), and weeds (18%). Forage on offer was higher in pastures with trees (2687 kg DM/ha) than in pastures without trees (1702 kg DM/ha). Forage on offer in the pastures with trees had higher crude protein (14%) than in pastures without trees (11%). There were no differences ($P > 0.05$) in daily milk yield and in milk composition (fat, protein and lactose) due to treatments. However, milk production per ha in pastures with trees (10163 kg/ha/yr) was higher ($P < 0.05$) than in pastures without trees (5081 kg/ha/yr), due to higher carrying capacity (1108 versus 569 kg LW/ha). The investment made on the silvopastoral system with alders was recovered in the fifth year after establishing the trees and the annual rate of return was 55% higher than in the pasture without trees.

Key Words: forage yield, forage quality, stocking rate

W321 Feeding native laying hens diets containing palm kernel meal with or without enzyme supplementations: 2. Manure nitrogen and microbial counts. Adrizal*[1], Yusrizal[1], S. Fakhri[1], Yatno[1], and C. R. Angel[2], [1]*Faculty of Animal Husbandry, University of Jambi*, *Jambi 36361, Jambi, Indonesia*, [2]*Department of Animal and Avian Sciences, University of Maryland*, *College Park*.

The objectives of this study were to evaluate effects of feeding native laying hens diets containing palm kernel meal (PKM) on nitrogen (N) excretion, excreta ammonia (NH_3), and excreta microbial counts. Hens (180, 48 wk old) were assigned to 180 cages (one bird per cage). Each of 12 diets was assigned at random to 15 cages. The 12 diets were the results of a factorial arrangement of 3 levels of PKM (0, 15, and 30%), 2 levels of fiber enzyme (0 and 0.03%), and 2 levels of a phytase-protease mixture (0 and 0.035%). Diets contained 2,753 to 2,758 kcal ME/kg and 17.5 to 18.4% CP and were fed for 10 wk. A 16L:8D lighting program was used. The results showed that at wk 4, excreta DM (but not N), increased as dietary PKM levels increased (19.4 vs. 21.9 vs. 23.0% for 0, 15, and 30% PKM, respectively; $P \leq 0.005$). There were no effects of enzyme supplementation on excreta DM and N. Lower excreta NH_3 due to increased PKM was observed at wk 4 and 10 ($P \leq 0.0001$). Ammonia reduction was also caused by fiber enzyme supplementation at wk 4 (197.9 vs. 161.7 ppm, at 0 and 0.03%, respectively) ($P \leq 0.05$). Interaction effect of fiber enzyme with PKM on NH_3 was observed at 4 and 10 wk ($P \leq 0.005$). Interactions were also observed on NH_3 between the phytase-protease mixture and PKM at 10 wk, between the fiber enzyme and PKM at 4 and 10 wk, and between the phytase-protease mixture and the fiber enzyme at 4 wk. Increasing dietary levels PKM from 0 to 15 to 30% resulted in increased *Lactobacillus* counts (107.8 vs. 106.8 vs. 169.8 $\times 10^8$ cfu, respectively) at wk 4. At 10 wk, dietary PKM levels did not clearly affect *Lactobacillus* counts, but reduced enteric bacteria (4.2 vs. 2.6 vs. 2.8 $\times 10^8$ cfu, respectively) ($P \leq 0.005$). Although enzyme had no clear effect on microbial growth, interaction effects of PKM and fiber enzyme on *Lactobacillus* and enteric bacteria or PKM with phytase-protease mixture on *Lactobacillus* counts were seen. Dietary PKM helped reduce N excretion, NH_3 emission, and favored nonpathogenic microbial growth.

Key Words: palm kernel meal, native laying hen, enzyme supplementation, excreta nitrogen, ammonia, excreta microbial count

W322 Effect of dietary protein concentration on ammonia emission from dairy manure. C. Lee*[1], A. N. Hristov[1], C. Dell[2], G. Feyereisen[3], J. Kaye[1], and D. Beegle[1], [1]*Pennsylvania State University*, *PA,* [2]*USDA-ARS*, *PA,* [3]*USDA-ARS*, *MN*.

The objective of this experiment was to investigate the effect of dietary crude protein concentration on ammonia (NH_3) volatilization from dairy cow manure. Two types of manure were prepared by feeding lactating dairy cows diets with 16% (DM basis; HighCP) or 14% CP (LowCP). The manure was used in 2 experiments. In Exp. 1, 400 g of each manure (1.7:1.0, feces:urine) was placed in sealed steady-state flux chambers connected to a photoacoustic infrared gas analyzer and incubated for 5 d at 25°C to measure the NH_3 emitting potential of manure. Ammonia emission rates were 202 and 132 (mg/h; $P < 0.001$) for HighCP and LowCP manure, respectively. Cumulative NH_3 emission was 45% less ($P < 0.001$) for LowCP compared with HighCP manure. In Exp. 2, LowCP and HighCP manure was applied to 61 × 61 × 61 cm lysimeters collected from a Hagerstown silt loam (fine, mixed, mesic Typic Hapludalf) in a complete randomized design. Manure was applied to each lysimeter immediately after mixing feces and urine (same ratio as in Exp. 1). The manure application rate was 9.3 g of N/lysimeter, corresponding to a field application rate of 300 kg N/ha. The HighCP manure had higher N content (4.4 vs. 2.8%, DM basis) and proportion of ammonium and urea-N in total manure N (51.4 vs. 30.5%) than the LowCP manure. As a result, more LowCP than HighCP manure (2.36 vs. 1.65 kg) was applied to each lysimeter. After manure application, NH_3 emissions were measured using a photoacoustic infrared gas analyzer at 3, 8, 23, 28, 50 and 100 h. Ammonia emission was greater ($P < 0.05$) from HighCP- than from LowCP-manure amended soil. The area under the cumulative (100 h) NH_3 emission curve for LowCP was smaller than the area for HighCP manure (56.8 and 114.8 mg $NH_3/m^2/min \times h$, respectively; $P < 0.05$). In conclusion, manure from dairy cows fed a 14% CP diet had decreased NH_3 emitting potential and resulted in 50% lower NH_3 emission when applied to soil, compared to manure from cows fed a 16% CP diet.

Key Words: dietary protein, ammonia emission, dairy manure

W323 Origin of ammonia nitrogen volatilized from dairy manure. C. Lee* and A. N. Hristov, *Pennsylvania State University*.

The objective of this experiment was to trace the origin of ammonia-N (NH_3-N) volatilized from dairy manure during storage. The experiment was conducted with ^{15}N-labeled or unlabeled feces and urine collected from dairy cows fed a 16% crude protein, 32% NDF diet. Ruminal microbes and consequently feces and urine were labeled with ^{15}N by dosing $^{15}NH_4Cl$ into the rumen. Two types of manure were prepared: FLM, ^{15}N-labeled feces and unlabeled urine; ULM, unlabeled feces and ^{15}N-labeled urine. Feces and urine were mixed in a 1:1 ratio (as-is basis) and incubated for 10 d at room temperature in a closed chamber system (n=4). Volatilized NH_3 was trapped in 0.5M sulfuric acid. The source of NH_3-N was estimated as: ^{15}N-enrichment (atom % excess) of NH_3-N ÷ ^{15}N-enrichment of ^{15}N-labeled urine or feces. Labeled and unlabeled feces or urine had similar N concentration (0.48 ± 0.01 and 1.01 ± 0.02%, respectively), but differed in ^{15}N-enrichment (0.090 vs. 0.005 and 0.133 vs. 0.0007 atom % excess, respectively). Total N, NH_3-N, and urea-N concentrations were similar between FLM and ULM. Cumulative NH_3 emissions were also similar between FLM and ULM (1,371 vs. 1,328 mg, $P = 0.51$). On average, 89% of the manure N lost during the incubation was recovered as ammonium in the acid trap. The proportion of NH_3-N originating from fecal N (FLM) was negligible in the first 48 h of the incubation, represented 0.04 ± 0.006 by d 5, and then gradually increased to 0.11 ± 0.019 of the emitted NH_3-N by d 10 (logistic regression model; adjusted $R^2 = 0.91$, $P < 0.001$). The proportion of NH_3-N originating from urinary N (ULM) represented 0.94 ± 0.027 at 24 h, 0.97 ± 0.002 at 48 h, 0.91 ± 0.004 at 72 h, and gradually decreased to 0.87 ± 0.005 at d 10 (exponential decay model; adjusted $R^2 = 0.92$, $P < 0.001$). This experiment demonstrated that the main source of NH_3-N volatilized from cattle manure during the initial 10 d of storage is urinary N, representing on average 90% of the emitted NH_3-N. The contribution of fecal N was relatively low, but gradually increased to about 10% by d 10, as mineralization of fecal N progressed.

Key Words: nitrogen-15, urine and feces, ammonia

W324 Air velocities in poultry houses raising large broilers. D. G. Overhults[1], A. J. Pescatore*[1], I. Lopes[1], G. Morello[1], J. P. Jacob[1], M. Miller[2], J. Earnest Jr.[1], and R. S. Gates[3], [1]*University of Kentucky*, *Lexington,* [2]*Kentucky Poultry Federation*, *Winchester,* [3]*University of Illiniois*, *Champaign*.

As part of a Kentucky poultry house energy efficiency project, bird level air velocities were measured in tunnel ventilated broiler houses used by three commercial broiler complexes. Although tunnel fans consume a considerable amount of energy, they also can generate significant airflow over the flock, creating a wind chill effect that mitigates heat stress related problems. Air velocities were recorded in 21 houses (9, 5, and 7 from complexes A, B, and C, respectively) raising 2.8-kg broilers. All but one house had a dropped cathedral ceiling. Velocity measurements were taken at four equally spaced locations across the house about 50 cm above the litter and 21 m upstream from the tunnel fans. Velocities were measured with no birds in the houses. Overall velocities averaged 2.50 m/s and ranged from 1.81 to 3.19 m/s. All but one house had velocities greater than 2.0 m/s (400 fpm), with eight houses exceeding 2.5 m/s (500 fpm) and two exceeding 3.0 m/s (600 fpm). In Complex A, the nine 12.2 × 152.4 m houses each had eight 1.22 m diameter exhaust fans with discharge cones. Three of the houses had an additional 1.32 or 1.37 m diameter exhaust fan, again with discharge cones. The additional fan produced higher air velocities in two of the three houses. Four houses (13.1 × 155.4 m) producing for Complex B each had ten 1.22 m diameter exhaust fans. A fifth shorter house (13.1 × 140.2 m) had only nine 1.22 m fans but had the lowest air velocity due to poor performing fans. The seven houses raising for Complex C (12.8 × 128m) all had at least eight exhausts fans of 1.22 m or greater in diameter. The presence of discharge cones, as well as the size and number of fans, did not consistently impact velocities which ranged from 2.05 to 2.82 m/s, with an average of 2.42 m/s for Complex C.

Key Words: air velocity, tunnel ventilation, broilers

W325 Effect of LED lights on growth performance of broiler chicks. R. D. Rierson*, C. M. Rude, M. A. Barrios, and R. S. Beyer, *Kansas State University*, *Manhattan*.

Light emitting diode (LED) light sources are relatively new and potentially beneficial to poultry producers due to lower energy cost. To test the efficacy of LEDs as a light source for growing broilers, the following experiment was completed, utilizing 5 treatments with different light intensities. Light intensities varied from 5 to 25 lx, in increments of 5 lx. There were 4 replications of each treatment, with 20 birds per pen for a total of 400 d old male Cobb 500 broiler chicks. Experiments were carried out in a single building using pens that were 5 × 12 feet in area. Pens were separated using black plastic to keep stray light from interfering with neighboring pens. Chicks were grown on the floor on used litter. The chicks were fed a standard NRC corn soy starter diet and were grown to 21 d of age. The light source for the experiment were white LEDs that were bunched into clusters and hung at 24 inches above the floor litter. Dimmers were installed in each pen to allow ease of adjusting lux intensities. Birds were raised for the first 3 d using incandescent ceiling bulbs, and on d 4 the LED lights were lowered to

treatment intensities and the overhead lights were turned off. The LED lights were left on a 24 h light schedule, but during daylight hours the curtains were occasionally dropped to prevent birds from overheating. All pens were given ad libitum access to feed and water. BWG and feed consumption was collected at 21 d. BWG under 5 to 25 lx was 1472g, 1480g, 1481g, 1536g, and 1541g, respectively, and the differences were not statistically significant when analyzed with the GLM procedure in SAS with an α of 0.05. Feed to gain ratios were not affected. It was observed that birds raised under higher intensities of light exhibited more physical activity than those raised under lower light intensity. No cannibalism was documented. The data concluded that it is possible to raise broilers under as low as 5 lx of light, from LED sources.

W326 Comparison of nutrient and microbial profiles in foaming and non-foaming swine manure pits. J. Rehberger*, E. Davis, A. Veldkamp, T. Parrott, and T. Rehberger, *Danisco*, *Waukesha, WI*.

Swine manure samples were collected from foaming and non-foaming deep pit storage units from three production systems and the nutrient and microbial compositions of these samples were assessed. Manure samples were obtained by sampling the entire depth of the manure storage pit with a 3 m-long PVC sampling rod and classified as having none (less than 2.5 cm of foam on the manure surface, n = 30), low (2.5 to 15.2 cm of foam on the manure surface, n = 25), or high (greater than 15.2 cm of foam on the manure surface, n = 14) levels of foam. Terminal restriction fragment length polymorphism (TRFLP) analysis was performed to assess microbial communities using four restriction enzymes; *Bfa* I, *Hae* III, *Msp* I, and *BstU* I. Manure samples obtained from deep-pit storage systems with a high degree of foaming had greater ($P < 0.05$) concentrations of fiber-bound protein compared to manure samples from non-foaming pits and those with a low degree of foam. Foaming pit samples also had a greater abundance ($P < 0.05$) of *Alphaproteobacteria*, *Betaproteobacteria*, *Deltaproteobacteria*, and *Actinobacteria* compared to non-foaming pit samples. Additionally, liquid and foam phases from three deep-pit swine manure storage systems experiencing foaming were sampled to compare differences in nutrient and microbial compositions between the liquid and foam portions. The concentration of crude fat was greater ($P < 0.05$) in foam samples compared to samples of the liquid portion, as were concentrations of copper, iron, and zinc. The liquid portions had a greater abundance ($P < 0.05$) of *Actinobacteria* and *Alphaproteobacteria* compared to foaming portions, and there was a greater abundance ($P < 0.05$) of *Flexibacter* in the foam as compared to the liquid portions. The divergent microbial communities present in foaming and non-foaming deep-pit swine manure systems coupled with greater fiber-bound nitrogen content in foaming pits suggests that differences in nutrient abundance and subsequent changes in the microbial environment may be factors associated with the foaming phenomenon.

Key Words: manure, pit, foam

W327 The effect of dietary alfalfa silage to corn silage ratios on cow performance and ammonia nitrogen emission. C. Arndt*[1], M. A. Wattiaux[1], and J. M. Powell[2], [1]*University of Wisconsin*, *Madison*, [2]*US Dairy Forage Research Center*, *Madison, WI*.

The objective was to determine the effect of varying alfalfa silage (AS) to corn silage (CS) ratio in a 55:45 forage:concentrate ratio (% DM) total mixed ration on performance of lactating cows and ammonia nitrogen (NH_3-N) emission. Sixteen multiparous Holstein cows (mean ± SD) 77 ± 35 DIM and 640 ± 84 kg of BW were blocked by DIM and randomly assigned to balanced 4 x 4 Latin squares. Cows were housed in modified tie-stall barns with 4 chambers designed to house 4 cows per chamber. Air samples were collected for about 17 h/d, on 3 consecutive days of each period and analyzed for NH_3 with a Photo-acoustic Multi-gas Monitor (Innova Model 1412). Dietary treatments were 20:80 (AS20), 40:60 (AS40), 60:40 (AS60), and 80:20 (AS80). As AS increased, expeller soybean meal substituted for soybean meal to maintain RUP above 6%. Dietary CP content of the diets increased with an increased proportion of AS in the diet and averaged 16.8, 17.2, 17.5, and 18.2% of diet DM for AS20, AS40, AS60, and AS80, respectively. No difference was observed for DMI (26.7 kg/d), milk yield (40.8 kg/d), milk efficiency (milk yield/DMI; 1.53), fat content (3.85%), protein yield (1.20 kg/d) and MUN (16.2 mg/dL). A linear and quadratic response was observed for fat yield which averaged 1.51, 1.59, 1.60 and 1.57 kg/d for AS20, AS40, AS60 and AS80, respectively, with the AS20 diet being lower than the other diets ($P < 0.05$). True milk protein content decreased ($P < 0.05$) from 3.01% in AS20 to 2.96% in AS40 and AS60, and was further reduced to 2.88% in AS80 compared to other treatments. Nitrogen intake increased linearly (701 to 791 g/d) with increasing proportion of AS in the diet whereas milk N decreased linearly (190 to 183g/d). No difference was observed in NH_3-N emission rate among treatments (averaging 0.70 ± 0.16g N/cow/h). Similarly, there was no difference in NH_3-N emission per unit of N intake (0.023 ± 0.006g NH_3-N/g N intake) or per unit of milk N (0.089 ± 0.020g NH_3-N/g milk N). Despite higher N intakes with increasing proportion of AS in the diet, no difference in ammonia emission was observed from cows fed and managed in a tie stall barn.

Key Words: forage, ammonia, emission

W328 Effect of inoculant and molasses on silage fermentation quality, protein fractions, nutritive value and aerobic stability in high dry matter alfalfa. M. Khorvash*[1], F. Hashemzadeh Cigari[1], G.-R. Ghorbani[1], and A. Taghizadeh[2], [1]*Isfahan University of Technology*, *Isfahan, Isfahan, Iran*, [2]*Tabriz University*, *Tabriz, East Azarbayjan, Iran*.

Microbial inoculants, containing lactobacillus plantarum and Propionibacterium acidipropionici (Lalsil) and molasses (0 and 50 g/kg) as a 2 × 2 factorial arrangement were studied on ensiled alfalfa fermentation indices, N fractions (Cornell net carbohydrate and protein system), in vitro degradability and aerobic stability. Forth cut of Alfalfa was wilted to 370 g/kg DM, chopped and ensiled for 90 days. Lalsil decreased pH, NDF, ADF and acetate but increased water soluble carbohydrate (WSC) and lactate: acetate ($P < 0.05$). Molasses addition also decreased pH, lactate: acetate and crude protein, but increased NDF and ADF. Ammonia-N content of the silages were decreased when treated with Lalsil but increased with molasses addition ($P < 0.05$). Lactate, butyrate and propionate were the same between treatments ($P > 0.05$). Inoculation without molasses improved silage fermentation quality more effective than other treatments. Protein fractions evaluation by CNCPS system showed that molasses decreased fraction A in the ensiled forage ($P < 0.05$). Both additives increased fraction B1 content of silages ($P < 0.05$). Fraction B2 was higher in inoculated silages than uninoculated silages ($P < 0.05$). No difference was observed for fraction B3 content among treatments. Fraction C was lower in inoculated silage than uninoculated, but was increased with molasses addition ($P < 0.05$). In vitro 12 h DM degradability assessed with Ankom DaisyII incubator, were highest in silages treated with Lalsil and not added with molasses. However, in vitro 48 h DM degradability were the same among treatments. All the silages treated with additives had better fermentation characteristics and remained more stable than control, after aeration. Silage treated with molasses or inoculant had the lowest rate of mold and yeast growth and pH value was increased rapidly in control but not in treated silages.

In conclusion, molasses and microbial inoculation improved silage fermentation parameters, decreased proteolysis and aerobic stability of high dry matter alfalfa.

Key Words: alfalfa silage, inoculant, CNCPS

W329 The effect of feed management software on whole farm nutrient balance. B. A. Stewart*, B. E. Cox, R. E. James, K. F. Knowlton, M. L. McGilliard, and C. C. Stallings, *Virginia Polytechnic Institute and State University*, *Blacksburg*.

Feeding nutrients more closely to a cow's nutrient requirements will reduce excretion of nitrogen and phosphorus by dairy cattle. The impact of improved feeding accuracy on whole farm nutrient balance through the use of feed management software was studied on 18 dairy herds located in Virginia. Nine herds began using the TMR Tracker feed management software in 2006 and were compared to 9 control herds not using feed management software. Each of the treatment herds was visited on a monthly basis. Annual inputs of nitrogen and phosphorus from purchased feed, fertilizer and animals were recorded from 2005 through 2008. Nitrogen and phosphorus exported from the farm as milk, animals, sold manure and feed were recorded. Whole farm nutrient balance was calculated using University of Nebraska software. After 2008, eight treatment herds and four control herds remained. Herd sizes averaged 290 and 325 for treatment and control farms. Milk production averaged 29.4 and 26.1 kg/d per cow respectively. Crop hectares averaged 326 and 284 respectively. Data were analyzed using proc mixed of SAS with repeated years, using 2005 data as a covariate. Measures of surplus (input-output) and ratio (input/output) were analyzed per farm and per cow. Measures on a per farm basis did not differ between treatment and control herds. Annual phosphorus ratios averaged 1.9 ± 0.9 (SD) and annual nitrogen ratios averaged 3.0 ± 1.5 (SD). On a per cow basis, annual phosphorus surplus averaged 16.1 ± 2.6 (SD) kg/yr and annual nitrogen surplus averaged 138.4 ± 12.7 (SD) kg/yr. Due to the large variation observed the use of feed management software did not have an effect on whole farm nutrient balance.

Key Words: whole farm nutrient balance, phosphorus, nitrogen

W330 Determining water usage on dairies. J. C. Potts*, B. J. Bradford, J. F. Smith, and M. J. Brouk, *Kansas State*, *Manhattan*.

A meta-analysis was performed on 65 studies that recorded water intake by dairy cattle. The meta-analysis was utilized to develop a prediction equation for water intake in lactating dairy cattle. Studies were selected based on quantitative measurements of DMI, water intake (WI), and milk yield. Published papers were selected throughout the world but they mainly came from the *Journal of Dairy Science*. Many of the studies used more than one parameter to determine WI values leading to 137 data points from the 65 studies. With the addition of Na in the meta-analysis, 41 data points were available from the studies to examine the effects of Na on WI. The effects of DMI, diet DM%, dietary Na, and levels of milk production on WI were evaluated. Including data from cows with higher levels of milk production (>30kg/d) improved the correlation (R^2 0.725) between WI and milk production. The meta-analysis results were then compared to on-farm measurements. Fresh water and waste water data from 11 freestall (FS) and 12 dry lot (DL) Kansas dairies were collected over a 9-year period (2000-2008). Fresh water usage was recorded from water pumping records. Data were first summarized annually by operation and then converted to a per cow per day basis prior to analysis. Data were then analyzed by using the proc mixed procedures of SAS. Fixed effects included in the model were dairy type (FS or DL) and year was considered a random effect. The DL dairies averaged 186 L/cow/day and were lower ($P < 0.05$) than the FS dairies which averaged 237 L/cow/day. Differences between DL and FS dairies may have been due to differences in waste management or cow cooling systems. Estimated drinking water accounted for 70% of the total water usage on DL dairies and 55% on FS dairies. Based on this data facility type may influence total water usage in dairy facilities.

Key Words: water intake, facilities, meta-analysis

W331 Dietary CP and tannin extracts impact ammonia emissions from manure deposited on dairy barn floors. J. M. Powell[1], M. J. Aguerre*[2], and M. A. Wattiaux[2], [1]*US Dairy Forage Research Center*, *Madison, WI*, [2]*University of Wisconsin*, *Madison*.

The impact of dietary CP and Quebracho-Chestnut tannin extracts on dairy cow performance and N partitioning are reported elsewhere at this meeting. Mixtures of feces/urine from these studies were applied to lab-scale ventilated chambers to measure ammonia-N emissions (ANE) from simulated concrete barn floors. Feces and urine were collected separately from lactating Holstein cows fed 2 levels of dietary CP (%DM): low protein, LP=15.5 and high protein, HP=16.8; each at 4 levels (%DM) of dietary tannin: T1=0, T2=0.45, T3=0.90 and T4=1.80. Feces and urine having a total weight of 16g were mixed in their excreted mass ratios (g/g) and applied to chambers. ANE were measured 1, 3, 6, 12, 24, 36 and 48h after application. Although patterns of ANE were similar over time, the 48h cumulative ANE (CANE, mg) was lower (P<0.05) for manure from the LP diets (12.1) than from the HP diets (24.7). As a percent of total N (%TN) and urinary N (%UN) applied, losses from the LP diets (16.9 and 46.2) were lower than from the HP diets (27.7 and 56.3). Tannins impacted CANE, %TN and %UN for both the LP and HP diets. For the LP diets, the non-tannin ration (T1) had CANE, %TN and %UN of 14.6, 19.6 and 48.0, respectively vs. 11.2, 16.1 and 45.7, respectively for the tannin-containing rations (average of T2, T3 and T4). Results were similar for the HP diets, except for %UN. Average CANE and %TN for manure from the HP non-tannin ration were 27.5 and 29.1, respectively vs. 23.7 and 27.2 for the HP tannin-containing rations. %UN was lower however for manure from the HP non-tannin ration (52.4) compared to the HP tannin-containing rations (57.5). These differences were likely due to overall higher excretions of urinary N by cows fed HP diets, and therefore higher amounts of urine N applied. For the LP diets, lowest CANE, %TN and %UN occurred at T2 and T4. For the HP diets, lowest CANE, %TN also occurred at T2 and T4, but %UN was lowest at T1 and T2 due to reasons mentioned above. The addition of tannin extracts to dairy rations can reduce ammonia emissions from dairy barns, but relative reductions depend on the amount of CP fed and therefore urinary N excretion.

Key Words: tannins, CP, ammonia emissions

W332 Emissions from a dairy waste management system in south-central Idaho. M. E. de Haro Martí*[1], R. E. Sheffield[2], and M. Chahine[3], [1]*University of Idaho*, *Gooding*, [2]*Louisiana State University*, *Baton Rouge*, [3]*University of Idaho*, *Twin Falls*.

This study evaluated the concentrations and emission rates of ammonia and hydrogen sulfide from a wastewater storage pond, manure processing area, and composting area from a 5,000 cow freestall scrape dairy located in south-central Idaho over a six months period. Pollutant concentrations were measured using an Ultraviolet Differential Optical Absorbance Spectrometer and emission rates were calculated using backward Lagrangian modeling via the WindTrax model. Measurements were collected continuously at a final 15-minute integration time. Average summertime concentrations adjacent to a 9.8-ha wastewater

storage pond were found to be 556.3 ppb for ammonia and 33.4 ppb for hydrogen sulfide, with emission rates averaging 28.5 μg/m^2/s and 4.3 μg/m^2/s, respectively. During the cold period, concentrations were found to average 366.3 ppb for ammonia and 310 ppb for hydrogen sulfide, with emission rates averaging 18.4 μg/m^2/s and 41.5 μg/m^2/s, respectively. Average concentrations downwind of a 13.3 hectare composting area during the warm period were found to be 472.2 ppb for ammonia and 83.1 ppb for hydrogen sulfide, with average emission rates of 33.4 μg/m^2/s and 15.9 μg/m^2/s, respectively. During the cold season, average downwind concentrations were 270.7 ppb for ammonia and 461.7 ppb for hydrogen sulfide, and emission rates averaged 17.3 μg/m^2/s and 81.6 μg/m^2/s, respectively. Significant seasonal variability in both concentrations and emission rates of all pollutants were observed between warm and cold periods.

Key Words: ammonia, hydrogen sulfide, emissions

W333 Nutritive value and silage conservation of mango industrial by products as animal feed in ruminants. A. Conde*[3,1], A. P. Sandoval[2], M. C. Cueto[1], N. M. Rojas[3], and L. M. Arevalo[4], [1]*Universidad de la Sabana*, *Bogotá, Colombia*, [2]*Corpoica*, *Nataima, Colombia*, [3]*Universidad de La Salle*, *Bogotá, Colombia*, [4]*Universidad UDCA*, *Bogotá, Colombia*.

Mango by-products were evaluated in order to define its potential as animal feed in ruminants. Seed and peels from Tommy Atkins and Keitt varieties in different days of industrial process were collected in Frutol Ltda, a fruit industrial company, located in Espinal - Tolima Colombia and analyzed in terms of chemical composition (dry matter DM, crude protein and its fractions A, B1, B2, B3 and C, residual insoluble ethanol RIE, NDF, ADF, lignin, structural carbohydrates: B2 and C, non structural carbohydrates (NSC): A and B, extract ether, ash and gross energy) and ruminal degradation kinetics with the methodology and model proposed by Orskov and McDonald. Tannins and saponins as antinutritive factors were analyzed. The effects of mango by-products as a feed supplement in dairy cows were simulated using the net carbohydrate and protein model, CNCPS. Different silage conservation conditions were evaluated in order to establish the best fermentation process. Peels showed better nutritional quality than seeds due to NSC, in special sugar fraction. Tommy Atkins variety had higher contents of DM, NSC and lower contents of NDF and lignin than Keitt. Higher degradability was found in peels 94%, 99% than in seeds 40%, 54% in Keitt and Tommy, respectively, when Orskov model parameters were estimated. Tannins and saponins were not detected. The principal problem in silage conservation was the low content of DM in mango agro-industrial by-products which was overcome with the 15% inclusion of rice meal before fermentation process. Simulations in the mechanistic CNCPS model predict that mango peels could be a good supplement in dairy cows because its metabolizable energy supply.

Key Words: carbohydrate fractions, mango by-products, silage conservation

W334 The ability of essential oils to inhibit *Salmonella* growth. K. S. Macklin*, J. T. Krehling, Z. T. Williams, and M. A. Bailey, *Auburn University*, *Auburn, AL*.

Salmonella is one of the leading causes of bacterial origin food borne illness in the US. This genus of bacteria is often associated with poultry and the ability to limit or eliminate it is of importance to the consumer as well as to the poultry industry. Historically antibiotics have been added to poultry feed to improve gut health and bird weight gain. Typically antibiotics are not added to control *Salmonella*. Regardless, there is growing sentiment by consumer and government groups to prohibit the use of antibiotics in animal agriculture. This has prompted the need to find a viable alternative to antibiotics; one such alternative is essential oils (EO). EO have been shown to inhibit bacterial growth in vitro and alter the intestinal microbial profile in vivo. In this trial, 13 different subspecies of *Salmonella* were tested against 11 essential oils and 3 antibiotics in a disc diffusion test. The tested EO consisted of red thyme, white thyme, tea tree, black pepper, tarragon, clove bud, Spanish sage, lemongrass, Comoric basil, cinnamon bark and cinnamon leaf. Antibiotics tested included penicillin G at 2 and 10 units, tetracycline at 30ug and chloramphenicol 30ug. EO discs were created by adding 5 ug of each oil onto a 6mm sterile disc and allowed to dry. Trypticase soy agar with 5% sheep blood plates were spread plated with each *Salmonella*. EO impregnated discs were than placed onto each agar plate (4/plate). Plates were then incubated aerobically at 37C for 24 hours. At that time the zone of growth inhibition (if any) for each disc was determined. In this trial, *Salmonella* isolates were considered susceptible if the zone of inhibition was greater then 15mm in diameter, anything less than is considered resistant. All of the essential oils and antibiotics were tested in triplicate against each *Salmonella* isolate. Among the EO tested, the three that *Salmonella* was most susceptible to were cinnamon bark, red thyme and white thyme oils. *Salmonella* isolates were resistant to tea tree, black pepper, tarragon, sage, and Comoric basil oils. The remaining four EO showed variable activity against the different subspecies of *Salmonella* tested.

Key Words: *Salmonella*, essential oils, disc diffusion

W335 Prediction of pregnancy by increased physical activity measured prior to timed insemination. A. H. Sanders*, A. De Vries, and J. Block, *University of Florida*, *Gainesville*.

This study considered activity increases close to timed-AI (TAI) following Ovsynch as predictors of pregnancy. Identifying cows with a greater probability of pregnancy could improve TAI efficiency through select use of semen. Data were 632 breeding records and activity recorded at twice daily milkings as average steps/hr by S.A.E. Afikim pedometers. The percent deviation of activity from the previous 10d rolling average of the same (a.m. or p.m.) milking session was calculated for the day before and day of TAI (4 milkings). At 32d after TAI, pregnancy was diagnosed by ultrasound. Overall, 45% of cows were pregnant. Logistic regression was used to evaluate the effect of activity deviations (AD) on probability of pregnancy (P32). When AD was modeled as a continuous effect, the AD from the first milking on the day of TAI (TAI-AM), and the second milking the previous day (PRE-PM) were significant predictors of P32 but model fit for PRE-PM was poor. For TAI-AM, 5 thresholds for AD were considered for dichotomizing activity signals. Zero, mean AD and mean plus SD (56.8% and 128.7% increase in AD) were 3 thresholds. ROC analysis was used to estimate an optimized threshold. Model fit for ROC was improved by ignoring AD <19.5%, which is the SD of a normal distribution with $\mu=0$ and lower half defined by recorded AD <0 (i.e baseline or non-estrus AD). The resulting optimal threshold was at 84.2% increase in AD (AUC=0.62). Finally, SD_{base} (19.5% increase in AD) was also considered as a threshold. For TAI-AM, the adjusted OR for P32 was significant when the mean AD or those thresholds greater than the mean were applied to AD, but OR was maximized (2.28) with the ROC determined threshold. The binomial probability for P32 was 39% (CI = 35-44%) for cows with AD below this threshold (n=465) and 60% (CI = 52-57%) for cows with AD above this threshold (n=167). For PRE-PM, adjusted OR for P32 was also maximized (1.55) with 84.2% threshold for AP, but fit was poor and CI for binomial probabilities overlap at all thresholds considered. With twice daily milking, AD for the milking interval prior to TAI is a useful indicator of probability of pregnancy.

Key Words: activity, pregnancy diagnosis, pedometer

W336 The influence of lipidic sources on the cholesterol plasma levels of beef heifers. M. C. A. Santana*[1], T. T. Berchielli[1], R. A. Reis[1], G. M. P. Melo[2], and P. H. M. Dian[2], [1]*São Paulo State University*, *Jaboticabal, São Paulo, Brazil*, [2]*Camilo Castelo Branco University*, *Descalvado, São Paulo, Brazil*.

This research aims to evaluate cholesterol responses under different lipid sources and supplementation frequencies. This research was conducted throughout a 4-mo period during the dry season. The experiment was completely random, using a 3 × 2 factorial arrangement (3 supplements and 2 supplementation frequencies). The supplements were derived from 3 different sources, soybean grains, soybean oil and protected fat (Megalac-E), the 2 supplement frequencies were (A) Monday, Wednesday and Friday and (D) daily. In the 4-mo experimental period, August–November, blood samples were taken from the jugular vein after the morning feeding. Subsequently, these samples were centrifuged and stored until the cholesterol blood level was evaluated. In all treatments, no cholesterol differences were observed in August and November ($P > 0.05$). The animals that were given soybean oil supplements Monday, Wednesday and Friday showed lower cholesterol plasma concentration values ($P < 0.05$) in September. The Megalac–E that was supplied daily presented a higher cholesterol level in comparison to the daily supplement of soybean grain in October ($P < 0.05$). Overall, this data indicated that the cholesterol blood level can be influenced according to the feeding strategy during the dry season.

Table 1. Cholesterol plasma levels of heifers supplemented with different lipid sources at two different frequencies

	D–SG	A–SG	D–SO	A–SO	D–ML	A–ML
August	194^{Aab}	181^{Aa}	224^{Aab}	222^{Aa}	221^{Aab}	245^{Aa}
September	250^{ABa}	220^{ABa}	296^{Aa}	210^{Ba}	292^{Aa}	280^{Aa}
October	171^{Bb}	197^{ABa}	199^{ABb}	193^{ABa}	257^{Aab}	214^{ABab}
November	161^{Ab}	168^{Aa}	163^{Ab}	164^{Aa}	185^{Ab}	$169A^{Ab}$

Lowercase in columns and capital letters in rows differ ($P < 0.05$).

D = daily; A = alternately; SG = Soybean; SO = Soy oil, and ML = Megalac-E .

Key Words: soybean grain, soybean oil, protected fat

W337 Substitution of soybean meal by inactive dry yeast in diets of beef cattle: nutrient intake and productive performance. A. F. Campos[1], O. G. Pereira*[1], S. C. Valadares Filho[1], K. G. Ribeiro[2], and L. O. Rosa[1], [1]*Federal University of Vicosa*, *Viçosa, Minas Gerais, Brazil*, [2]*Federal University of Jequitinhonha and Mucuri Valleys*, *Diamantina, Minas Gerais, Brazil*.

The objective of this study was to evaluate the nutrient intakes and productive performance of Nellore cattle fed diets containing different levels of inactive dry yeast (0, 25, 50, 75 and 100%, DM basis) in substitution of soybean meal. Diets consisted of 60% corn silage and 40% concentrate (DM basis), formulated to be isonitrogenous (12% CP, DM basis). Thirty-five Nellore steers non-castrated, with initial live weight of 350 kg were allotted in a randomized blocks design with seven replicates. The animals were kept in individual pens of approximately 10 m2, with protected feeders and waterier. The experiment lasted 84 days, divided in three periods of 28 days after 15 days of adaptation. There was a negative linear effect ($P < 0.05$) of yeast levels on dry matter and crude protein intakes, kg/d, while DMI as percentage of the BW had a quadratic effect with maximum intake of 1.81% BW at 26.98% of yeast level. Quadratic effects ($P < 0.01$) of yeast levels were observed on NDF intake, with maximum intakes of 4.36 kg/d and 0.82% BW at 36.19 and 39.37% of yeast, respectively. The ADG decreased linearly ($P < 0.05$) as yeast levels increased in diets. However, no effects of yeast levels ($P > 0.05$) were observed on ether extract intake, dressing percentage, carcass daily gain and feed conversion, which were, on average 0.215 kg/d, 56.3%, 0.90 kg/d, and 7.57, respectively. Our results suggest that soybean meal might be replaced by inactive dry yeast until 30% of concentrate. However, the utilization of this co-product depends of economic factors.

Financial support by CNPq and FAPEMIG.

Key Words: average daily gain, crude protein, carcass dressing

W338 Changes on growth performance and ruminal variables of finishing Dorper × Pelibuey lambs fed a sorghum grain diet plus an exogenous phytase. G. Buendía-Rodríguez[1], S. S. González–Muñoz*[2], R. Basurto-Gutiérrez[1], M. M. Crosby-Galván[1], L. A. Adame-López[1], and L. J. Montiel-Olguín[1], [1]*CENIDFyMA INIFAP*, *Ajuchitlán, Querétaro, México*, [2]*Colegio de Postgraduados*, *Montecillo, Edo. de México, México*.

The objective of this study was to evaluate the effect of an exogenous phytase (FINASE, AB Enzymes, from *Trichoderma reesei*; 40,000 FTU/g) on lambs fed a 70% ground sorghum grain diet. Thirty-six Dorper × Pelibuey lambs (24.09±2.95 kg BW) were fed the sorghum diet plus 0, 12.5, 25.0 and 37.5 g phytase/t diet, during 75 days. The experimental design was completely randomized, with four treatments and nine replications per treatment. Data collected over time was analyzed as repeated measurements using the MIXED option of SAS, and means were compared with the Tukey test. Variables were average daily gain (ADG), dry matter intake (DMI), feed conversion (FC), concentration of bacteria and volatile fatty acids (VFA) in the rumen, plus phosphorus fecal excretion (PFE). Phytase did not change ($P \geq 0.05$) ADG (199, 228, 232, 206 g/d), DMI (1068, 1127, 1126, 1212 g/d), FC (5.59, 5.01, 4.89, 6.40), or ruminal bacteria concentration (2.91, 3.15, 3.00, 3.06; 10^{10}/mL). However, phytase addition increased ($P \leq 0.05$) propionate concentration in the rumen (23.40^{c}, 24.68^{bc}, 31.37^{a}, 30.43^{ab} m*M*) and PFE (1.10^{b}, 1.18^{ab}, 1.37^{a}, 1.21^{ab} g/d). Therefore, it may be concluded that propionate ruminal concentration as well as phosphorus fecal excretion were affected when an exogenous phytase was added to a 70% sorghum grain diet, fed to finishing Dorper × Pelibuey lambs.

Key Words: phytase, finishing lambs, growth and ruminal variables

W339 Thawed semen quality of beef bulls supplemented with calcium soaps of polyunsaturated fatty acid. H. O. Patino*, M. M. H. Ramirez, R. M. Gregory, and D.d. Ré, *Universidade Federal de Rio Grande do Sul*, *Porto Alegre, RS, Brazil*.

Twenty Hereford, Angus, Brangus and Braford mature bulls (950 kg average body weight) were used in a completely randomized design to evaluate the effect of supplementation with calcium soaps of polyunsaturated fatty acids (CSPUFA) on the semen quality undergone the cryopreservation process and subsequent thawing. Bulls were fed diets with similar levels of crude protein and metabolizable energy consisting of green forage and concentrate supplemented with CSPUFA or energy supplement (ES). For 75 days bulls in the CSPUFA treatment received Megalac-E (200 g/day) and bulls in the ES treatment received Cassava

meal (750 g/day). Bulls were naturally stimulated by cows and semen samples were collected with an artificial vagina every 15 days. Then collected semen was evaluated, diluted and frozen in 0.5 mL straws for later thawing. Assessments of sperm motility, hypo osmotic swelling test (HO), heat resistance test (TTR) and staining with Trypan blue were performed to evaluate the quality of thawed semen. The type of supplement did not affect HO (53.7%) and TTR (27.8%) after freezing. Thawed semen of bulls supplemented with CSPUFA had a 22% increasing in sperm motility (37.5 vs. 30.5%; $P = 0.10$), percentage of spermatozoa with normal acrosome (48.0 vs. 39.2%; $P < 0.05$) and number of live spermatozoa (51.5 vs. 42.2%; $P < 0.05$) in relationship to thawed semen of bulls supplemented with cassava meal. Energy supplementation in the form of calcium soaps of polyunsaturated fatty acids may increase the resistance to the processes of sperm cryopreservation and subsequent thawing, increasing the sperm motility, percentage of live spermatozoa and percentage of spermatozoa with normal acrosome

Key Words: bypass fat, thawed semen, cassava meal

W340 Effects of non-protein nitrogen in diets containing 15% wet distillers grains with solubles and steam-flaked corn on feedlot cattle performance and carcass characteristics. C. H. Ponce*[1], M. S. Brown[1], N. A. Cole[2], C. L. Maxwell[1], J. O. Wallace[1], and B. Coufal[1], [1]*Feedlot Research Group, Department of Agricultural Sciences, West Texas A&M University*, *Canyon,* [2]*USDA ARS Conservation and Production Research Laboratory*, *Bushland, TX*.

Our previous data suggest that the non-protein nitrogen (NPN) need in diets with 15% wet distillers grains with solubles (WDGS) for optimum growth performance may be slightly less than in 0% WDGS diets. The objective of the present study was to more clearly define the NPN need in diets with 15% WDGS. Steer calves (n = 296; initial BW = 344 kg) previously grown for approximately 75 d were adapted to a common finishing diet, blocked by BW, and assigned to 36 soil-surfaced pens (18 m^2 of pen space and 33 cm of bunk space/animal). Treatments included a control diet without WDGS (contained 3% NPN from urea, and cottonseed meal) and 15% WDGS with either 1.5, 2.25, or 3.0% NPN (0.52, 0.78, and 1.04% urea, respectively). Steers were implanted on d 1 with Revalor-XS and were fed twice daily for 165 d. The WDGS was obtained 3 times/wk from a local plant, and grain composition of WDGS averaged 22% sorghum and 78% corn. Overall DMI was 6.1% higher ($P = 0.001$) for steers receiving WDGS than for the control. Similarly, steers fed WDGS had 8% greater ADG ($P < 0.008$) on either a live or a carcass-adjusted basis than the control. However, overall gain efficiency on either a live or adjusted basis was not different among treatments ($P > 0.15$). Dietary NPN concentration did not influence growth performance ($P > 0.21$). Hot carcass weight was 10.9 kg lighter for the control than for 15% WDGS ($P = 0.01$), whereas dressing percentage tended ($P = 0.12$) to increase in a linear manner as NPN increased in diets with WDGS. Remaining measured carcass characteristics were not altered by treatment ($P > 0.16$). The control group tended to have ($P < 0.12$) fewer average Choice and higher and more low Choice carcasses than those fed WDGS, but the distribution of remaining quality and yield grades did not differ among treatments. Data suggest that growth performance may not be improved by including more than 1.5% added NPN in diets with 15% WDGS derived from a blend of corn and sorghum grains.

Key Words: wet corn distillers grains, growth performance, beef cattle

W341 Effects of nutrient restriction and ruminally undegradable protein supplementation during early to mid-gestation on beef cow offspring intestinal growth. A. M. Meyer*[1], P. Moriel[2], W. J. Means[2], M. Du[2], B. W. Hess[2], and J. S. Caton[1], [1]*Center for Nutrition and Pregnancy, Department of Animal Sciences, North Dakota State University*, *Fargo*, [2]*Department of Animal Science, University of Wyoming*, *Laramie*.

Thirty-six Angus × Gelbvieh cows were blocked by parity and randomly allocated by BW to 1 of 3 dietary treatments from d 45 to 185 of gestation: a hay-based control (CON) diet formulated to meet NRC requirements for mid-gestation; a nutrient restricted (NR) diet providing 70% of CON NE_m; or an NR diet fed with a ruminally undegradable protein supplement (NRP) formulated to provide similar essential AA flow to the duodenum as CON. After concluding the dietary treatment period, cows were managed as a single group through calving and weaning. Calves were placed in the feedlot by sex and maternal dietary treatment, and managed similarly during the growing and finishing phases. Steers and heifers were slaughtered at 448 ± 1.0 (mean ± SE) and 466 ± 1.1 d of age, respectively. Detailed necropsies of the small intestine were performed and jejunal samples were collected. Data were analyzed using slaughter group as a block. Slaughter weight (552.4 ± 10.2 kg) did not differ ($P = 0.76$) among maternal treatments. Ileal mass (g) tended to be greater ($P = 0.12$) and proportional mass (g/kg BW) was greater (1.55 vs. 1.26 ± 0.09 g/kg BW; $P = 0.02$) for offspring of CON cows than NR, although liver, duodenal, jejunal, and total small intestinal mass did not differ ($P \geq 0.38$) among treatments. Offspring born to NR cows had greater ($P < 0.05$) jejunal length than CON and NRP, whereas NR had shorter ($P = 0.03$) ileal length compared with CON. Total small intestinal length was greater ($P = 0.02$) for offspring from NR cows than NRP (3,754 vs. 3,448 ± 92 cm). Per unit of BW, ileal length was less ($P < 0.09$) in NR compared with CON and NRP. There were no differences ($P \geq 0.20$) in small intestinal density (g/cm tissue) due to treatment. Additionally, offspring jejunal DNA, RNA, and protein concentration (mg/g tissue) and content (total g) did not differ ($P \geq 0.74$) among maternal treatments. In this study, maternal nutrition of beef cows during early to mid-gestation affected small intestinal length, but not mass, of market-weight offspring.

Key Words: developmental programming, intestine, ruminally undegradable protein

W342 Time of collection affects starch losses in Nellore and crossbred cattle in commercial feedlots. M. Caetano*[1], A. J. C. Nuñez[2], G. B. Mourão[1], and D. P. D. Lanna[1], [1]*University of Sao Paulo, ESALQ*, *Piracicaba, Brazil*, [2]*University of Sao Paulo, FZEA*, *Pirassununga, Brazil*.

Grain sources, grain processing and different feed formulations have been extensively studied in order to improve the efficiency of starch utilization and animal performance. Starch digestion is closely and directly related to fecal starch content (FS%), however we have observed large variations in FS% through a 24-h period in experimental animals. The objective of this study was to determine the magnitude and variability of starch losses in commercial feedlots, as well as the influence of collection period, diet starch content, grain particle size after grinding, genetic group and starch source (corn or sorghum) on pH and FS%. Samples (n=935) were collected on 9 commercial feedlots, with 13 different diets using ground corn or sorghum as starch sources. Diets contained between 40 and 88% concentrate and starch contents between 14.6 and 45.9% in the dry matter (DM). Animals were classified as Nellore or European crossbreds. Morning collections were taken between 0700 and 1200 h and afternoon collections between 1300 and 1800 h. Diets and feces were immediately put on ice and analyzed for DM, ash and starch. Diets were also analyzed for particle size while feces were analyzed for

pH. The average values for FS% were 9.8±7.50% and the range was 0.1% to 41.6% in the DM. There was a difference ($P \leq 0.05$) between FS% for samples collected in the morning or afternoon for both Nellore and crossbred (7.5% and 6.6% in the morning vs. 2.2% and 4.7% in the afternoon, respectively). There was an interaction between genetic group and period of collection ($P \leq 0.01$), however there was no difference in FS% between diets with corn or sorghum ($P \geq 0.29$). There was a linear and quadratic increase ($P \leq 0.06$) in FS% as starch content of the diet increased and no effect of particle size in FS% for both sources ($P \geq 0.21$). Fecal pH was higher for corn than for sorghum (6.55 vs. 6.04; $P \leq 0.01$), and there was a negative correlation between FS% and fecal pH ($r = -0.57$ for corn and $r = -0.51$ for sorghum; $P \leq 0.01$). In conclusion, FS% differs depending on time of sample collection, demonstrating the importance of standardization of sampling procedures.

Key Words: beef cattle, corn, sorghum

W343 Parenteral supplementation of cross bred Brahman steers with copper and zinc in the western plains of Venezuela. R. E. Mora*[1], A. M. Herrera[1], D. L. Sánchez[1], C. F. Chicco[2], and S. Godoy[2], [1]*Universidad Nacional Experimental del Táchira*, *Venezuela*, [2]*Universidad Central de Venezuela*.

To evaluate parenteral Cu and Zn supplementation on daily body gain (DBG), body measurements (BM) and blood chemistry of cattle, an experiment was carried out in the western plains of Venezuela, with 60 cross bred Brahman steers with an average BW of 201.6±20 kg. The animals were uniformly divided in four groups and assigned to four treatments: 1) oral mineral supplementation (OMS); 2) OMS with injected Cu (OMS-Cu); 3) OMS with injected Zn (OMS-Zn); and 4) OMS with injected Cu and Zn (OMS-Cu-Zn). Fifty mg of Cu and 80.2 mg of Zn/100 kg were injected subcutaneously every 73 and 28 days, respectively. The experiment lasted 129 days. The animals were kept under grazing conditions, in pastures of *Brachiaria arrecta* and *B. mutica* with a stocking rate of 0.9 animal/ha. In addition animals had access to a complete mineral mix and to a broiler litter, molasses and urea supplement (800 g/d) with 23.2% PC. Body weight changes were measured every 28 days. At the same time blood and forage samples were taken for chemical analyses. Changes in heart girth (HG) and wither height (WH) were measured at the beginning and at the end of the experiment. Data were analyzed by ANOVA in a complete randomize design using a 2 × 2 factorial arrangement. Forage contained 4.0 ± 1.4% CP; 77.8 ± 2.7% NDF; 5.6 ± 2.5 ppm Cu and 22.5 ± 6.2ppm Zn. Poultry litter supplement had 71.5 ppm Cu and 328.8 ppm Zn. No differences were found among treatments for DBG, with an average of 363.1±273.8 g/d, showing ($P < 0.05$) an interaction time × Cu, with greater gains of supplemented animals in the transition dry-wet season (552.6 ± 201 vs. 487.4 ± 131.1 g/d), and lower in the wet season, when compared with the unsupplemented animals (535.9 ± 263.9 vs. 632.1 ± 191.6 g/d). No differences in BM and blood chemistry were found. It is concluded that under the conditions of the experiment, subcutaneous Cu and Zn supplementation had no effect on animal performance and blood chemistry.

Key Words: parenteral supplementation, daily gain, body measurements

W344 Effect of wheat distillers dried grains with solubles (DDGS) as a replacement for barley grain and barley silage on ruminal pH and fermentation in finishing beef cattle. Y. L. Li*[1,2], W. Z. Yang[1], M. L. He[1], T. A. McAllister[1], and K. A. Beauchemin[1], [1]*Agriculture and Agri-Food Canada, Research Centre*, *Lethbridge, AB, Canada*, [2]*Feed Research Institute, Chinese Academy of Agricultural Sciences*, *Beijing, China*.

A study was conducted to evaluate whether wheat DDGS can partially, or entirely, replace grain and forage in a finishing diet fed to growing beef cattle without increasing the risk of ruminal acidosis. Eight ruminally fistulated Angus heifers were assigned to a replicated 4×4 Latin square design with 4 treatments: control, low (25%), med (30%) and high (35%) DDGS (% of dietary DM). The diets consisted of barley silage, barley concentrate, and wheat DDGS in ratios of 15:85:0, 10:65:25, 5:65:30 and 0:65:35 (DM basis), respectively. Heifers were fed once daily for ad libitum intake. Ruminal pH was monitored continuously for 5 d each period using a wireless system (LRCpH). Mean ruminal pH linearly ($P < 0.01$) decreased from 5.94, 5.88, 5.70, to 5.75 as DDGS was substituted for barley silage. Duration of which pH<5.8 was longer for med (14 h) and high (13 h) DDGS diets than for control (10 h) and low DDGS (10 h) diets. Total VFA concentration (m*M*) quadratically increased ($P = 0.04$) and was the highest for med DDGS (149) and lowest for control (135) and high DDGS (135) diets. Molar proportion of acetate linearly ($P < 0.01$) decreased, whereas that of propionate tended to linearly ($P = 0.06$) increase with the increase of DDGS and decrease of silage, so that the fermentation changed to a more glucogenic pattern. Concentration of NH_3-N tended to ($P = 0.07$) be higher for DDGS diets (averaged 10.6 m*M*) than for the control diet (6.5 m*M*). The results indicate that replacing barley grain and silage with wheat DDGS in finishing diets may improve feed efficiency and growth rate due to a more glucogenic fermentation. However, animals may experience more rumen acidosis, suggesting that fiber from wheat DDGS was not physically effective.

Key Words: wheat DDGS, ruminal fermentation, beef cattle

W345 Effect of levels of canola meal supplementation on intake and apparent digestibility in wethers. F. Hentz*, G. V. Kozloski, T. Orlandi, G. F. E. Pacheco, S. C. de Àvila, and P. S. Castagnino, *Universidade Federal de Santa Maria*, *Santa Maria, RS, Brasil*.

The effect of increasing levels of supplementation of meal from biodiesel production canola (44.4% CP and 29.5% NDF; DM basis) on intake and apparent digestibility by wethers was evaluated. Eight Texel wethers were used in a replicated 4x4 Latin square design with 15-d periods (10-d adaptation, 5-d collection). Wethers were housed in metabolism cages and fed a basal diet consisting of sudangrass ad libitum (10% refusals). Treatments were sudangrass only (control), or supplemented with 5, 10 or 15 g/kg BW of canola supplement (90% canola meal, 10% finely ground corn), offered twice daily at 0800 and 1700 h. Feed, orts and fecal output were recorded daily on day 10 to 15 and samples collected and composited within animal and period. Data were analyzed using the PROC GLM procedure of SAS. Forage DMI decreased linearly ($P < 0.05$) from 531 to 326 g/d as supplement intake increased. Total DMI, which included forage and supplement and nitrogen intake increased linearly ($P < 0.05$) from 531 to 778 g/d and 10 to 36 g/d, respectively. Apparent digestibilities of DM, OM, and NDF were similar for all treatments and averaged 0.69, 0.76 and 0.66, respectively, whereas N apparent digestibility increased linearly ($P < 0.01$) from 0.74 to 0.87 as supplement levels increased. In conclusion, supplementation with canola meal exerts a negative effect on forage intake while improves total nutrient intake by wethers.

Key Words: biodiesel byproducts, intake, digestibility

W346 Evaluation of including elevated levels of wet distillers grains in diets of beef steers. J. M. Carmack*[1], P. M. Walker[1], J. D. Fehr[1], R. L. Atkinson[2], and L. A. Forster[3], [1]*Department of Agriculture,*

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Few studies have been conducted evaluating inclusion rates of modified wet distillers grains with solubles (DGS) above 55% of the diet DM for finishing beef steers. The objective of this trial was to compare feedlot performance and carcass characteristics of feedlot steers fed increasing levels of DGS. The treatments (percent DM basis) were: 80 shelled corn/5 soybean meal/15 corn silage (CON), 25 DGS/60 shelled corn/15 corn silage (25 DGS), 40 DGS/45 shelled corn/15 corn silage (40 DGS) and 70 DGS/15 shelled corn/15 corn silage (70 DGS). Angus cross steers (n=140; 367±31 kg BW) were stratified by weight to 20 pens. Treatments were randomly assigned to pens with unequal pen replication. Seventy head were harvested on d 165 when 90% were estimated to have reached low choice or higher quality grade. The remaining 70 head were harvested on d 200 when 90% were estimated to have reached low choice or higher quality grade. Steers fed 70 DGS had higher ($P < 0.05$) ADFI and DMI compared to steers fed CON and 25 DGS. Mid trial G:F, end of trial G:F and final wt were lower ($P < 0.05$) for 70 DGS steers than steers fed CON, 25 DGS and 40 DGS. ADG tended to be higher ($P = 0.07$) for CON, 25 DGS and 40 DGS steers. No significant differences were observed for KPH percent and liver score. Dressing percent, carcass wt, ribeye area, and quality grade were lower ($P < 0.05$) for 70 DGS steers compared to other treatments. CON and 25 DGS steers had higher ($P = 0.02$) yield grades and 25 DGS steers had higher ribfat ($P = 0.02$) than 40 or 70 DGS steers. No significant differences in quality grade between treatments were observed (CON=100%, 25 DGS=97%, 40 DGS=100%, 70 DGS=87%) but 70 DGS steers did trend lower ($P = 0.07$) with 12% grading select. Results from this study suggest that steers fed DGS at 25 or 40% of the diet (DM) have similar or improved performance compared to control steers while steers fed 70 DGS have reduced performance but similar quality grades.

Key Words: high levels distillers grains, feedlot performance, carcass

W347 Performance, feed intake, residual feed intake and feed:gain ratio in progeny of Nellore steers housed in individual or group pens. M. L. Nascimento*[1], R. R. Tullio[2], M. M. Alencar[2], J. S. Lima[3], L. D. C. Vieira[4], M. L. P. Silva[4], and D. P. D. Lanna[1], [1]*University of Sao Paulo*, *Piracicaba, Sao Paulo, Brazil*, [2]*Embrapa Pecuaria Sudeste*, *Sao Carlos, Sao Paulo, Brazil*, [3]*Rural Federal University of Pernambuco State*, *Garanhuns, Pernambuco, Brazil*, [4]*State University of Sao Paulo*, *Jaboticabal, Sao Paulo, Brazil*.

Feed is the most expensive input within any livestock production system, including beef cattle. Residual feed intake (RFI), defined as the difference between observed intake and that predicted from average weight and daily gain, has been proposed as a criterion for genetic selection. There have been very little studies with this trait in *Bos indicus* breeds. The objective of this study was to assess the phenotypic variability in RFI in Nellore cattle. In addition to that, we re-evaluated the effect of housing type (group and individual pen) on ADG, G:F, DMI, and RFI. Hundred fourteen Nellore steers, progeny of eighteen bulls, were fed individually for 77 days, where 41 housed in individual pens and 73 in group pens with electronic gates feeders. The diet contained 40% corn silage and 60% concentrate on a dry matter basis, and was supplied ad libitum, twice a day. Animals were classed as low or high RFI if their RFI fell 0.5 SD or more below or above the mean (zero). There was no difference among ($P > 0.05$) between animals housed in individual or group pens for average daily gain (1.21 versus 1.23 kg/d, respectively), DMI (9.46 versus 9.44 kg DM/d, respectively), G:F (8.06 versus 7.83 kg/kg, respectively) and RFI. Housing type effects may be more evident under once daily feeding rather than with the twice daily interactions adopted in the present study. This study shows that individual pens may be used as long as animals are stimulated to come to the bunk more than once daily.

Key Words: beef cattle, intake, feeding

W348 Residual feed intake in progeny of Nellore bulls. M. L. Nascimento*[1], R. R. Tullio[2], M. M. Alencar[2], J. S. Lima[3], L. D. C. Vieira[4], M. L. P. Silva[4], and D. P. D. Lanna[1], [1]*University of Sao Paulo*, *Piracicaba, Sao Paulo, Brazil*, [2]*Embrapa Pecuaria Sudeste*, *Sao Carlos, Sao Paulo, Brazil*, [3]*Rural Federal University of Pernambuco State*, *Garanhuns, Pernambuco, Brazil*, [4]*State University of Sao Paulo*, *Jaboticabal, Sao Paulo, Brazil*.

Residual feed intake (RFI), defined as the difference between observed intake and that predicted from average weight and daily gain, has been proposed as a criterion for genetic selection. There have been very little studies with this trait in Bos indicus breeds. The objective of this study was to assess the phenotypic variability in RFI in Nellore cattle. Hundred thirty-eight Nellore steers, progeny of eighteen bulls, were fed individually for 77 days. The diet contained 40% corn silage and 60% concentrate on a dry matter basis, and was supplied ad libitum. The prediction equation was DMI = 0.1105 × Average $BW^{0.75}$ + 1.32 × Average Daily Gain (ADG). Animals were classed as low or high RFI if their RFI fell 0.5 SD or more below or above the mean (zero), where 39 were classed in the low RFI and 43 in the high group. Individual values of RFI ranged from –3.44 to 3.84 kg/d. Mean RFI for the low and high RFI groups were −1.11 and 1.06 kg/d, respectively; by definition, weights and ADG were similar between RFI groups. There was a difference among RFI groups for intakes and feed:gain where the high RFI group had intake 27.6% greater ($P < 0.0001$) than the low RFI steers (10.44 versus 8.18 kg of dry matter/d) and 0.5 percentage points more on a % BW basis. Furthermore, the high RFI group showed worse feed:gain ratio. The bulls were different from each other ($P < 0.05$) for ADG, feed intake and feed:gain (kg of dry matter/d and % BW). These results show the phenotypic variability in RFI and other traits among progeny of Nellore bulls.

Key Words: beef cattle, intake, genetic selection

W349 Effects of supplemental vitamin E with different oil sources on growth, health, and carcass parameters of preconditioned beef calves. C. J. Mueller*[1,2], C. Sexson[1], and R. R. Mills[1], [1]*Oregon State University*, *Corvallis*, [2]*Eastern Oregon Agricultural Research Center*, *Union*.

This trial was designed to evaluate the impact of supplemental vitamin E with or without different oil sources during a 35-d preconditioning period. Sixty-four (224 ± 33 kg) Angus-cross calves were stratified by weight and sex then randomly allotted to one of four treatments: CON (corn-soybean meal (base) diet with no added vitamin E or oil), SE (base diet plus 150 IU supplemental vitamin E), ELA (SE diet plus 1.5% safflower oil) and ELNA (SE diet plus 1.5% linseed oil). Following preconditioning, calves were shipped to a feedlot where they received a modified live intranasal vaccine for Infectious Bovine Rhinotracheitis (IBR) and Parainfluenze-3 (PI_3) on d37 and d56 to stimulate immune activity. Blood samples were obtained after preconditioning (d35), post-transit to the feedlot (d36), post-initial vaccination (d42), and post-secondary vaccination (d63 and 70) to quantify glucose and antibody titers. Weights were collected throughout the study with carcass data collected at harvest. Gain and carcass data were evaluated as a

randomized complete block design with sex as block, using the following preplanned contrasts: CON vs. vitamin E (mean of SE, ELA, and ELNA), SE vs. OIL (mean of ELA and ELNA), and ELA vs. ELNA. No differences ($P > 0.10$) were detected for ADG or body weights during the preconditioning and finishing periods. No differences ($P > 0.10$) were detected for carcass measurements between treatment contrasts, with the exception of backfat tending ($P < 0.10$) to be greater in SE calves versus OIL calves. Morbidity rates were less than 1% and consistent across treatments. Supplementation of vitamin E resulted in greater amounts of IBR titer at d35 and d36 ($P < 0.05$). The SE calves had higher PI_3 titers ($P < 0.05$) at d35 compared to OIL calves, but were similar ($P > 0.10$) through the feedlot phase. No differences ($P > 0.10$) were detected for PI_3 titers or glucose after the preconditioning period for any contrast. Supplementation of preconditioning diets with vitamin E with or without dietary essential fatty acids showed limited improvement in gain and immune response indicators in weaned calves.

Key Words: vitamin E, preconditioning, cattle

W350 Level of ammonia-nitrogen required to maximize ruminal microbial efficiency. Y. Liang* and M. S. Kerley, *University of Missouri*, *Columbia*.

Microbial efficiency (MOEFF) in the rumen is a function of dilution rate (D), with achievement of maximum efficiency dependent upon adequate supply of peptides and ammonia-nitrogen. Equations predicting maximum MOEFF at varying D were used to predict microbial requirements for peptides and ammonia nitrogen. The objective of this experiment was to determine accuracy of these prediction equations to estimate ammonia-nitrogen requirement of ruminal microbes. Our hypothesis was that MOEFF and organic matter digestion, when peptide-nitrogen supply was adequate and ammonia-nitrogen was limiting, would respond to increasing supply of ammonia nitrogen. Diets consisting of corn, Soyplus, bloodmeal and urea were formulated to provide adequate RDP (peptides) and inadequate to adequate levels of ammonia-nitrogen. Four diets were fed to continuous culture fermenters, varying in urea content (0, 0.2%, 0.45%, 0.7% urea on dry matter basis). The 0.7% urea diet was calculated to provide adequate ammonia-nitrogen. Ammonia, pH and VFA concentrations, organic matter and protein digestion and MOEFF were measured. As RDN (urea) increased digestibility of OM (linear, $P < 0.09$), MOEFF (linear, $P = 0.15$) and protein (quadratic; $P < 0.05$) increased. Increasing RDN level increased ammonia (quadratic, $P < 0.02$), butyrate (linear, $P < 0.01$) and total volatile fatty acid (linear, $P < 0.1$) concentrations. No differences were measured for pH, acetic and propionic acid concentrations or acetic to propionic acid ratio among treatments. Measured RDP and RDN were similar to predicted values. We concluded that increasing VFA concentrations, organic matter digestibility and MOEFF as RDN increased in diets occurred due to availability of ammonia-nitrogen increasing. Elevation of ammonia-nitrogen in 0.07% urea diet was believed to have occurred because ammonia-nitrogen requirement was met, as predicted. Requirement for RDN has been well established and this research demonstrated that ruminant diets can be balanced to supply required levels of RDN.

Key Words: MOEFF, rumen degradable nitrogen, ruminal fermentation

W351 Effects of polyunsaturated fatty acid supplementation (PUFA) on forage intake and digestibility in beef cows. R. F. Cooke*, A. B. Scarpa, F. M. Nery, F. N. T. Cooke, and D. W. Bohnert, *Oregon State University - EOARC*, *Burns*.

The objective was to compare DMI and in situ forage digestibility in beef cows supplemented or not with a rumen-protected PUFA source. Three Angus × Hereford cows (724 ± 39 kg of BW) fitted with ruminal cannulas were allocated to a 3 × 3 Latin Square design containing 3 periods of 21 d each. Treatments consisted of grain-based supplements without (CO) or with the inclusion (10%; as-fed basis) of a PUFA source (PF; Megalac-R, Church and Dwight, Princeton, NJ) or a saturated fatty acid source (SF; Megalac, Church and Dwight). Treatment intakes were formulated to be iso-caloric and iso-nitrogenous, and offered daily at a rate of 0.7% of BW/cow/d. Within each experimental period, mixed alfalfa-grass hay was offered in amounts to ensure ad libitum access from d 1 to 13, and hay DMI was recorded daily. Data collected from d 8 to 13 were used to determine treatment effects on hay and total DMI. From d 14 to d 21, cows were restricted to receive 90% of their voluntary hay DMI. Immediately before treatment feeding on d 16, polyester bags containing 4 g of hay (DM basis) were suspended within the rumen of each cow, and incubated in triplicates for 0, 4, 8, 12, 24, 36, 48, 72, and 96 h. After removal, bags were washed, dried for 96 h at 50°C in forced-air ovens and weighed. Triplicates were combined and analyzed for NDF content. Hay and total DMI were reduced ($P < 0.05$) in PF cows compared to SF and CO cows (2.19, 2.30, and 2.31% of BW for forage DMI, SEM = 0.29; and 2.86, 2.98, and 3.05% of BW for total DMI, SEM = 0.29). However, no treatment effects were detected ($P > 0.48$) for ruminal degradation rate of hay DM (6.81, 7.48, and 6.86%/h for CO, PF, and SF; SEM = 0.40) and hay NDF (6.05, 6.43, and 6.17%/h for CO, PF, and SF; SEM = 0.30). Similarly, no treatment effects were detected ($P > 0.63$) for effective ruminal degradability of hay DM (64.53, 64.93, and 64.94% for CO, PF, and SF; SEM = 0.38) and hay NDF (71.24, 71.76, and 71.57% for CO, PF, and SF; SEM = 0.36). In conclusion, PUFA supplementation did not impact forage digestibility, but decreased forage and total DMI in beef cows.

Key Words: forage digestibility, polyunsaturated fatty acids, beef cattle

W352 Use of real-time ultrasound (RTU) measurements and carcass traits to assess internal fat in residual feed intake (RFI)-indexed Brahman bulls under grazing conditions. C. A. Hughes*[1], J. A. Carter[1], T. D. A. Forbes[2], F. M. Rouquette, Jr.[3], L. O. Tedeschi[4], R. D. Randel[3], and F. R. B. Ribeiro[1], [1]*Texas A&M University-Commerce*, *Commerce,* [2]*Texas AgriLife Research*, *Uvalde,* [3]*Texas AgriLife Research*, *Overton,* [4]*Texas A&M University*, *College Station*.

This study evaluated RTU and carcass traits to determine total internal fat (IFAT) of Brahman bulls (n = 16) grazing Coastal bermudagrass ([*Cynodon dactylon* (L.) Pers]) at two stocking rates (SR) for 60 d. Prior to the grazing trial, animals were fed a high roughage diet for 70 d, stratified as efficient (LRFI) or inefficient (HRFI), and randomly assigned to high (HSR) or low (LSR) SR pastures. RTU measurements were collected 5 d prior to harvest off pasture and consisted of KPH depth (uKPH), backfat thickness (uBF), ribeye area (uREA), rump fat (uRUMP), i.m. (uIMF), and BW. Bulls were harvested at 16 to 18 mo of age and about 450 kg. Shrunk BW (SBW) was recorded after an 18 h fast prior to harvest. At harvest KPH and internal organs were separated, dissected, and weighed. Total internal fat was determined by adding the KPH and physically separated organ fat weights. After a 48-h chill complete carcass data was collected. Data were analyzed using a split-plot design in a 2 × 2 factorial arrangement with pastures within SR as random factors. Prediction equations were developed using the PROC REG procedure with the stepwise selection. There were no interactions or main effects of SR ($P > 0.05$) and RFI ($P > 0.05$) on any of the carcass traits or RTU measured; except for carcass backfat

that was significant ($P = 0.051$) with LRFI bulls having more backfat than HRFI bulls (0.22 vs. 0.13 cm, respectively). A linear regression to predict IFAT from KPH and uRUMP (R^2 of 0.61 and square root of mean square error of 1.54 kg) was developed. The stepwise selection indicated a partial R^2 of 0.53 for KPH and 0.08 for uRUMP. A previously published equation to predict IFAT from KPH accounted for 53% of the IFAT variation of our data. No differences between RFI and SR using RTU were detected for Brahman bulls harvested direct off pasture. The RTU may improve the predictions of IFAT when KPH is available. A second year of data will be used to improve the precision of the IFAT predictive equations.

Key Words: ultrasound, internal fat, carcass

W353 Effects of co-ensiling direct-cut grass with corn modified wet distillers grain plus solubles on beef steer diet digestibility. R. P. Arias*[1], L. J. Unruh-Snyder[1], E. J. Scholljegerdes[2], A. N. Baird[1], K. D. Johnson[1], D. Buckmaster[1], R. P. Lemenager[1], and S. L. Lake[3], [1]*Purdue University*, *West Lafayette, IN*, [2]*USDA-ARS Northern Great Plains Research Laboratories*, *Mandan, ND*, [3]*University of Wyoming*, *Laramie*.

Four crossbred beef steers fitted with ruminal cannulas (BW = 556 ± 31 kg) were used in a 4 × 4 Latin square to evaluate the effects of feeding co-ensiled corn modified wet distiller's grain plus solubles (WDG) with direct-cut grass (DC; 30% DM; 40% Tall Fescue) on diet digestibility characteristics. Steers were fed for four 14-d periods (10-d for adaptation and 4-d of samples collection). Diets were formulated to be isocaloric and isonitrogenous and consisted of: 1) a corn silage control-diet supplemented with soybean meal (CON); 2) DC co-ensiled with WDG in a 3:1 (DM basis; CO-EN); 3) Haylage (DC ensiled without WDG) mixed with WDG at feeding (H+WDG); 4) Haylage mixed with corn dry distiller's grain plus solubles (DDG) at feeding (H+DDG). Dry matter and N intake did not differ ($P > 0.05$) across treatments, however, steers fed the CON diet had lower ($P < 0.01$) NDF intake compared to other treatments. Apparent total tract DM and N digestibility were greatest ($P = 0.02$), and total fecal DM and N excretion were lowest ($P = 0.02$) for steers fed the CON diet compared to all other diets. Steers fed the H+DDG diet had lower ($P = 0.02$) rumen ammonia concentration compared to the CON and H+WDG diets, with the CO-EN diet being intermediate. The CON diet also had greater ($P = 0.03$) total VFA concentrations and lower ($P = 0.03$) acetate:propionate compared to the all other diets. Results from this study suggest that although the feeding value of the CON diet was higher; there was a similar feeding value between direct-cut grass co-ensiled with WDG, and haylage diets fed with either WDG or DDG added at the time of feeding.

Key Words: distillers grains, co-ensiled, digestibility

W354 Acetate utilization in young crossbred calves is age-dependent. K. Pike*, W. A. D. Nayananjalie, T. R. Wiles, M. A. McCann, D. E. Gerrard, and M. D. Hanigan, *Virginia Polytechnic Institute and State University*, *Blacksburg*.

Early weaning is a management strategy for reducing lifetime feed intake in beef cattle. As the age at weaning decreases, however, the ability of the calf to utilize energy substrates may limit the effectiveness of this approach. Volatile fatty acids are critical in ruminant metabolism and acetate is the primary energy yielding substrate. We hypothesized that acetate clearance rates would provide information on postabsorptive capacity of young calves to utilize acetate. Four Angus × Simmental bull calves weighing 113±9 kg at 87 ± 2 days of age and 4 calves weighing 133±10 kg at 111±5 days of age were given a bolus infusion of acetate (4 mmol of acetate/kg of BW) over a 5 min period via an indwelling jugular catheter. Blood samples (5 ml) were collected from the jugular catheter at 5 min intervals over the first 30 min post-infusion and at 15 min intervals over the next 60 min. Blood samples were placed on ice immediately after collection and plasma was prepared and stored at −20° C until analysis. Plasma acetate levels were determined by isotope dilution using gas chromatograph-mass spectrometry. Acetate clearance rates were determined for each calf by fitting an exponential decay curve to the observed acetate concentration data using the NLIN procedure of SAS. Resulting clearance rates were analyzed using the MIXED procedure of SAS. Although, differences in clearance rates between older (0.003 ± 0.0002) and younger animals [0.002 ± 0.0002 ($\min \times BW^{.075}$)$^{-1}$)] was not significant ($P = 0.26$), greater basal blood acetate concentrations for the younger animals (2.9±0.6 vs. 6.8±0.6 mmol, respectively; $P < 0.01$) are consistent with the numerical reductions in clearance rates. These data suggest that utilization of acetate by tissues of calves is age-dependent and suggest that the weaning age may be limited by the ability of the tissues absorb acetate from the peripheral circulation.

Key Words: acetate, calves, clearance rate

W355 Ergot alkaloids induce vasoconstriction of bovine foregut vasculature. A. P. Foote*[1], J. L. Klotz[2], D. L. Harmon[1], L. P. Bush[1], and J. R. Strickland[2], [1]*University of Kentucky*, *Lexington*, [2]*USDA-ARS, FAPRU*, *Lexington, KY*.

Alkaloids produced by the *Neotyphodium coenophialum* endophyte in association with tall fescue (*Lolium arundinaceum*) are imputed to cause peripheral symptoms of fescue toxicosis. We hypothesized that theses compounds could correspondingly affect foregut vasculature. The objective of this study was to determine vasoconstrictive potentials of ergovaline (ERV), ergotamine (ERT), ergocryptine (ERP), ergocristine (ERS), ergonovine (ERN), ergocornine (ERO), lysergic acid (LSA), and an ethanol-extract of ground endophyte-infected fescue seed (EXT) on right ruminal artery and vein. Segments of right ruminal artery and vein were collected from the ventral coronary groove of predominately Angus heifers (n = 7) shortly after slaughter and placed in a modified Krebs-Henseleit buffer on ice. Vessels were cleaned of excess connective tissue and fat, sliced into 2-3 mm segments and suspended in a multi-myograph chamber with 5 mL of continuously oxygenated Krebs-Henseleit buffer (95%O_2/5% CO_2; pH 7.4; 37°C). Arteries and veins were equilibrated to 1.0 g and 0.5 g respectively for 90 min followed by addition of 120 m*M* KCl. Increasing concentrations of each compound were added to the respective chamber every 15 min following buffer replacement. Data were normalized as a % of the contractile response induced by KCl and were analyzed as a completely randomized design using PROC MIXED of SAS. No venous response was observed until 1×10^{-5} *M* and no arterial response was observed until 1×10^{-6} *M* for ERV and ERT, 1×10^{-5} *M* for ERP, ERO, and ERN, and 1×10^{-4} *M* for ERS. Alkaloid, concentration, and vessel affected contractility ($P < 0.05$). A greater arterial maximal response was observed for ERO, ERT, ERV, and EXT ($P < 0.05$) and the arterial and venous responses were not different for ERN, ERP, ERS, and LSA ($P > 0.05$). These results indicate that ergot alkaloids have potential to alter blood supply and drainage from the bovine foregut and the differential artery and vein responses may contribute to the fescue toxicosis syndrome.

Key Words: ruminal artery and vein, vasoconstriction, tall fescue

W356 Comparison of methods to predict carcass composition in grass and grain fed Angus steers. G. Acetoze*, G. D. Cruz, and H. A. Rossow, *University of California*, *Davis*.

Interest in grass finished beef has been increasing. However more research is needed to apply grass finishing to current beef production systems. Methods to predict carcass composition were developed based on data from grain finished cattle. However data are limited on the accuracy of using these methods for grass finish cattle. The objective of this study is to examine the effects of grass or high grain diets on the carcass composition of Angus steers and compare results from two methods for determining carcass composition. Carcass composition was estimated using specific gravity (SG) and composition of 9-11th rib section (RS) from the right side (Lunt et al., 1985), to compare the percentages of muscle, fat and bone of 14 grain-fed and 13 pasture-fed Angus steers. Steers were slaughtered when their estimated quality grade by ultrasound was greater than low select. Average yield and quality grades for grass finish steers were 58% and high select, and 63% and average choice for grain finish steers. Average live weights at slaughter were 610 and 630 kg with standard deviations of 87 and 78 kg for grass and grain diets, respectively. Pasture was a mix of white clover and ryegrass (15.8% crude protein, 49.8% NDF) and the feedlot diet was a 90% corn, 10% alfalfa finishing diet (13.0% crude protein, 26.3% NDF) on a dry matter basis. Data were analyzed with the general linear models procedure of SAS (SAS Institute, 2004) for method, type of diet and method diet interaction with bodyweight as a covariate. Muscle and fat % were significantly different (P< 0.05) for method used to estimate carcass composition with least squares means for muscle of 60.3% and 52.0% and fat of 24.1% and 31.7% for RS and SG, respectively. Bone % for diet and method, interaction between diet and method and use of body weight as a covariate for muscle, fat and bone % were not significant. These results imply that carcass composition is different for grass and grain finish steers. However, equations estimating muscle and fat % may need to be re-evaluated for grass finish steers.

Key Words: grass finish, carcass composition

W357 Rumen bacterial population dynamics of steers grazing winter wheat forage and a yeast culture supplement. D. W. Pitta*[1], W. E. Pinchak[1], S. E. Dowd[2,4], J. Osterstock[3], V. Gontcharova[2], E. Youn[4,5], K. Dorton[6], I. Yoon[6], B. R. Min[1], J. D. Fulford[1], T. A. Wickersham[7], and D. P. Malinowski[1], [1]*Texas AgriLife Research*, *Vernon,* [2]*Research and Testing Laboratory*, *Lubbock,* [3]*Texas AgriLife Research*, *Amarillo,* [4]*Medical Biofilm Research Institute*, *Lubbock,*[5]*Texas Tech University*, *Lubbock,* [6]*Diamond V Mills*, *Cedar Rapids, IA,* [7]*Texas A&M University*, *College Station*.

A study was conducted to study the dynamics in rumen bacterial populations using bTEFAP technique in steers grazing winter wheat with and without yeast supplementation on the Southern Great Plains of Vernon, Texas over a 75-day period. Experimental design included 14 (Angus × Hereford) ruminally cannulated steers grazing a basal winter wheat forage and grouped into 3 treatments based on yeast supplementation i.e., treatment 1 (control; n=4), treatment 2 (7% yeast; n=5) and treatment 3 (14% yeast; n=5). Both fiber and liquid fractions of rumen samples were collected on day 14, 28, 56 and 76 to investigate their associated bacterial populations. Wheat forage grazed in the first 30 days was vegetative and had a higher nutritive value (crude protein of 21% and In vitro dry matter digestibility of 80%) while the wheat forage grazed in the latter half of the Experiment was reproductive (neutral detergent fiber of 50%). Using BLASTn search, sequences were compared to databases and assigned to genera based on the similarity indices. The number of bacterial genera identified increased with time from day 14 (93, 109) to day 76 (271, 233) in both fiber and liquid fractions respectively. *Prevotella* was the most predominant genera in both solid (up to 50%) and liquid (up to 60%) fractions on all sampling days. *Rikenella* was the second most abundant genus in both fractions, progressively increased with time from 8 to 20%, with increasing in fiber content. There was an increase in the number of bacterial genera identified in the yeast supplemented steers and the increases were mostly confined to the minor genera (<0.9% of 16S rDNA sequences found). Yeast supplementation increased *Ruminococcus* (a major genus) consistently with time and minor genera like *Lactobacillus, Lactococcus, Megasphaera, Atopobium and Enterococcus* which fall under Lactic acid bacteria cluster. In summary, yeast supplementation influenced major genera only to a limited extent but more prominent changes in the minor genera. Changes in the major genera were attributed more to the changes in nutritional quality of wheat forage.

Key Words: wheat, yeast supplementation, bTEFAP pyrosequencing

W358 Expression of phosphate transporter in small intestine, kidney, and parotid salivary gland of cattle fed differing levels of phosphorus from wet distiller's grains. A. P. Foote*[1], B. D. Lambert1,2, J. A. Brady[2], M. S. Brown[3,4], J. B. Osterstock[4], J. C. MacDonald[3,4], and N. A. Cole[5], [1]*Tarleton State University*, *Stephenville, TX*, [2]*Texas AgriLife Research*, *Stephenville*, [3]*West Texas A&M University*, *Canyon*, [4]*Texas AgriLife Research*, *Amarillo*, [5]*USDA-ARS, CPRL*, *Bushland, TX*.

Phosphorus (P) in the diets of animals in confined animal feeding operations (CAFOs) is of great importance with the increasing concern of environmental impact of animal agriculture. Excess phosphorus in diets of cattle is excreted in the manure and, if improperly managed, can be washed into local surface water causing an increase in algae growth, while a dietary deficiency can lead to poor growth and other detrimental symptoms. The objective of this study was to determine the expression of NaPi-IIb in the small intestine and parotid salivary gland and NaPi-IIa in the kidney of cattle fed increasing levels of P (0.29, 0.38, and 0.52% P; 0, 30 and 60% wet distillers grain, respectively). Samples of parotid salivary gland and kidney along with the mucosa of the duodenum, proximal jejunum, distal jejunum, and ileum were collected at slaughter and immediately frozen in liquid nitrogen. Relative amounts of NaPi-IIa or NaPi-IIb mRNA were determined using RT-PCR. Expression of NaPi-IIa in the kidney was not affected by diet ($P = 0.15$). Expression of NaPi-IIb was highest in the ileum and proximal jejunum ($P = 0.058$). NaPi-IIb expression in the parotid and small intestine were also not affected by varying dietary P ($P > 0.2$). It appears that dietary P may play a lesser role in regulation of P transporter expression in ruminants than in other animal species.

Key Words: phosphorus, transporters

W359 Supplemental vitamin E concentration in beef finishing diets containing wet distillers grains with solubles: feedlot performance and carcass characteristics. D. B. Burken*[1], K. G. Hanger[1], R. B. Hicks[1], D. L. VanOverbeke[1], J. L. Wahrmund[1], B. P. Holland[2], J. J. Martin[3], P. K. Camfield[3], and C. J. Richards[1], [1]*Oklahoma State University*, *Stillwater*, [2]*South Dakota State University*, *Brookings*, [3]*Oklahoma Panhandle State University*, *Goodwell*.

The objective of this study was to evaluate feedlot performance and carcass characteristics of finishing beef steers fed diets containing wet distillers grains with solubles (WDGS) and supplemented with vitamin E to target improvements in meat quality. One hundred ninety–nine steers (BW = 363 ± 31.1 kg) of mixed *Bos indicus*, *Bos taurus*, and *Bos indicus x Bos taurus* breeding were blocked by BW and randomly assigned to 1 of 4 supplemental vitamin E levels (0, 125, 250, and 500 IU/hd/day) fed for the last 97 d of the feeding period. Two blocks were

fed for a total of 129 d and 3 blocks were fed for a total of 150 d. Steers were fed a rolled corn-based finishing diet with 35% WDGS and 7% ground alfalfa (DM basis). Individual BW were measured initially on two consecutive days, the initial day of vitamin E supplementation, and the day of harvest. Carcass data were collected at harvest. There were no differences in ADG, G:F, and DMI for the pre-vitamin E supplementation period, the vitamin E supplementation period, or over the entire feeding period ($P \geq 0.11$). Final BW, HCW, and carcass-adjusted final BW did not differ among treatments ($P \geq 0.06$). Carcass characteristics (LM area, fat thickness, calculated YG, and KPH) were not affected by treatment ($P \geq 0.13$). Percentage of cattle grading upper 2/3 choice, low choice, and select did not differ ($P \geq 0.57$), nor did percentage calculated yield grades 2, 3, and 4 ($P \geq 0.07$). Data from this study illustrate that vitamin E can be supplemented in WDGS diets during the last 97 days of the feeding period to target improvements in meat quality with no adverse effects on animal performance or carcass characteristics.

Key Words: beef cattle, feedlot, vitamin E

W360 Abomasal direct infusion of L-arginine and *trans*-10, *cis*-12 conjugated linoleic acid affect to lipogenic gene expression and enzymes activities in angus steers. S. H. Choi*[1], G. Go[1], D. T. Silvey[1], L. A. Gilmore[1], K. Y. Chung[2], B. J. Johnson[2], G. Wu[1], and S. B. Smith[1], [1]*Department of Animal Science, Texas A&M University*, *College Station,* [2]*Department of Animal and Food Science, Texas Tech University*, *Lubbock*.

This study was conducted with a cattle model to exam the hypothesis that direct abomasal infusion of *trans*-10, *cis*-12 conjugated linoleic acid (CLA) and/or arginine would depress lipogenic enzymes activities and lipogenic gene expression in bovine subcutaneous adipose tissues. Sixteen Angus steers were assigned randomly to four treatments: direct infusion into the abomasums with L-arginine (50 g/d) or L-alanine (100 g/d; isonitrogenous control) and/or *trans*-10, *cis*-12 CLA (100 g/d) in steers fed a corn-based finishing diet. Infusion program was: the 1st period (15 d), steers were infused L-arginine or L-alanine, the 2nd period (15 d), steers were infused each amino acids and/or *trans*-10, *cis*-12-CLA. Subcutaneous adipose tissue and blood samples were collected at beginning and end periods. The BW gain and ADG were significantly decreased ($P = 0.03$) by abomasal infusion of CLA and feed:gain was significantly increased ($P = 0.01$). The activities of 6-phosphogluconate-dehydrogenase, glucose-6-phosphate-dehydrogenase and fatty acid synthase were not affected by arginine or CLA infusion. Arginine depressed NADP-malic enzyme (ME) activity, but this was reversed by co-infusion of CLA (arginine x CLA, $P= 0.02$). The concentration of *cis*-9, *trans*-11 and *trans*-10, *cis*-12 CLA in plasma was increased by CLA infusion, and arginine infusion increased plasma arginine. AMP-activated protein kinase (AMPK) and stearoyl Co-A desaturase (SCD) gene expression were significantly enhanced ($P \leq 0.025$) by arginine infusion but decreased PPARγ gene expression. CLA significantly depressed C/EBP-β gene expression. Because arginine increased AMPK gene expression and depressed PPARγ gene expression and ME activity, we predict that over time, arginine would depress adiposity. Unexpectedly, these effects were antagonized by CLA.

Key Words: conjugated linoleic acid, arginine, beef cattle

W361 Effects of different casein supplements on concentration of soluble non-ammonia nitrogen in the liquid phase of ruminal and omasal digesta in Korean native steers. C. W. Choi*[1], H. G. Lee[2], Y. K. Oh[1], S. C. Lee[1], M. K. Song[3], S. H. Choi[4], and S. B. Smith[4], [1]*National Institute of Animal Science, RDA*, *Suwon, Korea*, [2]*Department of Animal Science, Pusan National University*, *Mirang, Korea*, [3]*Chungbuk National University*, *Cheongju, Korea*, [4]*Texas A&M University*, *College Station*.

Three ruminally and duodenally fistulated Korean native steers were used to study the effect of different casein supplements on concentration of soluble non-ammonia N (SNAN) from the rumen and to compare SNAN estimates based on ruminal (RD) and omasal digesta (OD) samplings. The treatments in a 3 × 3 Latin square design consisted of a basal diet (control) of rice straw and corn based concentrate (30:70) and two casein protein supplemented diets. Crude protein intake for control (0.65kg/d of dry matter (DM)) was increased to 0.82 or 0.81kg/d of DM by replacing the basal diet with intact casein (0.24 kg/d) or acid hydrolyzed casein (0.46 kg/d), respectively. For SNAN analysis, digesta was collected from both the rumen and the omasum at 2 h intervals after a morning feeding, sequentially centrifuged to eliminate microbes, and precipitated with trichloroacetic acid followed by centrifugation. Different N fractions i.e., free amino acids (AA), peptides and soluble protein in RD and OD were assessed using the ninhydrin assay. Acid hydrolyzed casein supplement decreased ($P = 0.05$) rumen pH compared with control. Casein supplements increased (at lease $P < 0.05$) concentrations of peptide and total SNAN, whereas different casein types did not affect mean concentration of SNAN fractions in both RD and OD. Mean concentrations of free amino acid (58.1 vs. 46.8 mg N/L) and total SNAN (158.6 vs. 143.9 mg N/L) were significantly ($P < 0.05$) higher in OD than those in RD. In both RD and OD, despite relatively high concentration of free amino acid N, peptide N constituted the largest proportion of total SNAN suggesting that hydrolysis of peptides to AA rather than hydrolysis of soluble proteins to peptides or deamination of AA to ammonia is the most limiting step in rumen degradation.

Key Words: soluble non-ammonia nitrogen, casein supplements, omasal digesta:

W362 Similar performance and carcass quality of beef bulls weaned at 3 or 6 months of age when slaughtered at a fixed body weight. M. Vestergaard*[1], A. M. Graumann[2], F. Strudsholm[2], and C. F. Børsting[3], [1]*Aarhus University*, *Tjele, Denmark*, [2]*Agrotech A/S*, *Skejby, Denmark*, [3]*Danish Cattle Research Centre*, *Tjele, Denmark*.

In order to utilize dry beef cows to graze extensive pastures, where low yield of grass does not allow proper management and performance of cow-calf combinations, there could be prospective in using an earlier rather than a traditional weaning age. The present experiment focuses on the weaned calves and study the effects of three mo (3M) compared with six mo (6M) weaning age on growth performance and carcass quality. Furthermore, three feeding strategies were included at both weaning ages: concentrates ad lib (CON), total mixed ration of concentrate and first cut grass silage ad lib (TMR), and separately fed concentrate at a fixed amount (4 kg/d) and first cut grass silage ad lib (SEP). The pelleted concentrate and silage had a DM content of 87 and 39%, respectively, and an energy content of 8.7 and 7.7 MJ NE/kg DM, respectively. A total of 83 bull calves in 14 blocks of 6 were included. Each block represented a breed and included Hereford, Angus, Simmental, Charolais, Limousin and crossbreds of these breeds. Within breed a fixed BW at slaughter was chosen in order to produce carcasses of similar fatness degree. The mean BW across all breeds was 560 kg, ranging from 520 kg with Hereford to 610 kg with Charolais. The actual BW at weaning was 145 (3M) and 251 kg (6M) ($P < 0.001$). At 6 mo of age, 3M calves were 17 kg heavier than 6M calves ($P < 0.05$). DMI from 6 mo of age to slaughter (7.30 kg), ADG (1.63 kg/d), age at slaughter (370 d), carcass wt (314.5 kg), dressing percentage (58.1), and EUROP carcass conformation and fatness were not different between 3M and 6M bulls. There

were no major interactions between weaning age and feeding strategy. NE per kg DM was higher for CON than TMR and SEP rations ($P < 0.001$). DMI was highest in TMR ($P < 0.001$) leading to the highest Gain to Feed ratio in CON and lowest in TMR ($P < 0.001$). Carcass characteristics were not affected except carcass fatness that was lowest in CON ($P < 0.01$).

Key Words: beef production, weaning age, feeding strategy

W363 Development of a fescue toxicosis model using a fescue seed extract. A. F. Koontz*[1], L. P. Bush[2], J. L. Klotz[3], K. R. McLeod[1], F. N. Schrick[4], and D. H. Harmon[1], [1]*Department of Animal and Food Sciences, University of Kentucky*, *Lexington,* [2]*Department of Plant and Soil Sciences, University of Kentucky*, *Lexington,* [3]*Forage-Animal Production Research Unit, USDA-ARS*, *Lexington, KY,* [4]*Department of Animal Science, University of Tennessee*, *Knoxville*.

This study was designed to examine the efficacy of a fescue seed extract for inducing fescue toxicosis in cattle. Four growing Holstein steers (BW = 309±36kg) surgically fitted with ruminal cannulas were utilized in a four phase crossover design experiment. The basal diet consisted of endophyte free fescue hay fed ad libitum. In phases 1 & 2, steers were ruminally dosed twice daily with 1kg either ground endophyte infected seed (S_{E+}) or ground endophyte free fescue seed (S_{E-}) for 7 d in order to develop a baseline of physiological responses during fescue toxicosis. In phases 3 & 4, steers were ruminally dosed twice daily with an extract from endophyte infected seed (E_{E+}) or endophyte free fescue seed (E_{E-}) for 7 d. During d 4-7 of each phase room temperature was increased to 32°C (HS). Steers on both S_{E+} and E_{E+} had reduced serum prolactin on D7. Steers on S_{E+} and E_{E+} had a reduction in total intake ($P < 0.05$) during HS, while there was no difference between treatments during thermoneutrality. Rate of intake was also reduced for S_{E+} and E_{E+} during HS. Consequently, animals on S_{E+} and E_{E+} tended to lose weight (−2kg) while animals on S_{E-} and E_{E-} tended to gain weight (+8kg). Skin temperature was higher ($P < 0.01$) during HS for both S_{E-} and S_{E+}. Core body temperature was higher ($P < 0.0001$), for extract treated animals as compared to those dosed with ground seed for both E+ and E-. Heart rate measurements show the opposite effect for both form and endophyte comparisons. There was no effect of treatment on respiration rate at thermoneutrality, however, HS tended to increase respiration rate for all treatments ($P < 0.1$) with E+ dosed animals higher than E- ($P = 0.0002$), as well as S animals higher than E ($P = 0.0012$). Blood pressure was only measured during E treatment. Systolic pressure was unaffected by treatment ($P = 0.203$), while diastolic pressures were higher for E_{E+} ($P = 0.008$). HS resulted in a reduction in systolic and diastolic pressure for E_{E+} ($P < 0.05$), while E_{E-} pressures were unchanged. These data indicate a fescue seed extract model is able to mimic the symptoms of fescue toxicosis induced by seed.

Key Words: bovine, fescue, model

W364 Flint corn grain processing and protein adequacy in rations for feedlot finished Nellore bulls. A. M. Pedroso*, M. S. Peres, F. A. P. Santos, G. B. Mourao, and T. G. Neri, *ESALQ/USP*, *Piracicaba, SP, Brazil*.

This trial was designed to evaluate processing methods of flint corn grain and increasing urea levels effects on performance of finishing Nellore bulls fed rations containing 12% grass hay and 88% concentrate (%DM) for 101 d. Rations contained 3 urea levels (0.5; 1.0 or 1.5% DM) and 73.5 to 75% corn grains, either steam flaked (SF), dry rolled (DR) or fine ground (FG). 178 Nellore bulls, with 343 kg average initial LBW were used in a complete randomized blocks design with a 3x3 factorial arrangement. Animals were kept in 36 concrete floor pens. Parameters evaluated were dry matter intake (DMI), average daily gain (ADG), feed efficiency (FE – kg ADG/kg DMI), dressing percentage (DP), fat thickness (FT) and rib eye area (REA). Data were analyzed using PROC MIXED of SAS. Bulls fed SF flint corn showed 20.5% and 11.7% better FE than bulls fed DR and FG respectively ($P < 0.05$). Fine grinding of flint corn increased cattle feed efficiency in 7.9% compared with dry rolling ($P < 0.05$). SFC resulted in higher DP than FGC and DRC as well as higher REA than DRC ($P < 0.05$). Increasing urea levels resulted in linear increases ($P < 0.05$) on DMI, ADG and FE. There was an interaction of grain processing and urea levels for ADG ($P < 0.06$). Cattle fed DR and FG responded to urea up to 1% while cattle fed SF responded to urea up to 1.5% of diet DM. Increases in energy values with steam flaking and fine grinding were higher with the flint corn used in this trial than the increase reported by the literature for dent corn.

Table 1. Performance of finishing Nellore Bulls fed flint DR, FG or SF and different urea levels

	SFC	FGC	DRC	0.5% U	1.0% U	1.5% U	SEM	Effect (Pr>F) - Corn × Urea	Linear Regression (urea levels)
DMI (kg/d)	7.72b	8.26a	8.08ab	7.88	7.85	8.32	0.1338	0.5173	0.0312
ADG (kg/d)	1.40a	1.34ab	1.21c	1.21	1.32	1.43	0.0357	0.0514	0.0002
FE (ADG/DMI)	0.18a	0.16b	0.15c	0.15	0.17	0.17	0.0035	0.1353	0.0012
DP (%)	52.8a	52.7b	52.1c	52.7	52.6	52.4	0.2175	0.6933	NS
REA (cm^2)	57.9a	55.6ab	54.3b	58.3	56.0	53.5	0.7841	0.1363	NS
FT (mm)	3.89	4.23	4.00	4.15	3.93	4.05	0.2287	0.3124	NS

Key Words: feedlot, flint corn grain processing, protein adequacy

W365 Effects of ruminal energy-protein synchronization on intake, nutrient digestibility, performance, carcass traits and composition of carcass gain in beef heifers. M. S. Duarte, P. V. R. Paulino*, G. S. Viana, E. A. Fonseca, L. H. P. Silva, J. P. I. S. Monnerat, R. Mezzomo, J. Cavali, J. F. Lage, I. M. Oliveira, S. C. Valadares Filho, and M. F. Paulino, *Universidade Federal de Viçosa*, *Viçosa, MG, Brazil*.

This study was carried out aiming to evaluate the effects of ruminal energy–protein synchronization on intake, nutrient digestibility, feed conversion, animal performance, carcass traits and composition of carcass gain of beef heifers. Twenty crossbred heifers (average BW of 240 kg) were used. At the beginning of the trial, four animals were slaughtered as reference group and the sixteen remaining animals were randomly assigned to 4 treatments, in a 2 × 2 factorial design: two levels of concentrate (40 and 80%, based on dry matter) and two levels of rumen undegradable protein (RUP – 48.8 and 27.2% of the diet CP). At the end of the trial, the animals were slaughtered. There was no interaction (P>0.05) between concentrate and RUP level on any variable studied. Dry matter intake (DMI), nutrients intake and nutrients digestibility were not affected ($P > 0.05$) by RUP level. The animals fed the highest RUP level had higher ($P < 0.05$) average daily gain (ADG) and therefore greater feed conversion than the animals fed the lowest RUP level (1.18 kg/d; 6.44 and 0.96 kg/d; 7.38, respectively). Concentrate level did not affect ($P > 0.05$) DMI, feed conversion and ADG. The animals fed 80% concentrate diets had higher intake of TDN and EE, and lower intake of NDF ($P < 0.05$) compared to the animals fed 40% concentrate diets. The digestibilities of all nutrients, except the NDF, were greater ($P < 0.05$) for the 80% concentrate diets. There was no effect ($P > 0.05$) of RUP level on carcass traits and composition of carcass gain. Similarly, concentrate level did not affect ($P > 0.05$) the composition of carcass gain. The animals fed 80% concentrate diets had larger ($P < 0.05$) rib eye area than the animals fed 40% concentrate diets. Although feeding more

RUP led to improved feed conversion and increased ADG, the interaction of RUP and dietary energy level was not an important attribute in formulating beef heifer′s diet as no effect of ruminal energy-protein synchronization on performance, intake, nutrient digestibility, carcass traits and composition of carcass gain were detected.

Key Words: feedlot, performance, rumen undegradable protein

W366 The effects of restrictive feeding over the winter on the performance of prepartum crossbred beef cows. K. M. Wood*, I. B. Mandell, and K. C. Swanson, *University of Guelph*, *Guelph, Ontario, Canada*.

Eighty-seven mature pregnant beef cows, primarily of Angus and Simmental breeding, were used in a randomized complete block design to investigate the effects of restrictive feeding on performance over two separate winters. Cows were randomly assigned to one of three dietary treatments: Control (CON; n =24); fed free choice grass/alfalfa haylage, constantly restricted (CONST; n= 32); fed haylage at 1.8% of bodyweight, and stepwise (STEP; n = 31); fed haylage at 1.6% of bodyweight for 56 d and then fed 2% of bodyweight for 56 d. Individual feed intakes were recorded using the Calan gate system. Cows were weighed every 14 d to adjust intake and ultrasounded for rump fat, backfat and % intramuscular fat and body condition scored (BCS) on d 1, 56, 112. Calf birthweight was also recorded. Data were analyzed using Proc Mixed in SAS; the model included the effect of block (year of experiment), parity and dietary treatment, as well as the random effect of pen. Contrast statements were used to compare CON versus CONST and STEP, and CONST versus STP with significance declared at $P \leq 0.05$. Total DM intakes were similar ($P = 0.84$) for total DM intake between CONST and STEP; however cows fed CON had the greatest ($P < 0.001$) DM intakes. Average daily gains over the entire experiment were 1.1 ± 0.06 (LSM ± SEM) for CON, 0.83 ± 0.05 for CONST and 0.87 ± 0.05 for STEP and were greater ($P \leq 0.001$) for CON than the two restrictive treatments. There were no differences ($P > 0.17$) amongst dietary treatments for changes in backfat or calf birthweight. Cows fed CON deposited more ($P < 0.001$) rump fat and had a greater ($P < 0.001$) gain in BCS than cows fed CONST or STEP. Cows fed CONST or STEP did not differ (P = 0.95) for change in rump fat and CONST tended ($P = 0.08$) to have greater increase in change in BCS. In conclusion, method of restrictive feeding did not affect the overall performance of pregnant beef cows and may be an acceptable alternative to feeding free-choice haylage rations to prepartum beef cows over the winter.

Key Words: beef cows, restrictive feeding, winter rations

W367 Comparison of wheat dried distillers grains with solubles, alone or in combination with barley grain, as protein and energy sources for beef stocker calves grazing fall pasture and winter field bale grazing. L. P. Clark*[1] and H. A. Lardner[1,2], [1]*University of Saskatchewan*, *Saskatoon, Saskatchewan, Canada*, [2]*Western Beef Development Centre*, *Humboldt, Saskatchewan, Canada*.

Two experiments were conducted to evaluate and compare supplementing wheat dried distiller′s grains with solubles (DDGS) alone or in combination with barley grain on the performance of beef calves in a fall pasture (EXP1) or winter bale grazing (EXP2) program. In each experiment, weaned, cross-bred calves (n=54) were stratified by body weight and randomly allocated to 1 of 3 supplement strategies in a replicated (n=3) completely randomized design. In EXP1, calves (initial BW 211.9 ± 1.23 kg) were supplemented at 0.8% BW either (i) barley+canola meal (70:30 blend); (ii) barley+wheat DDGS (70:30 blend) or (iii) 100% wheat DDGS. In EXP2, calves (initial BW 205.8 ± 0.42 kg) were supplemented at 1.2% BW either (i) 100% wheat DDGS; (ii) 100% barley or (iii) wheat DDGS+barley (50:50 blend). The fall pasture study (EXP 1) was conducted on an 18 ha crested wheatgrass (*Agropyron cristatum*) pasture divided into 9, 2-ha paddocks. The winter bale grazing study (EXP 2) was conducted on a 5.4 ha paddock further divided into 9, 0.6 ha paddocks. In EXP2 calves had ad libitum access to grass-legume hay (12.5% CP, 57% NDF) fed in round bale feeders. Calves were weighed at start, every 14 d and end of both experiments. All weights were adjusted for a 4% shrink. Paddock was the experimental unit and data were analyzed using the Mixed model procedure of SAS. Average daily gains did not differ ($P = 0.33$) between supplement groups during the 33-d graze period on crested wheatgrass (EXP1) or the 109-d (EXP2) winter bale graze period ($P = 0.41$). These data suggest that wheat DDGS compared to barley supplementation will result in similar performance of stocker calves grazing fall pasture or winter bale grazing.

Key Words: wheat dried distillers grains with solubles, calves, grazing

W368 Carcass characteristics of Nellore heifers finished on pasture system with partial substitution of soybean meal for sunflower crushed seeds. S. L. N. Cerilo*, R. H. de Tonissi e Buschinelli de Goes, H. L. Lima, A. R. M. Fernandes, K. A. de Souza, K. C. da Silva Brabes, A. F. Marquez, and E. R. de Oliveira, *Universidade Federal da Grande Dourados*, *Dourados,MS, Brasil*.

The carcass characteristics of Nellore heifers finished in *Brachiaria humidicola* pasture, supplemented with partial substitution of soybean meal by sunflower crushed seeds were evaluated in the dry season. Twenty-four animals were used with initial body weight (BW) of 300 kg and initial body condition (BC) of 2 (in score 1 to 5), with approximately 24 months of age, were distributed at random into four paddocks of 3000 m^2, in a complete randomized design. The supplement was fed at 0.8% BW/animal/day. The supplements were based in corn and soybean meal, which soybean meal was replaced by sunflower crushed seeds in the proportions of 0, 20, 40 and 60%. All the concentrate containing 20% CP, varying oil levels (2.5, 4.7, 7.0, 9.2%). The animals were weighed and monitored for BC every 21 days and slaughtered at 378.5 kg and 3.8 of body condition. There was no difference ($P > 0.05$) between the levels of substitution for hot carcass weight (HC), cold carcass weight, carcass yield, carcass length, liver, fat thickness (FT), yield estimated grade (YG=72.92-0.489FT-0,02HC +0.119LEA), and Brazilian commercial cuts (BCC= 60,33-0,015HCW-0,462FT+0.11LEA), which presents a average of 197.05 kg, 193.33 kg, 52.03%, 1.2m, 3.59 kg, 4.52 mm, 74.18% and 62.14%, respectively. Effect ($P < 0.10$) was observed for the inclusion of sunflower crushed seeds for fat accumulation in peri-renal and loin eye area (LEA). The animals supplemented only corn and soybean meal presents a lower peri-renal fat (1.87kg), the substitution of 40% of sunflower crushed seeds, showed accumulation of 3.02 kg and those receiving 20 and 60% had an average of 2.69 and 2.05 kg, these values may be associated with oil levels of supplement. The loin eye area showed values of 69.2, 58.2, 57.8, 64.0 cm^2, and LEA/100 kg BW of 18.48, 15.01, 15.50, 17, 25, for the replacement levels of 0, 20, 40, 60%, respectively, which shows that the weight and size of animals can influence the area of loin eye. Partial substitution of soybean meal with sunflower crushed seeds, does not alter the carcass characteristics of Nellore heifers finished in grazing systems.

Key Words: fat thickness, loin eye area, yield grade

W369 Changes in ruminal parameters, of steers supplemented with sunflower crushed seeds in partial substitution of soybean meal. H. L. Lima*, R. H. de Tonissi e Buschinelli de Goes, S. L. N. Cerilo, A. L. Teodoro, K. A. de Souza, L. da Silva Fernandes, M. G. de Menezes Gressler, and E. R. de Oliveira, *Universidade Federal da Grande Dourados*, *Dourados, MS, Brasil*.

To evaluate the effect of partial substitution of soybean meal with sunflower crushed seeds on the ruminal pH and ammonia of steers supplemented at pasture, we used four animals fitted with permanent ruminal cannula, with initial weight of 300 kg, randomly divided into individual paddocks of *B. brizantha* cv. Marandu in 4 × 4 Latin square and a split-plot; the averages was compared by Tukey test at 5% probability. The supplements were provided in the amount of 0.8% BW/animal/day and consisting of corn, soybean meal and mineral, with 20% of crude protein. The soybean meal was replaced in the proportions of 0, 20, 40, and 60% for sunflower crushed seeds. The estimated ether extract of the supplements were 2.5, 4.7, 7.0, 9.2%, respectively. The determination of pH and ammonia ($N\text{-}NH_3$) occurred in the rumen at 0, 2, 4, 6 and 8 hours after supplementation. There was no effect ($P > 0.05$) for pH according to the level of substitution of soybean meal for sunflower crushed seeds and time of collection. This values had an average of 6.41, exceeding the limits of 6.2, for the occurrence of inhibition of fiber digestion. For contents of $N\text{-}NH_3$ have a significant effect ($P < 0.05$), and a quadratic response ($Y = 15.42 + 2.77x - 0.31x^2$, $r^2 = 0.55$), where the ammonia peaks occurred between 2 and 4 hours after the supplement supplied, with values of 22.56 and 21.40 mg/dL, these may be associated with the solubility of food constituents of the supplements, which have medium to high ruminal degradability. The $N\text{-}NH_3$ values remained above the limits of 10 mg/dL, which maximizing dry matter intake of animals, and digestion for grazing animals. Supplementation of steers on pasture with sunflower crushed seeds in partial replacement of soybean meal does not alter the ruminal pH and ammonia.

Key Words: supplement, pH, ammonia

W370 Effect of supplemental fat sources on rumen fermentation of a high-concentrate diet using a dual-flow continuous culture system. R. C. Araujo*[1], S. Calsamiglia[2], M. Rodríguez-Prado[2], S. Cavini[2], and A. Ferret[2], [1]*ESALQ, Universidade de São Paulo*, *Piracicaba, SP, Brazil*, [2]*Universitat Autònoma de Barcelona*, *Bellaterra, Spain*.

The negative effects of dietary fats on fiber digestion have been used as a criteria to limit the content of fat and degree of unsaturation in ruminants. However, the relevance of reduced fiber digestion in high-concentrate beef diets is questionable. Six 1320-mL dual-flow continuous culture fermenters were used in a complete randomized design (2 periods of 5 d adaptation and 3 d sampling each) to determine the effects of including 4.86% (DM basis) of hydrogenated palm oil (HIDROPALM, Norel S.A., Madrid, Spain), soybean oil, or olive olein on rumen fermentation of a high-concentrate diet. Temperature (38.5°C), and liquid (10%/h) and solid (5%/h) dilution rates were constant. The pH was allowed to fluctuate with an upper limit of 6.4, but average pH was not affected by treatments (average of 5.66). Fermenters were fed 95 g DM/d in 2 equal portions. Diets consisted of 10% barley straw, 45% ground corn, 22.6% barley, 16.2% soybean meal, 1.35% mineral and vitamin premix, and 4.86% supplemental fat source (DM basis). Diets were formulated to achieve 8.0% EE, with similar CP (14.4%) and NDF (16.9%) concentrations (DM basis). Data were analyzed using PROC MIXED of SAS and differences declared at $P < 0.05$ by Tukey test. True DM (average of 69.2%), CP (average of 77.4%), NDF (average of 19.2%) and ADF (average of 13.0%) degradabilities were not affected by treatments. No differences were observed for ammonia (average of 0.03 g/d), non-ammonia (average of 2.76 g/d), dietary (average of 0.50 g/d) and bacterial (average of 2.28 g/d) N flows. Total volatile fatty acids concentration (105.2 m*M*), acetate (average of 37.5%), and propionate (average of 53.0%) proportions as well as the acetate:propionate ratio (average of 0.70) were not affected by treatments. Results indicate that inclusion of soybean oil or olive olein at 4.86% of dietary DM does not affect rumen fermentation of a typical high-concentrate feedlot diet when compared with hydrogenated palm oil.

Key Words: hydrogenated palm oil, olive olein, soybean oil

W371 Dried distillers grains as a protein supplement to cattle consuming Bermudagrass hay. Z. J. Rambo*, J. E. Sawyer, C. L. Skaggs, and T. A. Wickersham, *Texas A&M University*, *College Station*.

We compared 3 protein supplements, cottonseed meal (CSM), dried distillers' grains (DDG), and DDG plus urea (DDGU), in steers fed Bermudagrass hay (7.4% CP). Ruminally and duodenally fistulated steers (463 kg) were used in a 13 × 4 incomplete Latin square with 13 treatments and 4 periods. Treatments were arranged as a 4 × 3 factorial plus a negative control (NC), which received no supplement. The factorial consisted of 4 levels of supplemental N (52, 104, 156, and 208 mg N/kg BW) from each of three sources of supplemental N (CSM, DDG, and DDGU; 49.6, 31.0, and 47.5% CP). Periods were 17 d long, with 10 d for adaptation, and 7 d for collection. A source by N level interaction ($P = 0.05$) was evident for forage OM intake. Forage OM intake increased quadratically ($P = 0.02$) with increasing amounts of CSM, numerically ($P = 0.16$) with increasing amounts of DDGU, and were not influenced by increasing amounts of DDG. Forage OM intake increased from 39.5 g/kg $BW^{0.75}$ for NC to 43.4, 45.3, 45.9, and 41.9 g/kg $BW^{0.75}$ for 52, 104, 156, and 208 mg N/kg BW from CSM, respectively. Total digestible OM intake increased (linear; $P < 0.01$) with increasing level of supplementation for all three sources. Total digestible OM intake was 21.0 g/kg $BW^{0.75}$ for NC and 27.7, 27.3, and 28.4 g/kg $BW^{0.75}$ for CSM, DDG, and DDGU, respectively, at the highest level of N. Organic matter digestion increased (linear; $P \leq 0.03$) for all sources. At the highest level of supplementation OM digestibility averaged 59% versus 53% for steers receiving NC. There was a source by level interaction ($P = 0.03$) for ruminal ammonia concentration. This interaction is explained by linear increases ($P \leq 0.05$) in ammonia concentrations for all three sources; however, increases were greatest for DDGU, followed by CSM, and DDG. When N was provided at 208 mg N/kg BW, ruminal ammonia averaged 4.84, 3.29, and 8.61 m*M* for CSM, DDG, and DDGU, respectively. Dried distillers' grains were effective at increasing total digestible OM intake although the mode of action differed from CSM.

Key Words: Bermudagrass, dried distillers grains, protein

W372 Effect of residual feed intake, gender, and breed composition on blood urea nitrogen concentration in an Angus-Brahman multibreed herd. R. O. Myer*[1] and M. A. Elzo[2], [1]*University of Florida*, *NFREC, Marianna*, [2]*University of Florida*, *Gainesville*.

Blood urea N can be used as an indicator of N use and excretion by an animal. The objective of this research was to asses the effect of residual feed intake (RFI) and post weaning growth rate on blood plasma concentration of urea N (PUN) in 188 bulls, heifers, and steers (mean = 296.5 kg, SD = 37.3 kg) ranging from 100% Angus to 100% Brahman. Calves were assigned to pens in a GrowSafe feeding facility by sire group and

sex, and self-fed a total mixed ration (corn, cottonseed hulls, chopped grass hay, cottonseed meal, molasses, and mineral-vitamin supplement; 90% DM, 14% CP, 1.5 mcal/kg DM NEm, and 0.9 mcal/kg DM NEg). The pre-trial adjustment period lasted 21 d. Individual daily feed intake was collected during the 70 d feeding trial; BW were recorded every 2 wk. Blood (jugular) was drawn on d 0 and d 56 for PUN. Residual feed intake (RFI) was computed as the difference between actual and expected intakes. The RFI groups were high (RFI > mean + 0.5 SD), medium (RFI between mean ± 0.5 SD), and low (RFI < mean - 0.5 SD; SD = 2.0 kg DM/d). Data (PUN) were analyzed using a mixed model. Fixed effects were sex of calf, RFI group, and Brahman fraction of calf; daily feed intake and mean exit velocity were covariates. Random effects were sire and residual. Overall ADG was 1.25 ± 0.26 kg/d. Brahman had higher d 0 and d 56 PUN concentrations than Angus ($P < 0.01$). Sex affected both d 0 and d 56 PUN ($P < 0.01$) concentrations with bulls having the lowest and heifers the highest. Day 0 PUN concentration was negatively associated with ADG ($P < 0.01$). Only d 56 PUN concentration was related to RFI ($P = 0.02$), indicating that more feed efficient animals also had lower PUN.

Key Words: beef cattle, feed efficiency, blood urea

W373 Body composition and tissue deposition in Nellore, F1 Simmental × Nellore and F1 Angus × Nellore steers fed at maintenance or ad libitum with two levels of concentrate in the diet. I. M. Oliveira*, P. V. R. Paulino, M. I. Marcondes, C. A. Neves, S. C. Valadares Filho, E. Detmann, J. Cavali, V. R. M. Couto, and N. K. P. Souza, *Universidade Federal de Viçosa*, *Viçosa, MG, Brazil*.

The objective of this study was to evaluate the effects of feeding regimen (FR) and genetic group (GG) on body weight gain (EBWG) composition and tissue deposition rate in beef steers. Forty eight steers, 18 months old, were used (20 Nellore (NE), 20 F1 Simmental × Nellore (NS) and 20 F1 Angus × Nellore (NA) with initial BW of 265.6±6.4 kg; 325.3±4.7 kg and 324.6±6.0 kg, respectively). Four animals from each GG were slaughtered at the beginning of the trial in order to estimate initial body composition. A 3 × 3 factorial arrangement was used, being 3 GG and 3 FR (maintenance and ad libitum with 2 concentrate allowance levels: 1 and 2% of BW), with 6 replicates for the ad libitum treatments and 4 animals fed at maintenance. After 136 days on feed all animals were slaughtered and their body and carcass composition were directly determined. There was no interaction ($P > 0.05$) between GG and FR on any variable assessed. Animals fed at maintenance had larger ($P < 0.05$) proportions of bones and muscle in the carcass than the ad libitum fed animals (19.7; 65.11 vs. 15.2%; 60.5% respectively) and less fat (17.97 vs. 23.45%). NE carcass had larger proportion of muscle (62.74%) and smaller ($P < 0.05$) proportion of fat (19.94%) than that observed in the carcass of the crossbred animals (61.10 and 22.19%). The rate of tissue deposition (adipose and muscular) in the carcass was lower in NE animals (168.55 and 152.08 g/d) and in those fed with 1% of concentrate (192.42 and 200.89 g/d) when compared to crossbred animals (229.11 and 259.51 g/d) and those fed with 2% of concentrate (225.43 and 246.50 g/d). Protein accretion in the EBWG was largest ($P < 0.05$) in the animals that received more concentrate (201.51 vs. 166.02 g/d, for 1 and 2% of BW on concentrate, respectively). NE animals deposited less fat and protein ($P < 0.05$) in the EBWG (477.22 and 145.81 g/d, respectively) than crossbred animals (660.68 and 202.75 g/d), while NA had more ($P < 0.05$) fat deposition in the EBWG than NS animals (720.28 vs. 601.08 g/d).

Key Words: feedlot, empty body weight, crossbred cattle

W374 Effect of supplementing a combination of lysine and methionine on growing cattle performance and carcass composition. N. D. Luchini*[1] and M. J. de Veth[2], [1]*Adisseo*, *Alpharetta, GA*, [2]*Balchem Corporation*, *New Hampton, NY*.

Lysine (Lys) and methionine (Met) have been identified as the two amino acids (AA) most limiting growth of beef cattle. The objective of this study was to determine the effect of supplementing metabolizable Lys and Met on growth and carcass composition of growing bulls. One hundred and twenty bulls (333 ± 52 kg; mean ± SD), randomly allocated to one of two treatments were fed a basal diet composed of corn grain, distillers grains, grass hay and a mineral/vitamin premix at 56.8, 14.8, 25.2 and 3.2% DM, respectively with no supplemental AA (CON) or the basal diet with supplemental Lys (4.59 g/kg DM of a lipid-encapsulated Lys (AminoShure-L) and Met (1.24 g/kg DM of the isopropyl ester of 2-hydroxy-4-(methylthio) butanoic acid (Metasmart) (L+M). Using CNCPS V.6.1, estimated concentrations of Lys and Met in metabolizable protein were 5.43% and 1.95% for CON and 6.41% and 2.18% for L+M. The AA products were mixed with ground corn and mixed into the TMR. Daily DMI was recorded for each animal using the GrowSafe feeding system. Bulls were weighed on 2 successive days at the start and end of the study. Ultrasound (for carcass quality) was made at the start and end of the study. Data was analyzed using the PROC Mixed procedure of SAS and pretreatment measurements were used as a covariate. For average daily gain (ADG) and backfat thickness there was an interaction with the covariate (pretreatment body weight (BW) and backfat thickness, respectively) and therefore covariates were treated as categorical variables with two levels (low and high groups). L+M increased BW gain ($P < 0.05$) and tended to increase DMI ($P < 0.15$) compared to CON. ADG (kg/d) increased ($P < 0.01$) in the high BW (1.88 and 1.68) for L+M and CON, respectively There was an increase (17%; $P = 0.02$) in backfat thickness for the high group of animals on L+M treatment compared to the CON. There were no effects of L+M on longissimus muscle area or intramuscular fat. Results indicate that supplementing a balanced ratio of the two most limiting AA can improve growth and ADG of growing bulls.

Key Words: beef cattle, lysine, methionine

W375 Effect of protein and energy supplementation on voluntary intake and ruminal parameters in steers. F. P. Portilho* and L. F. Barros, *University of Brasilia*, *Brasília, DF, Brazil*.

Supplementation may have associative effects (positive or negative) between the forage and concentrate with important consequences on the efficiency of nutrient use. This study aimed to evaluate the effects of different amounts of protein and energy supplement on the behavior of the parameters pH and N-NH3 in rumen fluid and on the voluntary intake and degradability of dry matter (DM) and NDF) of forage in cattle receiving hay Coast-cross (*Cynodon dactylon*). We used five steers with mean of 290 kg of BW, cannulated in the rumen, fed ad libitum hay of Coast-cross, and minerals. Five treatments were evaluated, consisting of 4 levels of daily protein and energy supplementation (0.25, 0.50, 1.00 and 1.50 kg DM to 100 kg BW / day) of corn meal, soybean meal and urea, and one control treatment received only hay and mineral mix ad libitum. Data were collected from voluntary intake, degradability of dry matter and NDF of hay, the pH and N–NH3. The intake was calculated daily by the leftovers. The potential degradation in situ was made according to Mertens (1993). The pH of the samples was measured according to the technique described by Fenner 1965, adapted by VIEIRA (1980). The experimental design used was the Latin square (5 × 5) and analysis were performed using SAS (1990) GLM procedure. The highest level of protein and energy supplementation (1.5 kg DM to 100 kg BW /

day) reduced the pH, reducing ruminal degradation of DM and NDF of Coast-cross hay, however, insufficient to modify intake. The highest concentrations of ruminal N–NH3 were observed at the highest levels of intake of protein-energy supplement (1.0 and 1.5 kg DM to 100 kg BW / day). These levels of supplementation, concentrations of ruminal N–NH3 remained longer near the plateau and decreased slower than the other treatments supplemented. There was no additive effect of intake of different amounts of protein-energy supplement on the intake of DM and NDF of hay. The rumen degradation of DM and NDF was not influenced by intake of protein-energy supplement to the level of 1.0 kg DM to 100 kg BW / day.

Key Words: steers, intake, degradation

W376 Energy requirements adjusted by milk yield of beef cows in Uruguay. V. Gutiérrez Castro*, M. Carriquiry Fossemale, and A. C. Espasandín Mederos, *Facultad de Agronomía, UdelaR*, *Montevideo, Uruguay*.

Maintenance energetic cost is affected by body composition, weight (BW) and metabolic activity of organs, such as mammary gland, therefore, the potential of milk production has been associated with maintenance requirements. Thirty-two beef cows (Hereford, n=10; Angus, n=10; F1, n=12) were used to predict maintenance requirement based on milk yield in grazing conditions. The experiment was carried at the Experimental Station Bernardo Rosengurtt (Cerro Largo, 32°35′S, 4°15′W). Cows grazed native pastures with two different forage allowances average of 10 vs. 6 kg DM/100 kg BW/d for HI and LO, respectively). Milk yield and composition were measured once a month from 30 to 120 days postpartum. Cows were milked and separated from their calves 12 overnight before being milked using an portable machine (previous injection with oxytocin, 10 IU/cow). Milk was weighed and a sample obtained for protein, fat, and lactose analyses. Data were analyzed with a mixed model that included forage allowance, cow and calf breed, calf sex, and forage allowance by breed interaction as fixed effects, cow within breed as a random effect, and days postpartum as a covariate. Cow BW and milk production were affected ($P < 0.05$) by breed and forage allowance. Cow BW was greater for F1 than purebred cows in both HI and LO (average 460 vs. 434 ± 7 for F1 vs. purebred cows, respectively). Milk peak productions were greatest for F1 cows in HI and lowest for purebred cows in LO (9.3, 9.1, 8.4, and 6.1 ± 0.6 kg/d for F1 and purebred cows in HI and LO, respectively). These differences influenced energy requirements during lactation with the greatest values in HI forage allowances (18.7 to 14 Mcal/d and 13.8 to 8.9 Mcal/d from first to fourth month postpartum, for HI and LO, respectively) and F1 cows (18.7 to 14.8 Mcal/d and 17 to 13.3 Mcal/d from first to fourth month postpartum, for crossbred and purebred cows, respectively). Forage allowances affected maintenance requirement adjusted by milk yield by modifying BW and body condition score, and milk production, being only greater for F1 cows in HI forage offers.

Key Words: milk, beef cattle, Mcal/d

W377 Productive performance during fattening phases of Nellore and F1 Nellore x Brahman fed with three different diets. I. S. Silva*, F. A. Barbosa, J. M. S. Diogo, R. A. Mandarino, and F. C. E. Botelho, *Faculty of Agronomy and Veterinary Medicine, University of Brasília - UnB*, *Brasília/DF, Brazil.*

The experiment evaluates productive performance in fattening cattle, divided into two genetic groups and subjected to three diets in a feedlot. The experiment was conducted from August to November 2009, lasting 96 days, 14 days of adaptation of animals. The herd was composed of 42 bulls with an average age of 23 months, 21 breed Nelore (NEL) and 21 crossbreed Nelore × Brahman (NBR). Each genetic group was divided into three diets, with 7 animals each: SIL - corn silage and concentrate (corn grain, soybean meal, soybean hulls, urea and mineral supplement) at a ratio of 25:75 (dry in matter), PEL - exclusive diet of pellets; GRN - diet with whole grain corn and pellets. The experiment was conducted in a completely randomized in a 2 × 3 factorial, divided as follows: NBRSIL, NBRPEL, NBRGRN, NELSIL, NELPEL and NELGRN. In all treatments the food supply was ad libitum divided into three treatments daily. The average initial body weights (BWI) were: 350.7, 350.6, 355.8, 379.2, 375.7, 376.1 kg, for NELSIL, NELPEL, NELGRN, NBRSIL, NBRPEL and NBRGRN respectively. The final body weights (BWF) averages were: 500.0, 464.4, 479.7, 410.8, 471.9 and 501.5 kg for NELSIL, NELPEL, NELGRN, NBRSIL, NBRPEL and NBRGRN, respectively. The average hot carcass yield (HCY) was 58.51, 58.44, 57.34, 58.4, 58.61 and 58.05 for NBRSIL, NBRPEL, NBRGRN, NELSIL, NELPEL and NELGRN, respectively. The genotypes and diets did not affect the PI, PF and HCY ($P > 0.05$). The average daily gain (ADG) was 1.346 and 1.219 kg for NEL and NBR, respectively, without differences in the genetic group. There was influence of diet on the weight gain SIL was higher than PEL and similar to the GRN, 1.470, 1.093 and 1,299 kg, respectively ($P < 0.05$). The dry matter intake averaged was 9.25 and 9.65 kg /animal/day for NEL and NBR, respectively. The feed conversion was 7.17 and 8.26 for NEL and NBR, respectively ($P > 0.05$). The genetic group had no influence on average daily gain and hot carcass. The diet affected the average daily gain with better results for SIL and GRN, but had no differences for yield and hot carcass weight.

Key Words: carcass yield, genetic group, weight gain

W378 Effects of feeding monensin or polyclonal antibody preparation against lactate–producing rumen bacteria on blood lipoprotein concentrations of feedlot cattle. J. R. Rochesel*[1,2], F. S. Parra[1], M. D. B. Arrigoni[1], C. L. Martins[1], S. R. Baldin[1], L. M. N. Sarti[1], R. S. Barducci[1], N. R. B. Consolo[3], D. D. Millen[1], R. D. L. Pacheco[1], D. Tomazella[1], A. L. Campanini[1], F. A. S. Miquilin[1], and A. M.Lopes[1], [1]*São Paulo State University (UNESP)*, *Botucatu, São Paulo, Brazil*, [2]*Supported by FAPESP*, *São Paulo, São Paulo, Brazil*, [3]*University of São Paulo (USP)*, *Pirassununga, São Paulo, Brazil*.

This study, conducted at the São Paulo State University feedlot, Botucatu Campus, Brazil, was designed to test the effects of feeding polyclonal antibody preparation (PAP) against lactate-producing rumen bacteria or monensin (MON) on blood lipoprotein concentration of feedlot cattle fed high-concentrate diets. Ninety-six 9-mo-old bullocks (285.9 ± 38.7 kg) were assigned to 24 pens (4 bullocks/pen) and used in a completely randomized design with a 2 x 2 factorial arrangement of treatments using repeated measures over time, replicated 6 times. Factors were inclusion or not of PAP or MON, at a dose of 300 mg•kg^{-1} of DM or at 30 mg•kg^{-1} of DM, respectively. Blood samples were collected from jugular vein of 48 animals (2 bullocks/pen) chosen randomly to evaluate the concentrations of cholesterol (CHL), triglycerides (TRG) and VLDL, LDL and HDL in each phase of feeding: adaptation (ADP), growing (GRO) and finishing (FNS). No significant ($P < 0.05$) PAP and MON main effects or interactions were observed for any of the variables measured. Nevertheless, it was observed ($P < 0.05$) a phase main effect for CHL, HDL, LDL, VLDL and TRG. Bullocks presented greater ($P < 0.05$) concentration of CHL in the GRO and FNS phases when compared to ADP phase (GRO=124.24, FNS=112.02 vs. ADP=68.97 mg•dL^{-1}). Likewise, greater ($P < 0.05$) concentration of HDL was found in the GRO and FNS phases (GRO=76.22, FNS=74.59 vs. ADP=37.13 mg•dL^{-1}). LDL concentration increased ($P < 0.05$) from ADP to GRO phase (27.54 vs. 52.34 mg•dL^{-1}); however, its concentration decreased ($P > 0.05$) in the FNS phase at similar concentrations (31.84 mg•dL^{-1}) as those in ADP phase. Furthermore, VLDL and TG concentrations decreased ($P < 0.05$) in the FNS phase. Concentration of HDL remained unaltered in FNS when compared to GRO phase, while VDLD and LDL concentrations were reduced. Thus, the feed additives tested had no effect on blood lipoproteins concentration; however the concentrations were altered by diet energy level. With respect to blood lipoproteins, feeding PAP may be eventually an alternative to substitute MON.

Key Words: blood, lipoproteins, feed additives

W379 Effects of feeding polyclonal antibody preparations against lactate–producing rumen bacteria or monensin on feeding behavior of feedlot cattle. T. M. Mariani[1,2], R. D. L. Pacheco[1], M. D. B. Arrigoni[1], C. L. Martins[1], S. R. Baldin[1], L. M. N. Sarti[1], R. S. Barducci[1], T. M. Mariani[1], J. R. Ronchesel[1], F. S. Parra[1], D. Tomazella[1], J. P. S. T. Bastos[1], E. S. Ogawa[1], and D. D. Millen*[1], [1]*São Paulo State University (UNESP)*, *Botucatu, São Paulo, Brazil*, [2]*Supported by FAPESP*, *São Paulo, São Paulo, Brazil*, [3]*University of São Paulo (USP)*, *Piracicaba, São Paulo, Brazil*.

This study was designed to test monensin (MON) and polyclonal antibody preparations (PAP) against lactate-producing rumen bacteria on feeding and rumination efficiencies of DM and NDF of Brangus (BR) and Nellore (NE) cattle. The experiment was designed as a 2 × 2 factorial arrangement using repeated measures over time, replicated 4 times (4 bullocks/pen), in which 32 9-mo-old bullocks (254.1 ± 12.7 kg) of each of two breeds (BD) evaluated were fed diets containing either MON at 30 mg•kg^{-1} of DM or PAP at 300 mg•kg^{-1} of DM for 144-d. Measures over time were taken according to the phases evaluated: adaptation (ADP), growing (GRO), finishing 1 (FN1) and finishing 2 (FN2). The level of concentrate fed in those phases was 55%, 70%, 80% and 85%, respectively. Visual appraisal was made every five minutes during 24-h, and the feeding behavior (eating and ruminating times) data collected in min was used to calculate the efficiencies. It was evaluated in min per kilo of DM and NDF the feeding efficiency of DM (FEDM) and NDF (FENDF) and rumination efficiency of DM (REDM) and NDF (RENDF). No significant ($P > 0.05$) feed additive (FA) main effects were observed for any of the efficiencies evaluated. However, it was observed a BD main effect ($P < 0.05$) for some variables, in which BR bullocks presented better FEDM (29.75 vs. 35.65 min•kg^{-1} of DM), REDM (52.07 vs. 62.92 min•kg^{-1} of DM) and RENDF (191.64 vs. 257.43 min•kg^{-1} of DM) when compared to NE cattle. In addition, it was found an interaction ($P < 0.05$) between BD and phases for FENDF, where BR bullocks were more efficient than NE bullocks only in the FN1 (86.79 vs. 141.41 min•kg^{-1} of DM) and FN2 (95.81 vs. 166.66 min•kg^{-1} of DM) phases. FEDM, REDM and RENDF got better ($P < 0.05$) from ADP to FN1 phase; however, bullocks were less efficient ($P < 0.05$) in FN2 when compared to FN1 phase. Bullocks fed PAP presented similar efficiencies when compared to those fed MON. Overall, BR cattle were more efficient than NE in terms of FEDM, REDM and RENDF, and for FENDF when diets contained levels of concentrate of 80% or more.

Key Words: efficiencies, feedlot, Zebu

W380 Effects of feeding polyclonal antibodies preparations against lactate–producing rumen bacteria or monensin on blood gas profile, DMI fluctuations and rumenitis incidence of feedlot cattle. R. D. L. Pacheco*[1,2], D. D. Millen[1], M. D. B. Arrigoni[1], C. L. Martins[1], S. R. Baldin[1,2], L. M. N. Sarti[1], R. S. Barducci[1], T. M. Mariani[1], J. R. Ronchesel[1], F. S. Parra[1], D. P. D. Lanna[3], J. P. S. T. Bastos[1], and G. B. Mourão[3], [1]*São Paulo State University (UNESP)*, *Botucatu, São Paulo, Brazil*, [2]*Supported by FAPESP*, *São Paulo, São Paulo, Brazil*, [3]*University of São Paulo (USP)*, *Piracicaba, São Paulo, Brazil*.

This study was designed to test monensin (MON) and polyclonal antibody preparations (PAP) against lactate-producing rumen bacteria on blood gas profile, DMI fluctuations (DMIF) and rumenitis (RUM) incidence of Brangus (BR) and Nellore (NE) cattle. The experiment was designed as a 2 × 2 factorial arrangement using repeated measures over time, replicated 6 times (4 bullocks/pen), in which 48 9-mo-old bullocks of each of two breeds (BD) evaluated were fed diets containing either MON at 30 mg•kg^{-1} of DM or PAP at 300 mg•kg^{-1} of DM for 112-d. Measures over time were taken according to the phase: adaptation (ADP), growing (GRO) and finishing (FNS). The DMIF was calculated as the difference in DMI between consecutive days on the first four days of GRO and FNS phases. At harvest RUM incidence was determined, on the entire washed rumen, using a scale of 0 (no lesions noted) to 10 (severe ulcerative RUM). A significant ($P < 0.01$) feed additives (FA) and BD main effects were found for bicarbonate (PAP = 28.35 vs. MON = 26.72 mmol•L^{-1}; BR = 28.10 vs. NE = 26.96 mmol•L^{-1}), total CO_2 (PAP = 29.67 vs. MON = 27.95 mmol•L^{-1}; BR = 29.38 vs. NE = 28.24 mmol•L^{-1}) and base excess in extracellular fluid (PAP = 4.16 vs. MON = 2.49 mmol•L^{-1}; BR = 3.89 vs. NE = 2.77 mmol•L^{-1}). Likewise, BR cattle and bullocks receiving PAP had ($P < 0.01$) higher blood pH in the ADP phase than NE (7.423 vs. 7.404) and bullocks fed MON (7.427 vs. 7.400), respectively. Bullocks receiving PAP showed greater ($P <$

0.01) DMIF in GRO phase than those fed MON (0.339 vs. 0.243 kg); however, was not observed ($P > 0.05$) any difference between FA in the FNS phase. No significant BD ($P > 0.05$) main effect was found for DMIF. Moreover, NE presented greater ($P < 0.05$) incidence of RUM than BR (2.60 vs. 1.26); on the other hand, no significant FA ($P > 0.05$) main effect was observed. Thus, feeding PAP may be eventually an alternative to MON to reduce the risk of acidosis, because even showing greater DMIF, it improved the blood gas profile without impacting negatively rumen wall epithelia in terms of RUM.

Key Words: feedlot, MON, PAP

W381 Effects of feeding polyclonal antibodies preparations against lactate–producing rumen bacteria or monensin on blood lipoproteins concentrations and fatty acid profile of feedlot cattle. D. D. Millen*[1,2], R. D. L. Pacheco[1], M. D. B. Arrigoni[1], C. L. Martins[1], S. R. Baldin[1], L. M. N. Sarti[1], R. S. Barducci[1], T. M. Mariani[1], J. R. Ronchesel[1], F. S. Parra[1], D. P. D. Lanna[3], J. P. S. T. Bastos[1], G. B. Mourão[3], and A. M. Lopes[1], [1]*São Paulo State University (UNESP)*, *Botucatu, São Paulo, Brazil*, [2]*Supported by FAPESP*, *São Paulo, São Paulo, Brazil*, [3]*University of São Paulo (USP)*, *Piracicaba, São Paulo, Brazil*.

This study was designed to test monensin (MON) and polyclonal antibody preparations (PAP) against lactate-producing rumen bacteria on blood lipoprotein concentrations (BL) and fatty acid profile (FAP) of Brangus (BR) and Nellore (NE) cattle. The experiment was designed as a 2 x 2 factorial arrangement, replicated 6 times (4 bullocks/pen), in which 48 9-mo-old bullocks of each of two breeds (BD) evaluated were fed diets containing either MON at 30 mg•kg^{-1} of DM or PAP at 300 mg•kg^{-1} of DM for 112-d. Before slaughter blood samples for BL analysis were collect from jugular vein. At harvest, samples from s.c. adipose tissue were collected for FAP analysis. No significant ($P > 0.05$) feed additives (FA) main effect was observed for cholesterol concentration in LM and for BL, with the exception of HDL ($P < 0.05$), where bullocks receiving PAP had greater concentrations than those fed MON (59.85 vs. 54.04 mg•dL^{-1}). With respect to BD, NE bullocks presented ($P < 0.01$) lower VLDL concentration. Regarding FAP, no significant ($P > 0.05$) FA and BD main effect was found, with the exception of trans–vaccenic acid, where bullocks receiving MON and BR cattle had greater ($P < 0.05$) concentrations than those fed PAP (2.40 vs. 1.77 g•100g^{-1}) and NE (2.44 vs. 1.73 g•100g^{-1}), respectively. However, it was found significant ($P < 0.05$) interaction between BD and FA for C14:0, C16:0, C18:1, C18:2, CLA, C18:3 n-3, SFA, MUFA, and PUFA. Despite greater ($P < 0.05$) concentration of SFA than NE fed MON, NE bullocks receiving PAP presented greater ($P < 0,05$) concentrations of some UFA including C18:2, C18:3 n-3, PUFA (1.85 vs. 1.61 g•100g^{-1}), and CLA (0.58 vs. 0.49 g•100g^{-1}). On the other hand, feeding MON led to greater ($P < 0.05$) concentrations of C18:1 and MUFA, and lower ($P < 0.05$) C14:0 and C16:0 than PAP in NE bullocks. No differences were detected ($P > 0.05$) between BR cattle fed either FA. Thus, feeding PAP may be an alternative to MON, as feeding PAP increased the concentration of some UFA beneficial to human health, what may have led to greater concentrations of HDL in blood.

Key Words: feedlot, HDL, fatty acid

W382 Economic analysis of beef steer finishing diets containing elevated levels of wet distillers grains with solubles. J. M. Carmack*[1], P. M. Walker[1], J. D. Fehr[1], R. L. Atkinson[2], and L. A. Forster[3], [1]*Department of Agriculture, Illinois State University*, *Normal,*[2]*Animal Science, Food and Nutrition, Southern Illinois University*, *Carbondale,* [3]*Archer Daniels Midland Co*, *Decatur, IL*.

With increased production of ethanol in the Midwest over the past several years, increased supplies of wet distillers grains with solubles (DGS) has created an opportunity to decrease feed costs through their inclusion in finishing diets. This study consisted of an economic analysis (as fed basis) of a feeding trial conducted at Illinois State University in which 140 Angus cross steers were fed diets containing 0, 25, 40 or 70% DGS (percent DM basis). The treatments were: 80 shelled corn/5 soybean meal/15 corn silage (CON), 25 DGS/60 shelled corn/15 corn silage (25 DGS), 40 DGS/45 shelled corn/15 corn silage (40 DGS) and 70 DGS/15 shelled corn/15 corn silage (70 DGS). Seventy head were harvested on d 165 when 90% were estimated to have reached low choice or higher quality grade. The remaining 70 head were harvested on d 200 when 90% were estimated to have reached low choice or higher quality grade. Cost of feedstuffs, expressed as cents/kg were: 2.81:kg shelled corn, 7.54:kg soybean meal, 1.22:kg DGS, 0.59 corn silage, 8.86:kg trace mineralized salt, 4.13:kg limestone and 1.13/hd/d Rumensin/B1 premix. Average $:cwt of carcass was different ($P < 0.05$) with CON = 25DGS = 40DGS > 70DGS. Gross return:steer was lower ($P = 0.01$) for 70 DGS compared to the other treatments with no differences between CON, 25 DGS and 40 DGS diets. Differences were observed ($P < 0.05$) for total cost of feed:steer to harvest with CON > 25DGS > 40DGS > 70DGS. Gross dollar return over feed cost:steer was different ($P = 0.01$) as follows: 25 DGS = 40DGS > 70DGS > CON. Diets containing either 25 or 40% DGS (DM basis) returned more gross dollars over feed cost. Based on the analysis of this study, diets containing higher levels of DGS can return more dollars over feed cost.

Key Words: finishing diets, distillers grains, economic analysis

W383 Interactive effects of yeast and yeast cell wall material on feedlot performance during the receiving period of stressed beef cattle. D. N. Finck*[1], S. L. Parr[1], T. R. Young[1], J. A. Carroll[2], J. R. Corley[3], A. G. Estefan[3], and B. J. Johnson[1], [1]*Texas Tech University, Dept. of Animal and Food Sciences*, *Lubbock,* [2]*USDA-ARS, Livestock Issues Research Unit*, *Lubbock, TX,* [3]*Lesaffre Feed Additives*, *Milwaukee, WI*.

The objectives of this experiment were to determine the effect of live yeast and yeast cell wall supplements on performance and health of cattle during the receiving period. Newly-weaned crossbred steers (n = 184; 9 pens/treatment; initial BW = 203 kg) were blocked by BW and randomly assigned to pen (4 pens/block; 5 or 6 hd/pen). Pens within a block were randomly assigned to one of four treatments: 1) control (CON; no yeast additive), 2) live yeast (LY; 5 g•hd^{-1}•d^{-1} live yeast product), 3) yeast cell wall (YCW; 5 g•hd^{-1}•d^{-1} yeast cell wall product), 4) live yeast + yeast cell wall (LY+YCW; 5 g•hd^{-1}•d^{-1} live yeast and 5 g•hd^{-1}•d^{-1} yeast cell wall). A randomized complete block design was used; data were analyzed either as 4 separate treatments, or treatments 2 and 3 were combined to analyze the overall effect of yeast product inclusion level (0, 5, and 10 g inclusion). Daily DMI was recorded and individual BW were collected every 14 d for the 56 d feeding period. Steers receiving 5 g of LY or YCW showed a 7% numerical increase in ADG and a 7.7 kg increase in BW at d 56. Cumulative DMI was increased ($P < 0.05$) for the LY, YCW, and LY+YCW compared to CON (5.47, 6.02, 5.96, and 5.89 kg/d, respectively). Interim DMI differed for d 0 to 28 (5.03, 5.59, and 5.42 kg/d for 0, 5, or 10 g LY or YCW, respectively; $P = 0.02$, quadratic), d 0 to 42 (5.17, 5.75, and 5.62 kg/d; $P = 0.02$), and cumulative (5.46, 5.99, and 5.88 kg/d; $P = 0.03$). Steer morbidity and mortality were not affected by LY or YCW supplementation ($P > 0.10$). Collectively, these data indicated that the use of LY or YCW additives increase total

feed consumed by the steers during the first 56 d of the feeding period, which contributed to a trend for increased growth rate.

Key Words: receiving, steers, yeast

W384 Condensed tannins supplementation on feedlot performance of growing bulls. R. Barajas*[1], B. J. Cervantes1,2, A. Camacho[1], E. A. Velazquez[1], M. A. Espino[1,3], F. Juarez[1], L. R. Flores[1], and M. Verdugo[1], [1]*FMVZ-Universidad Autonoma de Sinaloa*, *Culiacan, Sinaloa, Mexico*, [2]*Ganadera Los Migueles SA de CV*, *Culiacan, Sinaloa, Mexico*, [3]*Técnología de Máxima Producción, S.A. de C.V.*, *Culiacan, Sinaloa, Mexico*.

This study was conducted to determine the influence of condensed tannins on feedlot performance of growing bulls. An 84-days feedlot experiment involving sixty bull-calves 183.94 ± 1.2 kg was performed. Animals were blocked by starting weight and in groups of five placed in ground flour pen (2 × 12 m). The experiment was conducted as a randomized complete block design. Treatments were: 1) Feedlot diets without additional tannins containing 0.56% of additional urea (CTRL); 2) Diets with 0.56% additional urea, added with equivalent of 0.20% of condensed tannins (TAN); and 3) Diets with 1.12% additional urea and 5% less canola meal than CTRL diets, and added with equivalent of 0.20% of condensed tannins (TAN-U). Supplementary condensed tannins were provided in form of an extract of condensed tannins from quebracho trees (SilvaFeed ByPRO; Indunor, S.A., Buenos Aires, Argentina). Both diets containing tannins increased ($P < 0.01$) ending weight, and average daily gain respect to bull-calves fed the unsupplemented CTRL diets. The ADG of TAN and TAN+U treatments were 14.8% and 12.6% higher ($P = 0.05$) than control, respectively. DMI was not affected by treatments ($P > 0.15$). Feed/gain ratio was enhanced ($P = 0.08$) by the two tannins contained treatments. TAN treatment reduced ($P < 0.01$) in 18.5% blood urea nitrogen in relationship to CTRL, while BUN values in TAN+U were similar ($P > 0.10$) to CTRL bull-calves. It is concluded, that supplementation with 0.2% of condensed tannins of quebracho trees improves feedlot performance of growing bull.

Key Words: condensed tannins, bulls, feedlot performance

W385 Factors influencing intake: Diet composition and carcass characteristics in finishing yearling steers. M. G. Dib*[1], G. E. Erickson[1], T. J. Klopfenstein[1], and M. L. Spangler[1], [1]*University of Nebraska*, *Lincoln,* [2]*Archer Daniels Midland*, *Columbus, NE*.

The effects of dietary components and carcass characteristics on average daily DMI were investigated using 930 individually fed yearling steers representing 13 experiments using a Calan gate system. Dietary treatments considered in the current study included the percentage of corn, either dry or high moisture (DRC_HMC), byproducts, and forage in the diets. Carcass and performance traits evaluated were 12th rib fat thickness (FAT), marbling score (MARB), calculated USDA Yield Grade (YG), HCW, and ADG. Pearson correlations between DMI and FAT, MARB, YG, HCW, and ADG were 0.16, 0.10, 0.15, 0.48, and 0.50, respectively, and were significant at the 0.05 level. The Mixed procedure of SAS was used to obtain coefficients for the regression of DMI on each carcass trait individually fitting experiment as a random variable. Estimated regression coefficients for FAT, YG, MARB, and HCW were 107.2 mm ±13.5, 1.15 calculated USDA YG ± 0.12, 0.003 marbling score unit±0.0009 and 0.01 kg±0.0004 respectively. The Mixed procedure of SAS was used to obtain regression coefficients for varying levels of the two dietary treatments. The most appropriate model included experiment as a random effect and the nested effect of forage within level of DRC_HMC. The inclusion rate of byproducts was not fit in the model but accounted for the balance of the diets. Nested effects were necessary in the current study given the inability to uncouple differing dietary treatments across experiments. Significant estimates were 0.89 (SE±0.45), 1.86 (SE±0.48), 2.06 (SE±0.48), 1.07 (SE±0.48), 0.61 (SE±0.29), 1.06 (SE±0.38), 0.99 (SE±0.35), 0.70 (SE±0.33) and 1.83 (SE±0.46) for 60:5 (corn:forage), 66:5, 76:5, 65:7, 0:7.5, 52.5:7.5, 67.5:7.5, 82.5:7.5 and 83.5:7.5, respectively ($P < 0.05$). The model accounted for 30% of the variation in DMI. Results show a positive and moderate correlation between DMI and both HCW and ADG and weak relationships with carcass characteristics.

Key Words: carcass traits, dry matter intake, feedlot cattle

W386 Effect of increased Rumensin dosage level and timing on performance of steers fed in confinement to harvest. G. J. Vogel*, *Elanco Animal Health*, *Greenfield, IN*.

One-thousand nine-hundred eleven crossbred steers (357 kg) were randomly allotted to 18 pens in a randomized complete block design of 3 treatments with 6 replications to evaluate the effects of an elevated level of Rumensin. Experimental treatments included: 1) Rumensin fed at 36.4 mg/kg of the diet, (R); 2) Rumensin fed at 48.5 mg/kg of the diet, (HR); and 3) Rumensin fed at 36.4 mg/kg of the diet before reimplant and then at 48.5 mg/kg of the diet post reimplant, (R-HR). All treatments were fed Tylan at 9.5 mg/kg of the diet. Reimplanting occurred on d 65 of the 151 d long study. A 2 ration step-up program was used to adapt steers to the final diet by d 22. Steers were fed 3 times daily. The final diet was formulated to contain 1.65 Mcal NEg/kg, 13.2% CP, 20.9% NDF, 7.9% EE, 0.72% Ca and 0.52% P. Performance parameters were analyzed using PROC MIXED with treatment as fixed effects and block as random effects. HR resulted in an improvement ($P < 0.02$) in feed to gain of 3.8 and 3.2%, respectively, over R and R-HR. Feed intake was not affected by feeding the elevated level of Rumensin. Carcass traits were not affected by treatment. These data indicate that feeding elevated levels of Rumensin for the entire finishing period enhance animal performance.

Table 1. Effect of increased Rumensin dosage

	Treatments				
	R	HR	R-HR	SEM	P
Final BW, kg	595.3	600.8	596.6	4.5	0.66
DM Intake, kg	9.49	9.41	9.49	0.11	0.70
Daily Gain, kg/d	1.58	1.63	1.59	0.03	0.17
Feed / Gain	6.01[a]	5.78[b]	5.97[a]	0.04	0.02

[ab]Means with different superscripts differ ($P < 0.05$).

Key Words: Rumensin, monensin level, cattle

W387 Blood gas profile, rumenites and liver abscesses incidences of feedlot bullocks fed high-concentrate diets containing monensin or polyclonal antibodies preparations against lactate-producing rumen bacteria. L. M. N. Sarti*[1,2], R. S. Barducci[1], M. D. B. Arrigoni[1], C. L. Martins[1], S. R. Baldin[1], D. D. Millen[1], R. D. L. Pacheco[1], T. M. Mariani[1], J. R. Ronchesel[1], F. S. Parra[1], A. L. Campanini[1], J. P. S. T. Bastos[1], D. Tomazella[1], and F. A. S. Miquilin[1], [1]*São Paulo State University (UNESP)*, *Botucatu, São Paulo, Brazil*, [2]*Supported by FAPESP*, *São Paulo, São Paulo, Brazil*.

This study was designed to test the effects of polyclonal antibody preparation (PAP) against lactate-producing rumen bacteria or mon-

ensin (MON) on blood gas profile (BGP), rumenites (RUM) and liver abscesses (LVA) incidences of feedlot bullocks fed high concentrate diets. Nine-mo-old Brangus (BR) bullocks (n=72) (261.04 ± 34.73 kg) were assigned to 24 pens (3 bullocks/pen) and used in a completely randomized design with 2 × 2 factorial arrangement of treatments using repeated measures over time, replicated 6 times. Factors were inclusion or not of PAP or MON, at a dose of 300 mg/kg DM or at 30 mg/kg DM, respectively. Measures over time were taken according to the phase: adaptation (ADP), growing (GRO) and finishing (FNS). Blood samples were collected from jugular vein of 48 animals (2 bullocks/pen) chosen randomly. At harvest RUM incidence was determined, on the entire washed rumen, using a scale of 0 (no lesions noted) to 10 (severe ulcerative RUM). No significant ($P > 0.05$) PAP or MON main effects were observed for RUM. On the other hand, feeding PAP reduced ($P < 0.01$) the LVA (5.56% vs. 19.44%), but no significant ($P > 0.05$) MON main effect was found (13.89% vs. 11.11%). No significant ($P > 0.05$) MON main effect was observed for any of the BGP variables; however, a significant ($P < 0.01$) PAP main effect was found, in which bullocks receiving PAP presented lower concentrations of bicarbonate (BICARB; 25.83 vs. 27.35 mmol/L), base excess in blood (BEB) and in the extracellular fluid (BEECF) than cattle fed no PAP. A significant ($P < 0.01$) interaction between PAP and MON was observed, in which bullocks receiving both feed additives presented lower blood pH than bullocks fed either PAP or MON (7.38 vs. 7.42 and 7.43, respectively). The phase affected ($P < 0.01$) the concentrations of BICARB, BEB and BEECF, where greater concentrations were observed in the GRO phase, followed by ADP phase, which had greater concentrations than FNS phase. Thus, even reducing the LVA, feeding PAP reduced the buffering capacity of the blood.

Key Words: blood, MON, PAP

W388 Effect of intermittent roughage delivery and roughage type on intake and digestibility by beef steers fed concentrate diets. A. Lopez[1], J. I. Arroquy*[1,2], M. Avila[2], H. Coria[3], and O. Hernandez[3], [1]*CONICET*, *Santiago del Estero, Argentina*, [2]*INTA EEA Santiago del Estero*, *Santiago del Estero, Argentina*, [3]*FAyA - Univ. Nac. Santiago del Estero*, *Santiago del Estero, Argentina*.

The objective of the trial was to evaluate the effect of three roughage delivery systems and two roughage sources on dry matter intake and digestibility by beef steers. Six ruminally fistulated beef steers (BW = 287 ± 35 kg) were used in a six treatments by four periods (6 × 4) trial. Treatment structure was 2 × 3 factorial. First factor was roughage delivery in a total mixed ration (TMR) or the same proportion of ingredients but forage offered once every 3-d (FE3D) or 6-d (FE6D) separated of the concentrate. The second factor consisted of two forages in the ration: middle-quality alfalfa hay (AH) vs. cotton plant byproducts (CPB). Roughage source was incorporated in the diet at 11% and 7% in DM basis to AH and CPB, respectively. There were not roughage delivery system × roughage source interaction for total (TDMI), concentrate (CDMI), and roughage (RDMI) DM intake, as well as total tract DM digestion (DMD) and total digestible DM intake (TDDMI). Roughage delivery system did not affect TDMI (73.6, 90.7, and 85.2 [SEM = 13.9] g/ kg BW0.75 for TMR, FE3D, and FE6D respectively), CDMI (67.0, 82.2, and 74.5 [SEM = 14.4] g/kg BW0.75 for TMR, FE3D, and FE6D respectively), RDMI (6.6, 6.9, and 6.4 g/kg BW0.75 [SEM = 1.1] for TMR, FE3D, and FE6D respectively), TDDMI (51.7, 69.7, and 62.1 g/kg BW0.75 [SEM = 8.7] for TMR, FE3D, and FE6D respectively) and DMD (696.5, 768.4 vs. 729.2 g/kg BW0.75 [SEM = 22.5] for TMR, FE3D, and FE6D respectively). Forage source affected RDMI ($P < 0.01$; 8.8 vs. 4.5 g/ kg BW0.75 [SEM = 0.8]). Whereas TDMI (85.7 vs. 80.6 [SEM = 8.5] g/ kg BW0.75 for AH and CPB respectively), CDMI (76.9 vs. 72.2 [SEM = 8.8] g/kg BW0.75 for AH and CPB respectively), TDDMI (62.9 vs. 59.4 g/kg BW0.75 [SEM = 5.5] for AH and CPB respectively) and DMD (730.9 vs. 731.7 g/kg BW0.75 [SEM = 18.4] for AH and CPB respectively) were similar among roughage sources. According to our experiment it is concluded that roughage portion of a finishing ration might be supplied in a discontinuous way without any effect on DM intake and digestibility utilizing either a middle-quality or low-quality roughage source.

Key Words: roughage delivery, finishing diet, digestibility

W389 Effect of wheat straw level and processing method on site and extent of digestion by cattle consuming finishing feedlot diets. J. A. Valdez*[1], J. O. Chirino[1], M. F. Montaño[1], N. G. Torrentera[1], E. G. Alvarez[1], J. F. Calderón[1], O. M. Manriquez[1], M. A. Lopez[1], V. M. Gonzalez[1], A. Perez[1], J. Salinas[2], and S. A. Soto-Navarro[3], [1]*Universidad Autónoma de Baja California*, *Mexicali, BC, MX*, [2]*Universidad Autónoma de Tamaulipas*, *Victoria, TAM, MX*, [3]*New Mexico State University*, *Las Cruces*.

Holstein steers (n = 4; 216 kg BW), fitted with cannulas in the rumen and proximal duodenum, were used to evaluate wheat straw inclusion level (7 and 14%; DM basis) and roughage processing method (ground vs. pellet) on characteristics of digestion of steam-flaked corn finishing diets. The experimental design was a 4 × 4 Latin square with a 2 × 2 factorial arrangement of treatments. Wheat straw was ground in a tub grinder with a 3.81 cm screen, while the pellet dimensions were 2 cm long × 0.5 cm diameter. An interaction was detected between straw level and processing method for DM intake ($P < 0.01$). With 14% straw, processing method did not affect ($P = 0.83$) DM intake. With 7% straw, DM intake was lower (2.3%, $P < 0.01$) for pelleted straw than for ground. Digestibility of ruminal OM (6%), true ruminal N digestibility (9.7%), total tract OM (3.9%), and total tract N (4.2%)were greater ($P \leq 0.05$) for diets that contained 7% wheat straw than for those that contained 14%. Ruminal starch digestibility (88.7, and 84.9 ± 0.74%, for pelleted and ground, respectively) was greater ($P = 0.04$) and ruminal pH (5.44, and 5.76 ± 0.22, for pelleted and ground, respectively) was lower ($P = 0.05$) for diets that contained pelleted straw than for those that contained ground straw. Steers fed 7% wheat straw had greater OM and N digestibility. The greater ruminal starch digestibility and lower pH of steers consuming pelleted wheat straw might be responsible for the lower DM intake observed for steers consuming pelleted wheat straw at 7%. Wheat straw is a viable roughage source for feedlot diets. However, when included at low levels, the pelleted form does not elicit the optimum rumen function stimulation.

Key Words: digestion, processing, wheat straw

W390 Milk production response to incremental levels of crude glycerol on diets of grazing dairy cows. R. Echeverria, A. Mackinnon, J. Rotulo, and P. Chilibroste*, *Universidad de la Republica, EEMAC*, *Paysandu, Uruguay*.

An experiment was carried out to determine milk production response of Holstein dairy cows to incremental levels of crude glycerol in the diet. The experiment was conducted between June 15 and July 31 of 2009 at the Experimental Station M. A. Cassinoni, Agronomy Faculty, Republic University, Uruguay. A complete randomize block design was set up and a repeated measurement in time model used to analyze the data. Thirty six autumn-calving dairy cows were blocked by parity, days in milk, milk production and body weight and randomly allocated to one of the following treatments: T0 = control diet, T1= 0.72 kg of glycerol/cow/day and T2= 1.44 kg of glycerol/cow/day. Control diets were based on grazing of a daily strip of oat plus 5 kg DM of a commercial concentrate (18.2% CP, 14% FDA, 25% NDF and 7.3% ASH) offered half at each milking. The crude glycerol (3.5% humidity, 6.9% ash, 1,5% fat and 17% methanol) was mixed with the concentrate just before each milking session. Cows body weight and milk production at the beginning of the experiment were 585±57, 576±67, 564±49 and 24.4±3.2, 24.9±4.3, 26±3.1, for T0, T1 and T2, respectively. Cows fed glycerol (T1 and T2) produced 2.15 L extra milk than control cows (T0=23.5 L; $P < 0.05$). Milk production of glycerol fed cows was not significantly different (25.4 vs. 25.9 for T1 and T2, respectively). A marginal response of 2.6 L extra milk per kg extra of glycerol was obtained with a supplementation of 0.72 kg of glycerol/cow/day. Milk response to crude glycerol in this experiment was higher than responses obtained with other energy sources which open opportunities to the use of this byproduct on diets of dairy cows.

Key Words: crude glycerol, dairy cows, milk production

W391 Nutrient balances in California dairy farms. 2. Factors associated with feed conversion and nitrogen utilization efficiencies. A. R. Castillo*[1], N. Silva del Rio[2], and N. St-Pierre[3], [1]*University of California Cooperative Extension*, *Merced,* [2]*University of California Cooperative Extension*, *Tulare,*[3]*The Ohio State University, Department of Animal Sciences*, *Columbus*.

The aim of this survey was to study dietary factors associated to nitrogen utilization efficiency and feed conversion in lactating cows on commercial farms. Forty dairies in Merced, California (mean 787 ± 592 lactating cows/farm) were characterized based on the total salt (TS) in drinking water (mean 560 ± 343 TS mg/L) and 3.5% fat-corrected milk yield/cow (MY) (mean 31.8 ± 5.2kg/d). TS were estimated by oven drying (105°C, 24 h), and MY and fat content on DHIA information. Duplicated samples of Total Mixed Rations (TMR) were collected on 2 non-consecutive days and wet chemistry analyzed. TMR nutrient content per farm (% DM, NDF, ADF, Lignin, N, Fat, Ash, non-fiber carbohydrates [NFC], was analyzed for each production group (n = 118). CP balance (CPB) was estimated according to the NRC, 2001. DMI per farm was calculated for each lactating group based on the total daily amount of TMR supplied, divided by the number of cows in each feeding group, and corrected by estimated refusal. Pearson correlation analysis was used to study the linear association of feed conversion (FC = MY/DMI) and nitrogen utilization efficiency (NUE = N milk/N intake), and TS, MY, DMI, TMR nutrient content, number of TMR/dairy for lactating cows, and cow number/dairy. A correlations table shown results were only r > 0.30 and $P < 0.05$ are reported. FC and NUE were positively associated to MY, NFC and number of TMR/dairy, and both were negatively associated to CPB. FC and NUE were also negatively associated to dietary NDF and N concentrations, respectively. FC and NUE were high and positive correlated.

Table 1. Correlation table: factors associated with FC and NUE

	MY	%NDF	%N	%NFC	CPB	TMR/dairy	FC
FC	0.88**	–0.33*	ns	0.37*	–0.35*	0.39**	–
NUE	0.70**	ns	–0.64**	0.55**	–0.70**	0.36**	0.86**

ns = non-significant, *$P < 0.05$, **$P < 0.01$.

Key Words: dairy farms, feed conversion, nitrogen utilization efficiency

W392 Effects of glucose, propionate, insulin and gut peptides on neuropeptide mRNA concentrations in the ovine hypothalamus. A. E. Relling*[1,3], K. Lee[1], S. C. Loerch[1], and C. K. Reynolds[2], [1]*The Ohio State University*, [2]*University of Reading*, *UK*, [3]*Universidad Nacional de La Plata*, *Argentina*.

The effects of glucose, propionate, or hormones of splanchnic origin on appetite regulating neuropeptides in the hypothalamus of ruminants have not been described. Therefore, the objective of the present study was to measure the effect in vitro of glucose, propionate, insulin, cholecystokinin (CCK), glucagon-like peptide-1 (GLP-1), or polypeptide YY (PYY) on hypothalamic mRNA concentrations for neuropeptide Y (NPY), agouti-related peptide (AgRP), and proopiomelanocortin (POMC). In an incomplete block design, hypothalamic tissue from market lambs was obtained at slaughter and immediately incubated in culture media for 2 h at 36°C. Treatments included a control Dulbecco's Modified Eagle Medium (DMEM) containing 1 m*M* glucose (n=8) or DMEM with the following additions: 10 m*M* glucose (n=8), 1 m*M* propionate (n=4), 1 n*M* insulin (n=4), 120 pM GLP-1 (n=4), 100 p*M* PYY (n=4), 80 p*M* CCK (n=4), or 10 m*M* glucose plus 1 n*M* insulin (n=4). The abundance of mRNA for NPY, AgRP, and POMC was measured using quantitative reverse transcriptase PCR, and normalized to peptidylprolyl isomerase B mRNA expression in the same sample. Dunnett's mean separation was performed to compare treatment means to the control using mixed model procedures testing the random effects of lamb and block, and the fixed effects of treatment. There was a 4-fold increase in POMC mRNA concentration for the media containing glucose plus insulin ($P < 0.05$), but NPY or AgRP mRNA concentration was not affected. There were no effects observed for the other treatments ($P > 0.20$). Results of the present study suggest insulin is required for effects of glucose on hypothalamic POMC expression in sheep. Therefore, it is likely that the effect on the neuropeptides that regulate dry matter intake are due to additive effects of multiple signals, not solely changes in single hormone and metabolite concentrations.

Key Words: hypothalamic neuropeptides, gut peptides, insulin

W393 Relationship between prolamin content and in situ starch digestibility of barley grain. M. Oba*[1], D. Gibb[2], and T. McAllister[2], [1]*University of Alberta*, *Edmonton, AB, Canada*, [2]*Agriculture and Agri-Food Canada*, *Lethbridge, AB, Canada*.

The objective of this study was to evaluate the relationship between prolamin content and in situ digestibility at various incubation times for barley grain. Forty lots of barley grain samples were obtained from

an agronomic study evaluating effects of seeding and fertilization rates at two locations in Alberta (Beaverlodge and Lacombe). Barley grain was ground through 6-mm screen of the Wiley mill before in situ incubation. In situ digestibility of starch was determined after 0, 3, 6, and 24 h of incubation in the rumen of three non-lactating cows fed a 75% concentrate diet. Barley grain samples from Beaverlodge contained more prolamin than those from Lacombe (2.6 ± 0.1 vs. 1.3 ± 0.1%; $P < 0.001$). However, barley grain from Beaverlodge was greater in 6-h in situ digestibility compared with those from Lacombe (60.1 ± 1.1 vs. 56.7 ± 1.1%; $P < 0.05$). Prolamin content of barley grain (% dry matter) was not correlated to in situ starch digestibility at 0-h ($r = 0.15$), 3-h ($r = -0.17$), or 6-h ($r = 0.19$) of incubation, but was positively correlated to 24-h in situ digestibility ($r = 0.37$; $P = 0.05$). Prolamin content of barley grain was not correlated to in situ DM digestibility at any incubation time. These results indicate that growing environment potentially affects prolamin content of barley grain, but that prolamin in barley grain may not negatively affect starch digestion in the rumen.

Key Words: barley grain, starch digestibility, prolamin

W394 Effect of crude glycerin supplementation on the performance of dairy cows under high altitude tropical conditions. L. Mestra[1], Y. Avellaneda*[1], P. Medina[1], G. Garcia[1], C. Ariza-Nieto[1], D. Cifuentes[1], D. Galindo[1], J. Palomino[1], and G. Afanador[1,2], [1]*CORPOICA*, *Bogota, Colombia*, [2]*Universidad Nacional de Colombia*, *Bogota, Colombia*.

This study evaluated the effect of crude glycerin (10% moisture, 87% glycerol and <0.5% methanol) supplementation on dairy cow performance under grazing conditions during the first stage of lactation. The experiment was carried out at the Colombian Corporation for Agricultural and Livestock Research located at 2650 above mean sea level. Pastures of *Pennisetum clandestinum* + *Lolium perenne* (cutting age, 45 days) sward were grazed by cows in a strip-grazing system. Cows had access to corn silage and an energy-protein nucleus (22.1% CP and 2.0 Mcal/kg NEmilk) which offer was adjusted according to the expected lactation curve. A total of 12 Holstein cows were randomly assigned to three glycerin levels (0, 300, 500 ml/day). Cows were individually weighed every other month. Feed intake and milk production were recorded daily. Additionally milk samples were collected at 0, 90 and 150 days of the study to determine fat, protein and lactose content. Data were analyzed as a completely randomized design with repeated measures over time using the MIXED procedure of SAS (Ver. 9.0, SAS Institute, Cary, NC, USA). Glycerin level did not affect productive performance ($P > 0.05$) of the dairy cows, although cows supplemented with 300 and 500 ml/day increased milk production by 10% and 6.3%, respectively compared to control group. Body weight gain was higher in cows supplemented with glycerin at 300 ml/d (0.108 kg/d) when compared to cows without glycerin (0.067 kg/d). The percentage of lactose was higher ($P < 0.05$) in milk of cows supplemented with crude glycerin compared to control group (4.8% vs. 4.4%). At the end of the experiment (150 days) milk fat showed a tendency ($P = 0.095$) to be higher in the group of cows supplemented with glycerin (3.7%) compared to the control group (3.1%). Thus, it can be concluded that there is a trend in the improvement of milk quality of cows supplemented with crude glycerin.

Key Words: glycerin, dairy cow, milk quality

W395 Effect of the germinated corn on feed intake, milk production, milk quality and blood metabolites of lactating cows. B. W. Kim*[1], J. W. Ju[1], J. K. Choi[2], and J. S. Shin[1], [1]*Kangwon National University*, *Chuncheon, Kangwon-Do, South Korea*, [2]*Dae Han Feed Company*, *Incheon, South Korea*.

This study was conducted to evaluate the effect of germinated corn on the feed intake, milk production, milk quality and blood metabolites of lactating cows. Five lactating cows were randomly assigned to 3 replicates of 3 treatments to determine the effects of feeding 0 (control), 10 (T1), 20% (T2) of the germinated corn in partial replacement of alfalfa hay and commercial concentrate in the diet. The trial lasted for 3 months. The feed intake was not significantly affected. However, the lactating cows fed on the germinated corn consumed more feed: 21.5kg in T1 and 21.7kg in T2 than those in the control (20.9 kg). The T1 and T2 resulted in a 5.8 and 11.1% increase in milk production, respectively, compared to the control ($P < 0.05$). The feed efficiency improvements were observed in treatments with germinated corn by 3.0 and 7.4% in T1 and T2, respectively. No significant difference was found in milk fat and lactose contents, but milk protein and solid-not-fat contents were higher in T1 and T2. The somatic cell counts were significantly lower for the cows fed on the germinated corn (78.67×10^3 /mL in T1 and 79.68×10^3 /mL) than those fed the control diet (158.33×10^3 / mL). Thus, these findings indicate that germinated corn can be useful as feed supplementation for increasing milk production and milk quality of lactating cows.

Key Words: germinated corn, feed intake, lactating cows

W396 Influence of hypocalcemia on plasma biochemical parameters, lipid mobilization, and liver lipid infiltration in cows. W. G. Chamberlin*, J. R. Middleton, J. N. Spain, G. C. Johnson, and M. R. Ellersieck, *University of Missouri*, *Columbia*.

This study was conducted to evaluate the effects of calcium status at calving on plasma metabolites and liver lipid infiltration in Holsteins. One hundred multiparous Holsteins were assigned to one of two groups 1) hypocalcemic (n=51; ionized calcium [iCa] <1.0 mmol/L) or 2) normocalcemic (n=49; iCa >1.0 mmol/L) based on whole blood iCa concentrations at calving. Cows were blocked by parity and calving date (3.5 for hypocalcemic, 2.8 for normocalcemic). Blood samples were collected to measure iCa, NEFA, and serum chemistry profiles at −14d, calving, 3d, 7d, 14d, 21d, and 35d. Liver biopsies were collected from 22 cows (8 hypocalcemic and 14 normocalcemic) on the day of calving, and 7 and 35 days postpartum for analysis of lipid infiltration in the hepatocytes. Data are reported as LSMeans ± SE. On day 0, [iCa] differed with hypocalcemic cows having lower whole blood [iCa] (0.88 ± 0.01 mmol/L) versus normocalcemic cows (1.08 ± 0.01 mmol/L; $P < 0.0001$). Hypocalcemic cows also had lower mean total plasma calcium concentrations on day 0 than normocalcemic cows (7.03 ± 0.08 mg/dl vs. 8.20 ± 0.08 mg/dL; $P < 0.0001$). Hypocalcemic cows had lower plasma phosphorus levels on days 0 (3.96 ± 0.16 mg/dL), 7 (5.33 ± 0.17 mg/dL), 14 (5.10 ± 0.18 mg/dL), and 21 (5.75 ± 0.18 mg/dL) versus normocalcemic cows on days 0 (4.7 ± 0.17 mg/dL; $P = 0.002$), 7 (5.81 ± 0.17 mg/dL; $P = 0.05$), 14 (5.67 ± 0.18 mg/dL; $P = 0.03$), and 21 (6.28 ± 0.18 mg/dL; $P = 0.04$). Hypocalcemic cows had significantly higher mean NEFA concentrations on days 0 (1034.4 ± 61.04 uEq/L) and 21 (613.42 ± 61.42 uEq/L) versus normocalcemic cows on days 0 (823.17 ± 62.65 uEq/L; $P = 0.01$) and 21 (444.67 ± 63.48 uEq/L; $P = 0.02$). Hypocalcemic cows also had more lipid in the hepatocytes on day 35 (17.33 ± 3.36%) than normocalcemic cows (6.98 ± 2.6%; P = 0.02). No differences were detected between groups for total or direct bilirubin concentration, gamma glutamyl transferase or aspartate aminotransferase activity ($P > 0.05$). These data provide evidence of an association between calcium status at calving, fat mobilization, and liver lipid infiltration.

Key Words: transition, hypocalcemia, liver

W397 Effects of a low energy diet prepartum on subclinical ketosis in dairy cows. L. A. Vickers*[1], D. M. Weary[1], D. M. Veira[2], and M. A. G. von Keyserlingk[1], [1]*Animal Welfare Program, University of British Columbia*, *Vancouver, British Columbia, Canada*, [2]*Agriculture and Agri-Food Canada*, *Agassiz, British Columbia, Canada*.

Despite decades of research the dairy industry remains challenged with high rates of disease after calving, often attributed to prolonged periods of negative energy balance (NEB). In an effort to reduce NEB it is common practice to provide an energy dense diet 3 wks before calving, but this may lead to over consumption of energy and actually increase the risk of metabolic disease post-partum. The aim of this trial was to compare the metabolic status of transition cows on a traditional pre-calving diet (NE_L=1.45 Mcal/kg) versus a low energy, high forage diet (NE_L=1.34 Mcal/kg). Cows were randomly assigned to either the control diet (cows were switched to the close up ration 3 wks prepartum) or the treatment diet (cows remained on the low energy diet until parturition). After parturition, all cows were fed a common lactation diet (NE_L =1.65 Mcal/kg). Treatment groups were balanced for parity, previous 305-day milk production and body condition score. DMI was measured daily from 3 wks before to 2 wks after calving for 78 multiparous Holstein cows. Blood BHBA was measured daily for 10 d after calving. The MIXED procedure in SAS was used to test the fixed effect of treatment on BHBA for each day postpartum, and on DMI in the prepartum and the postpartum period. Cows on the low energy diet prepartum had lower BHBA levels than did control cows (0.48 ± 0.03 vs. 0.65 ± 0.03mmol/L; $P < 0.0001$). Using a threshold of $1.0 \leq$ BHBA ≤ 1.4 mmol/L, fewer cows on the low energy diet prepartum were diagnosed as having subclinical ketosis compared to cows on the control diet (4.8% vs. 20.6%; χ^2 =7.17, $P = 0.007$). Cows on the low energy diet had lower DMI compared to the cows on the close up diet (13.57 ± 0.09 kg/d vs. 16.45 ± 0.12 kg/d; $P < 0.05$) and consumed slightly less DM in the first 2 wks postpartum (18.64 ± 0.41 vs. 17.65 ± 0.40 kg/d; $P < 0.05$). Feeding a low energy diet before calving can reduce the risk of subclinical ketosis.

Key Words: transition diets, intake, subclinical ketosis

W398 Impacts of maternal selenium supply and nutritional plane on offspring intestinal vascularity. R. D. Yunusova*, A. M. Meyer, T. L. Neville, K. A. Vonnahme, C. J. Hammer, J. J. Reed, D. A. Redmer, L. P. Reynolds, and J. S. Caton, *Center for Nutrition and Pregnancy, Department of Animal Sciences, North Dakota State University*, *Fargo*.

Objectives were to investigate the effects of maternal nutritional plane and Se supply during gestation on offspring intestinal vascularity. Rambouillet ewe lambs (n = 82 in Exp. 1, n = 84 in Exp. 2; approximately 240 d of age; 52 kg BW at breeding) were allocated to a 2 × 3 factorial. Treatments included dietary Se (adequate Se [ASe, 9.5 (Exp.1) or 11.5 (Exp. 2) μg/kg BW] or high Se [HSe, 81.8 (Exp. 1) or 77.0 (Exp. 2) μg/kg BW]) initiated at breeding and nutritional plane (60% [RES], 100% [CON], and 140% [HIGH] of requirements) initiated at d 50 (Exp. 1) or d 40 (Exp. 2) of gestation. Ewes were fed pelleted diets and housed individually indoors. At parturition, lambs were immediately removed and fed artificial colostrum for the first 20 h followed by ad libitum milk replacer. At 180 ± 2 d (Exp. 1) and 20 d (Exp. 2) of age lambs were euthanized and tissues were harvested. Collected jejunal tissues were perfusion fixed with Carnoy's solution, paraffin embedded, and vascular structures were visualized microscopically. Data were analyzed for effects of Se supply, nutritional plane, and their interaction. In Exp. 1, capillary area density (% tissue) was greater ($P = 0.08$) in 180-d old offspring from ewes fed HSe compared with ASe (15.3 vs. 13.8 ± 0.6%, respectively). In addition, area per capillary (μm^2) was greater ($P \leq 0.09$) in CON compared with RES. In Exp. 2, capillary surface density ($\mu m/\mu m^2$) was greater ($P \leq 0.05$) in 20-d old offspring from ewes fed CON than RES. Maternal nutritional plane tended ($P \leq 0.11$) to alter total small intestinal vascularity (mL), with lambs from CON being greater than RES. Area per capillary was affected by the interaction of Se × nutritional plane ($P = 0.09$). In offspring from ewes fed ASe, RES had greater area per capillary than CON and HIGH, whereas area per capillary was not affected by nutritional plane in HSe offspring. In conclusion, maternal Se supply and nutritional plane during gestation resulted in measurable changes in offspring intestinal vascularity at both 20 and 180 d of age. Additional work is needed to determine impacts on intestinal function and nutrient uptake.

Key Words: intestine, maternal nutrition, selenium

W399 Performance of high-yielding dairy cows supplemented with fat or concentrate under hot and humid climates. U. Moallem*[1], G. Altmark[2], H. Lehrer[1], and A. Arieli[2], [1]*Agriculture Research Organization*, *Bet Dagan, Israel*, [2]*Faculty of Agriculture, Hebrew University*, *Rehovot, Israel*.

Multiparous Israeli-Holstein mid-lactation cows were used to examine the effects of energy source under hot and humid conditions on performance, metabolic heat production (MHP) and efficiency. Cows (n = 42) were individually fed and assigned into 3 groups: 1) control - were fed a lactating-cow ration (1.75 Mcal NEL/kg DM); 2) HG - supplemented with 0.825 kg/d per cow of ground corn grain (2.7% of diet); 3) HF - supplemented with 0.300 kg/d per cow of calcium salts of fatty acids (1.5% of diet). Indirect MHP was calculated as: metabolizable energy intake – (energy output in milk + energy retention in body-mass + energy for maintenance). Data were analyzed as repeated measurements using the PROC MIXED procedure of SAS. Mean daily maximum ambient temperature, relative humidity and temperature-humidity index (THI) were 31.5°C, 86.6% and 76.8, respectively. DMI was lower in HF and HG than in controls, and milk yields were higher in the control group than in HG. Milk-fat percentage was 0.38 units higher and fat yields were 11% greater in HF than in HG. Fat-corrected milk (FCM) yield was 5.5% higher in HF than in HG, but not than in control. Body weight gain (kg/d) of the HG cows tended to be higher than that of the others. Efficiency of conversion of DM or energy intake to milk and FCM was higher in HF than in other groups; however, when taking the energy retention in body-mass into account, no difference in energy utilization between HF and HG were observed. Indirect MHP was similar in HG and HF cows, and lower than in controls. HF cows channeled more metabolizable energy for milk production (43.1, 40.5 and 41.6% for HF, HG and control groups, respectively). In contrast, HG cows directed more energy for body-mass retention (1.89, 0.53, and 0.99% for HG, HF and control, respectively). In conclusion, increasing the energy density in diets of heat-stressed mid-lactation cows over 1.75 Mcal/kg DM was not effective in enhancing production; however, HF increased the efficiency for milk production. Moreover, HF cows prioritized milk-fat production, whereas HG cows channeled more energy for body-mass retention.

Key Words: heat stress, fat supplementation, energy partitioning

W400 Concentrations of plasma metabolites and hormones in periparturient Holstein cows fed two sources of fat. C. Caldari-Torres[2], E. D'Agosto[1], M. C. Perdomo[1], C. R. Staples[1], and L. Badinga*[1], [1]*University of Florida*, *Gainesville,* [2]*Virginia Tech*, *Blacksburg*.

This study examined the effect of feeding diets enriched in saturated fatty acids (SFA; RBF Cargill, 91% saturated fat, 1.5% of DM) or linoleic acid (LA, Prequel 21, Virtus Nutrition, 63% n-6 FA, 1.8% of DM) to transition Holstein cows (n = 18) on plasma metabolites and hormones related to energy metabolism. Dietary treatments were initiated at approximately 28 d prior to calculated calving date and continued through 49 d postpartum. Blood samples were collected weekly beginning 1 wk before estimated calving date through 7 wk postpartum. Plasma NEFA concentration increased ($P < 0.01$) between wk 1 before (231 ± 88 μeq/L) and wk 1 after parturition (829 ± 80 μeq/L) and returned to pre-calving concentrations by wk 7 postpartum (404 ± 80 μeq/L). Blood NEFA concentrations in cows consuming the LA-enriched diet tended to be lower ($P = 0.06$) than those receiving the SFA-supplemented diet at wk 3 and 4 postpartum. Blood glucose concentrations were consistently greater ($P < 0.01$) across wk in cows fed the LA-enriched diet compared to those consuming the SFA-supplemented diet. Concentrations of plasma insulin were only numerically greater for cows fed additional LA (0.73 vs. 0.67 ng/mL). Mean peripheral concentration of IGF-I decreased ($P < 0.01$) from 130.8 ± 14.7 ng/mL at 1 wk before calving to 60.9 ± 13.4 ng/mL at 2 wk after calving, and then increased to 119.8 ± 13.4 ng/mL by wk 7 postpartum. Pre- and postpartum plasma IGF-I concentrations were greater ($P < 0.01$) in Holstein cows fed the LA-enriched diet than those consuming the isocaloric control diet supplemented with SFA. Plasma IGF-I concentration at wk 7 postpartum was positively correlated (r = 0.58, $P < 0.01$) with conception rate to first insemination. Results indicate that peripartum supplementation of LA may improve the metabolic status and increase the risk of pregnancy of early postpartum dairy cows.

Key Words: fat, hormone, cattle

W401 Weaning dairy cows to a new diet: The effectiveness of a gradual dry-off procedure. K. L. Proudfoot*, D. M. Weary, and M. A. G. von Keyserlingk, *University of British Columbia*, *Vancouver, British Columbia, Canada*.

Gradual dietary transitions for animals are typically favored over abrupt switches. However, a common method to end the lactation of a dairy cow (i.e. dry-off) is to abruptly switch cows from a high to low energy diet. Gradual weaning at dry-off may be beneficial, but no work has assessed if it is equally effective at reducing milk output. Here we assessed the effect of a gradual versus abrupt switch from a lactating cow diet (60:40 forage:concentrate ratio) to grass hay on dry matter intake (DMI) and milk yield. Four pens of 6 cows were followed for 14d. Cows were paired, with one cow from each of 2 treatments based on parity and previous milk yield. During the first 2d (baseline) both treatments were fed the same lactation diet of 60% forage. Cows on the gradual treatment were switched to a diet 10% higher in forage every 2d until d9; cows on the abrupt treatment were switched directly to 100% forage on d9. Each cow had access to one feed bin that recorded DMI. Data were summarized into 5 periods: Four 2-d periods before treatments were switched to 100% forage and one 4-d period following the switch (d10 to 14). Differences between treatments were tested using Proc Mixed in SAS with the feed bin was the experimental unit and period as a repeated measure. The model included pair, pen, period, treatment and period × treatment interaction. No baseline differences were detected between cows on the gradual and abrupt treatment for milk yield (15.5±1.2 vs. 14.8±1.2 kg/d, $P = 0.74$) or DMI (18.0±0.5 vs. 17.7±0.5 kg/d, $P = 0.67$). The gradual increase in % forage resulted in treatment × period interactions for both milk yield ($P < 0.01$) and DMI ($P < 0.01$); as % forage in the diet increased cows on the gradual treatment produced less milk and had lower DMI than did the cows on the abrupt treatment. After both groups were switched to the 100% forage diet no differences were detected between cows on the gradual and abrupt treatment for milk yield (9.3±0.9 vs. 7.5±0.9 kg/d, $P = 0.17$) or DMI (10.4±0.4 vs. 10.2±0.4 kg/d, $P = 0.64$). These results indicate that a gradual dietary transition at dry-off is as effective at reducing DMI and milk yield as an abrupt switch in diet.

Key Words: dry-off, weaning

W402 Effects of feeding different levels of guar meal on performance of Holstein dairy cows. A. Vatandoust[1], A. A. Naserian*[2], F. Boldaje[1], and S. Zerhdaran[1], [1]*University of Gorgan*, *Gorgan, Iran*, [2]*University of Mashhad*, *Mashhad, Iran*.

Eight multiparous (n = 2) early lactating Holstein cows were used in a 4 × 4 Latin square design to determine effects of different levels of guar meal on the performance of dairy cows. Treatments were including 4 levels of guar meal: T1) 0, T2) 4, T3) 8, T4) 12% of DM that substitute to soybean meal. Treatments effect on DMI (kg/d) were not significant ($P > 0.05$). Milk yield were increased for cows fed T2 compared with other treatments (43.392, 46.480, 44.100 and 43.080, respectively) ($P < 0.05$). Milk fat (%) was increased for T2 compared with T3 and T4 ($P < 0.05$), but had no difference between T1 and T2 ($P > 0.05$). Milk protein was not influenced by treatments ($P > 0.05$). Treatments effect on pH were significant ($P < 0.05$), cows fed T2 had lower pH than control (6.58 vs. 6.36). It was concluded that substitution 4% of soybean meal with guar meal had the best effect on performance.

Table 1. Effects of different levels of guar meal on DMI, rumen pH, milk yield and composition

	T1	T2	T3	T4	SE	P-value
DMI (kg/d)	26.805	26.975	26.717	26.968	0.445	>0.05
Milk yield (kg/d)	43.392b	46.480a	44.100b	43.080b	0.806	<0.05
Milk Fat (%)	3.717ab	4.101a	3.380b	3.424b	0.162	<0.05
Milk protein (%)	2.803	2.592	2.688	2.715	0.110	>0.05
rumen pH	6.588a	6.367b	6.381ab	6.406ab	0.070	<0.05

T1, T2, T3 and T4= levels of guar meal (0, 4, 8 and 12% of DM respectively). SE= standard error of means.

Key Words: guar meal, lactating Holstein cow, soybean meal

W403 Feed sorting and feeding behavior of transition dairy cows fed glycerol as a replacement for corn. E. R. Carvalho*, N. S. Schmelz, H. White, and S. S. Donkin, *Purdue University*, *West Lafayette, IN*.

Feed sorting is a natural behavior of dairy cows that can result in inconsistencies in nutritive value of a TMR. The objective of this work was to study the effects of glycerol on the feed sorting and feeding behavior of transition dairy cows. Twenty-six multiparous Holstein cows were paired by expected calving date and fed diets containing either high moisture corn or glycerol from −28 through +56 days relative to calving (DRTC). Glycerol was included at 11.5 and 10.8% of the ration DM for the pre- and post-partum diets, respectively. Cow activity was continuously videotaped for 24 h on −17, −10, +8, +15 and +50 DRTC. Feeding behavior was evaluated for 1 h intervals at 0, 1, 5.5, and 11 h relative to feed delivery and feed sorting was determined during the next 24-h period by measuring the particle size distribution of feed consumed at 4, 8, 12 and 24 h post feeding. The TMR at feeding and

at each time post feeding was size separated across 18, 9, and 1.18 mm screens and a bottom pan to yield long, medium, short, and fine particles, respectively. Adding glycerol to the prepartum diet increased ($P \leq 0.05$) the DM% retained as long particles and reduced ($P \leq 0.05$) short and fine particles but did not change the medium particles ($P \geq 0.05$). Feed intake did not differ ($P \geq 0.05$) between diets and was 14.7 ± 0.4 and 20.2 ± 0.5 kg/d for the pre- and post-partum intervals, respectively. Glycerol increased ($P \leq 0.05$) the preference for long particles during the prepartum period (17.8 vs. 9.2%, glycerol vs. control) and increased ($P \leq 0.05$) sorting against short (37.3 vs. 42%, glycerol vs. control) and fine particles (13.6 vs. 17.9%, glycerol vs. control). There was no effect of glycerol on preference for medium particles ($P \geq 0.05$). There was no effect ($P \geq 0.05$) of diet on feed sorting after parturition as well as on feeding behavior during the whole study. The data indicate that although glycerol in transition diets has no effect on overall DMI, there is increased preference for long particles that occurs during the prepartum interval.

Key Words: glycerol, sorting, transition cows

W404 Impact of climate on chemical composition and in vitro organic matter digestibility of semi-arid barley grain varieties determined by gas production technique. E. Abdi Ghezeljeh[1,2], M. Danesh Mesgaran*[1], H. Nasiri Moghaddam[1], H. Fazeli[3], and A. R. Vakili[1], [1]*Ferdowsi University of Mashhad*, *Iran*, [2]*East Azarbaijan Research Center for Agriculture and Natural resources*, *Tabriz, Iran*, [3]*Animal Science Research Institute*, *Karaj, Iran*.

The objective of this study was to investigate the effect of three semi-arid climates (cold, moderate and warm with the annual temperature range of –20 to 22, –2 to 24, and 2 to 35°C respectively) on crude protein (CP), starch (ST), soluble sugar (SC), bulk density, acid detergent fiber (ADF) and organic matter digestibility (OMD) of sixteen barley grain varieties obtained in year 2008 (10 samples per each variety). Samples were ground (1 mm) and the chemical compositions were determined as proposed by standard methods. Three ruminally fistulated sheep (49.5 ± 2.5 kg) were used as rumen liquor donor for gas production technique. The animals were fed 0.8 kg DM alfalfa hay and 0.5 kg DM concentrate (165 g CP/kg of DM). Rumen fluid was collected before the morning feeding and strained through 4 layers of cheesecloth into a CO_2-filled flask. In vitro incubation of the samples was done using a manual pressure transducer technique. Approximately 200 mg of each sample was weighed into 120 ml serum bottles (n= 4). The bottles were pre-warmed at 39°C before the injection of 30 ml rumen fluid-buffer mixture into each bottle followed by incubation in a water bath at 39°C. Gas produced were recorded at 72 h after the incubation. These data were used to estimate the organic matter digestibility of the samples. Starch content of cold region varieties was significantly ($P < 0.05$) higher (65.65%) than those of warm region (55.29). The samples obtained from the warm climate had the highest amount of crude protein (11.68%), while it was the lowest (10.57%) in the cold region samples. Soluble sugar contents of moderate climate varieties was more than the cold and warm climate samples and the differences were significant ($P < 0.001$). Varieties of the cold and warm climates had the highest (80.03%) and the lowest (78.03%) organic matter digestibility ($P < 0.05$), respectively.

Key Words: barley grain, climate, digestibility

W405 Effect of flax oil and flax hulls on mRNA abundance of antioxidant enzymes and lipogenic-related genes in the mammary gland of dairy cows. M. F. Palin*, H. V. Petit, D. Beaudry, C. Côrtes, N. Gagnon, P. Lacasse, and C. Benchaar, *Dairy and Swine Research and Development Centre, Agriculture and Agri-Food Canada*, *Sherbrooke, Quebec, Canada*.

Flax oil is a good source of n-3 fatty acids and flax hulls are rich in plant lignans which are strong antioxidants. Flax lignans induce the expression of peroxisome proliferator-activated receptor gamma (PPARG) in 3T3-L1 adipocytes and feeding rats with flax seed upregulates hepatic expression of antioxidant enzymes such as superoxide dismutase (SOD), catalase (CAT), and glutathione peroxidase (GPX). In this study, we determined the effect of dietary flax oil and/or flax hulls on mRNA levels of antioxidant enzymes (CAT, GPX1, GPX3, SOD1, SOD2 and SOD3) and lipogenic-related genes (acetyl-Coenzyme A carboxylase alpha (ACACA), fatty acid synthase (FASN), lipoprotein lipase (LPL), PPARG1, PPARG2, stearoyl-CoA desaturase (SCD) and sterol regulatory element binding transcription factor 1 (SREBP1c)) in the mammary gland of dairy cows. Eight Holstein cows were assigned to 4 dietary treatments in a double 4 × 4 Latin square design (21-d periods). Treatments were a control diet without flax products (CO), CO with 500 g/d flax oil infused in the abomasum (CO500), CO with 10% flax hulls in the DM (HU) and HU with 500 g/d flax oil infused in the abomasum (HU500). Biopsies of the mammary gland were taken on d 21 of each period. Relative quantitation of gene expression was performed using real-time PCR analyses and the comparative CT method. Addition of flax hulls increased mRNA abundance of ACACA, FASN, LPL, PPARG1, SCD and SREBP1c ($P < 0.05$) genes in the mammary gland and flax oil reduced mRNA abundance of the same genes ($P < 0.05$). The mRNA level of CAT, GPX1, GPX3, SOD1 and SOD3 decreased ($P < 0.05$) with flax oil addition. Flax hulls reduced ($P < 0.05$) mRNA abundance of GPX3, SOD2 and SOD3 genes. In conclusion, flax oil and flax hulls can modulate the expression of genes in the mammary gland of cows. However, contrasting effects were observed with flax oil reducing, while flax hulls increasing mRNA abundance of lipogenic-related genes

Key Words: flaxseed, gene expression, dairy cows

W406 An effective method for total RNA isolation from ruminal contents. P. Wang*[1,2], M. Qi[2], L. B. Selinger[1], T. A. McAllister[2], and R. J. Forster[2], [1]*University of Lethbridge*, *Lethbridge, AB, Canada*, [2]*Agriculture and Agri-Food Canada, Lethbridge Research Centre*, *Lethbridge, AB, Canada*.

Gene expression analyses including RT-PCR, microarrays and metatranscriptomics are techniques that could significantly expand our understanding of the rumen microbial ecosystem. The ability to isolate and stabilize representative RNA samples is critical to obtaining reliable results in all of these procedures. In this study, we established an improved RNA isolation method for extracting high quality total RNA from both liquid and solid phases of ruminal contents. This method is based on liquid nitrogen-mortar disruption and acid guanidinium-phenol-chloroform extraction combined with column purification. Yield of total RNA using this procedure was as high as 150 μg per gram of ruminal content. The typical large subunit/small subunit (LS/SS) rRNA ratio ranged from 1.8 to 2.0 with an RNA integrity number (Agilent) greater than 8.5. The rRNA profile associated with solid ruminal contents was more complex than that associated with the fluid, exhibiting broader rRNA peaks with discrete shoulders. This result is consistent with the isolation of both prokaryotic and eukaryotic rRNA from the particle-associated microbial consortia. The addition of RNAprotect reagent (Qiagen) to the samples resulted in partially degraded RNA, with LS/SS rRNA ratio lower than 1.0, and noticeable smearing of the RNA bands upon electrophoresis. We therefore recommend that this reagent not be used for the isolation of RNA from rumen samples. The integrity of total RNA isolated by our optimized procedure was tested by

reverse transcription PCR. We detected three *Fibrobacter succinogenes* S85 glycoside hydrolase transcripts: (*celF*, *cel3* and *xynD*) from RNA isolated from the solid phase of ruminal contents. Our research team is currently applying this new technique to obtain high quality ruminal RNA to characterize the rumen microbiome on a metatranscriptomics level, using next generation sequencing.

Key Words: total RNA, rumen, RNA quality

W407 Supplementation of embryo recipients heifers with rumen bypass fat. H. O. Patino*, J. C. C. Angel, M. M. H. Ramirez, R. M. Gregory, and D. d. Ré, *Universidade Federal de Rio Grande do Sul*, *Porto Alegre, RS, Brazil*.

Forty-four Angus × Hereford embryo recipients heifers (385 kg average body weight) were used in a completely randomized design to evaluate the effect of bypass fat supplementation on performance and plasma parameters. Embryo recipient heifers were kept in the same paddock of improved native pasture and individually feeding daily with isocaloric energy supplements. The treatments were: functional supplement, with inclusion of 150g of calcium soaps of fatty acids (CSFA)(Megalac-E); energy supplement, without inclusion of calcium soaps and without supplementation. Heifers estrus synchronization was performed using two PGF2α doses with an interval of 11 days. Seven days after estrus detection embryo transfer was performed. Blood samples were collected on the embryo transfer day and pregnancy confirmation day as well. The supplement type offered did not affect pregnant rate (34%) and plasma insulin concentration (14.1 μIU/mL; $P > 0.05$). Between the date of embryo transfer and the date of pregnancy confirmation heifers supplemented with CSFA had a 49% increase in ADG in relationship to heifers supplemented with energy supplement and without supplementation (0.90 vs. 0.64 vs. 0.57 kg/day; $P < 0.05$). On embryo transfer day and pregnancy confirmation day heifers supplemented with CSFA had a 17% and 33% increase in plasma cholesterol concentration in relationship to heifers supplemented with energy supplement and without supplementation (171 vs. 147 vs. 147 mg/dL; 198 vs. 154 vs. 143 mg/dL; $P < 0.05$). On embryo transfer day and pregnancy confirmation day heifers supplemented with CSFA had a 48% and 71% increase in plasma progesterone concentration in relationship to heifers supplemented with energy supplement and without supplementation (5.4 vs. 3.6 vs. 3.7 ng/dL; 7.3 vs. 5.8 vs. 4.3 ng/dL; $P < 0.05$). Daily weight gain, plasma cholesterol and progesterone concentration of embryo recipient heifers were increased by inclusion of calcium soaps of fatty acids into energy supplements.

Key Words: progesterone, cholesterol, pregnancy rate

W408 Effects of infusing different doses of free α-linolenic acid to the duodenum on the immune function of lactating dairy cows. P. Sun, J. Q. Wang*, G. Yang, and Khas-Erdene, *State Key Laboratory of Animal Nutrition*, *Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China*.

The purpose of this study was to determine the effects of infused a high C18:3 free fatty acid mixture to duodenum on the immune function of dairy cows. A crossover design was adopted and four primiparous Chinese Holstein cows (BW = 476 ± 6 kg, DIM = 100 ± 2 d) fitted with duodenal cannulas were divided into two treatments, in which homogenized aqueous mixtures of α-linolenic acid (LNA; 82.4% cis-9, cis-12, cis-15 18:3; 14.7% cis-9, cis-12 18:2; 2.8% cis-9 18:1) or control containing only the emulsifying ingredients were used. The control infusate contained 15 g/d of xanthan gum, 5 g/d sodium alginate, and 25 g/d of Tween 80 in 10 liters of water. Each period lasted 5 wk, during which two cows received 0, 100, 200, 300, and 400 g/d of LNA for 1 wk each, and the other two cows received only the carrier infusate. Blood was collected at the end day of each infusion amount and concentrations of serum IgA, IgG, IgM, prostaglandin E2 (PGE2) and Th1/Th2 cytokines were determined using bovine ELISA Kit. The results showed that increasing the supply of LNA to the small intestine increased serum IgG and Th1 cytokines including interferon-γ ($P < 0.05$), whereas the concentrations of PGE2 and Th2 cytokines, such as interleukin (IL)-4 decreased ($P < 0.05$) when infused no more than 300 g/d. However, the influence was affected by the higher dose of LNA at 400 g/d as the incidence of diarrhea occurred in some dairy cows. Throughout the whole experiment, no difference was observed in serum IgA and IgM. This study demonstrated that post-ruminal infusion of LNA affected the naïve T lymphocytes and modified the balance of Th1/Th2 type immune response, which suggest immunomodulatory properties of LNA.

Key Words: lactating dairy cow, α-linolenic acid, immune function

W409 Supplementation of methionine hydroxy analog, trace mineral chelates and dietary antioxidants in the diet of dairy cows for milk production, milk composition, and hoof status. G. Conti[1], G. Castillo*[3], M. Gallardo[2], S. Toffano[3], and M. Vazquez-Anon[3], [1]*University of Veterinary Medicine - Universidad del Litoral*, *Santa Fe, Argentina*, [2]*CICV National Institute for Agricultural and Livestock Technology (INTA)*, *Buenos Aires, Argentina*, [3]*Novus International*, *St. Louis, MO*.

In the Argentinean Central Dairy Region during Fall of 2009, 266 lactating dairy cows in a commercial herd were randomly assigned to a control or a treatment group. The treatment group consisted of a mixed supplementation of methionine hydroxy analog (12 g/head/day; MFP), mineral chelates (2 g/d of Mintrex-Zn (320 mg/d Zn), 2 g of Mintrex-Cu (300 mg/d of Cu), 2 g/d of Mintex- Mn (260 mg/d of Mn)) and dietary antioxidants (5 g/d/h Feedgard) in order to evaluate lactation performance and hoof health response. 266 primiparous and multiparous cows (132± 90 DIM and 2.94± 1.8 lactations) were on trial for a minimum of 90 and maximum of 180 d. Cows were fed twice a day after milking an isoenergetic (1.82 Mcal NEL) and isoproteic (17% CP) diet consisted of 30% corn silage, 30% alfalfa, 20% corn, and 20% soybean meal, and a mixture of vitamins and trace minerals. Minerals were formulated according to NRC 2001. The treatment cows produced 9% more milk (32.6 vs. 29.7 l/d $P < 0.05$), 4% FCM (30.5 vs. 27.8 kg/d; $P < 0.05$), milk fat (1.15 vs. 1.06 kg/d; $P < 0.05$) and protein yield (1.1 vs. 0.99 kg/d; $P < 0.05$) than control cows. There were no differences in milk composition or body condition between treatments. Treatment cows showed fewer hoof injuries ($P < 0.05$) due to lower incidence in heel (49%), white line (46%), and sole (59%) injuries and dermatitis (46%). The locomotion score showed fewer treatment cows with grades 2 to 4 (29.15% vs. 45.7% $P< 0.05$). From this study it can be concluded that the combination of methionine hydroxy analog, chelated trace minerals, and dietary antioxidant significantly improved milk yield and hoof health status

Key Words: methionine and mineral chelates, antioxidant, hoof health status

W410 Effects of *Bacillus subtilis* natto on the immune function of weaned calves. P. Sun, J. Q. Wang*, and H. T. Zhang, *State Key Laboratory of Animal Nutrition, Institute of Animal Science*, *Chinese Academy of Agricultural Sciences, Beijing, China*.

The effects of *Bacillus subtilis* natto on the immune function of weaned calves were investigated in this study. Twenty-four Holstein male calves

of 7 ± 1 d of age were randomly allotted to three treatments of eight calves. The calves were weaned when their starter intake reached 2% of their body weight. The *Bacillus subtilis* natto including Na type and N1 type was mixed with milk before weaning or mixed with the starter diets directly to the calves after weaning in the two experimental treatments and no *Bacillus subtilis* natto was fed to the control group. The experiment ended on the seventh week after weaning, when blood was collected and IgA, IgE, IgG, IgM and cytokine levels including interleukin (IL)-4, IL-10 and interferon-γ (IFN-γ) were determined in the serum of all the calves. Data were analyzed using the ANOVA procedure of SAS. No difference was observed in serum IgE concentration in the two *Bacillus subtilis* natto supplemented treatments (52.87 and 53.30 mg/L for Na and N1 group) compared to the control (56.37 mg/L). IgA and IgM in the serum of the calves were not different, whereas serum IgG was greater ($P < 0.05$) in the *Bacillus subtilis* natto supplemented calves than in the control calves. Furthermore, calves fed with Na type of *Bacillus subtilis* natto were found to secrete more IFN-γ ($P < 0.05$) but tended to produce less IL-4 ($P < 0.1$) in the serum than the control calves, although serum IL-10 was not affected. This study demonstrated that *Bacillus subtilis* natto did not stimulate IgE-mediated allergic reactions, but induced nonspecific immune responses associated with increased serum IgG and IFN-γ levels in the probiotic-fed calves, which suggests that the probiotic characteristics of *Bacillus subtilis* natto (especially for Na type) benefit the immune function.

Research was supported by Youth Foundation from Institute of Animal Science (2009qn-8).

Key Words: *Bacillus subtilis* natto, immune function, calf

W411 Nutrient balances in California dairy farms. 1. Effects of salt content in drinking water and milk yield per cow on nutrient utilization efficiency. A. R. Castillo*[1], N. Silva del Rio[2], and N. St-Pierre[3], [1]*University of California Cooperative Extension*, *Merced,* [2]*University of California Cooperative Extension*, *Tulare,* [3]*The Ohio State University, Department of Animal Sciences*, *Columbus*.

The aim of this survey was to study nutrient utilization efficiency and feed conversion in lactating cows on commercial farms. Forty dairies in Merced, California (mean 787±592 lactating cows/farm) were selected to study the effect of total salt in drinking water (TS) and average milk yield (MY, as 3.5% fat-corrected milk yield/cow) in each dairy farm on TMR nutrient content, feed management, feed conversion (FC=MY/DMI) and nitrogen utilization efficiency (NUE=N milk/N intake). Data was analyzed as 2 x 2 factorial with high TS (HTS) and low TS (LTS), and high MY (HMY) and low MY (LMY) as the main factors. The four treatments were: HTS-HMY, HTS-LMY, LTS-HMY, and LTS-LMY. Levels of TS were, 809 and 307 mg/L for HTS and LTS, respectively. Levels of MY were 35.9 and 27.6 kg/cow per day per dairy farm for HMY and LMY, respectively. The mean TMR nutrient content were: ADF (23.6%), lignin (4.3%), nitrogen (2.8%), fat (4.5%), and ash (8.3%) and not affected by water TS or MY. Differences were observed with TMR NDF content (34% and 36%) and non-fiber carbohydrates (NFC, 36% and 33%) for HMY and LMY, but not affected by water TS. The TMR DCAD content was affected by water TS (HTS=23 and LTS=29mEq/100 g DM). But, the other variables were different only for H and L milk yield, as follow: FC (HMY=1.5, LMY=1.25), ENU (HMY=0.26, LMY=0.22), cow number/dairy (HMY=1061, LMY=513), TMR/dairy for lactating cows (HMY=3.7, LMY=2.2).

Key Words: dairy farms, feed conversion, nitrogen utilization efficiency

W412 Evaluation of estimated diet energy intake and impact on energy use of the lactating dairy cow. K. J. Clark*[1], P. J. Kononoff[1], and L. O. Tedeschi[2], [1]*University of Nebraska-Lincoln*, *Lincoln,* [2]*Texas A&M University*, *College Station*.

A meta-analytical procedure was used to evaluate the impact of observed intakes of diet net energy for lactation (NE_L) on use of energy by lactating dairy cows. Data from nine nutrition experiments, which included 29 dietary treatments and 778 observations collected at the University of Nebraska-Lincoln Dairy Research Unit, were used. All studies were cross-over designs in which cows were fed diets for either 21 or 28 d periods. Data were analyzed using SAS and a random coefficient model to account for the random effects of different experiments. For each experiment, TMR and fecal samples were collected, dried, ground, and analyzed for DM, CP, ash, NDF, NFC, ether extract (EE) and ADF. Diet concentration of total digestible nutrients (TDN) and NE_L were computed using NRC (2001) equations. Total NE_L use was estimated based on maintenance and lactation requirements plus energy needed to meet observed BW changes. Apparent digestibility of nutrients was estimated based on the concentration of indigestible ADF in the TMR and feces. Apparent digestibility (mean ± SD) was 61.5 ± 8.3, 64.0 ± 9.1, 42.4 ± 13.6, 88.5 ± 7.5, and 82.6 ± 10% for DM, CP, NDF, NFC, and EE, respectively. Mean DMI and 3.5% FCM averaged 23.9 ± 4.7 and 35.4 ± 12.4 kg/d, respectively. The TDN and concentration of NE_L in each diet were estimated to be 65.9 ± 17.4% and 1.58 ± 0.55 Mcal/kg, respectively. Results suggested NE_L intake was a weak predictor of NE_L use ($R^2 = 0.01$). The resulting regression equation was y = 32.0 +0.12 x; where y = NE_L use (Mcal/d) and x = measured NE_L intake (Mcal/d). Although also poor, DMI served as a better predictor of NE_L use ($R^2 = 0.16$). The resulting regression equation was y = 12.9 +0.98 x; where y = NE_L use (Mcal/d) and x = measured DMI (kg/d). These results suggested the measured NE_L intake of the ration is not a good predictor of NE_L utilization in the animal.

Key Words: energy, lactation, digestibility

W413 Regulation of hepatic gluconeogenic enzymes by dietary glycerol in transition dairy cows. H. M. White*, E. R. Carvalho, and S. S. Donkin, *Purdue University*, *West Lafayette, IN*.

Nutritional status is a known regulator of gluconeogenic gene expression. Glycerol can replace corn in diets fed to dairy cow and is linked to increased rumen propionate production. The effect of dietary glycerol on the regulation of gluconeogenic enzymes is unknown. The objective of this study was to examine the effect of glycerol on expression of pyruvate carboxylase (PC), cytosolic phosphoenolpyruvate carboxykinase (PEPCK-C), mitochrondrial phosphoenolpyruvate carboxykinase (PEPCK-M), and glucose-6-phosphatase. Twenty-six multiparous Holstein cows were fed either a control diet or a diet where corn grain was replaced by glycerol from −28 through +56 days relative to calving (DRTC). Liver tissue was collected via percutaneous liver biopsy at −28, −14, +1, +14, +28, and +56 DRTC for RNA analysis. Expression of PC mRNA was increased ($P < 0.05$) by 6-fold at +1 and by 4-fold at +14 DRTC relative to precalving levels. Dietary glycerol did not alter ($P \geq 0.05$) expression of PC mRNA expression. Expression of PEPCK-C was increased ($P < 0.05$) by 2.5-fold at +14 and 3-fold at +28 DRTC compared to +1 DRTC. Overall, dietary glycerol increased ($P < 0.05$) PEPCK-C expression compared to cows fed control diets (2.94 vs. 1.61 ± 0.8 arbitrary units, main effect of glycerol vs. control, respectively). The ratio of PC to PEPCK-C was increased ($P < 0.05$) by 3-fold at +1 DRTC in all cows. There was no effect ($P \geq 0.05$) of diet or DRTC on PEPCK-M or glucose-6-phosphatase mRNA. There were no interactions of dietary treatment and DRTC for any transcript measured. Substituting

corn with glycerol increased the expression of PEPCK-C mRNA during transition to lactation and suggests that dietary energy source alters hepatic expression. The observed increase in PEPCK-C expression with glycerol feeding may indicate regulation of hepatic gene expression by changes in rumen propionate production.

Key Words: glycerol, gluconeogenesis, transition cow

W414 Effects of dietary betaine on milk yield and milk composition of mid-lactating dairy cows. S. E. Peterson*[1], J. K. Kinch[1], J. E. Williams[1], M. A. McGuire[1], M. Chahine[2], and P. Rezamand[1], [1]*Univeristy of Idaho*, *Moscow,*[2]*University of Idaho*, *Twin Falls*.

Betaine, naturally found in plants and an oxidative product of choline, is converted to acetate in the rumen, and transferred to the mammary gland where it may be used for milk fat synthesis. The objective of this study was to determine the effect of supplemental dietary betaine on bovine milk yield and milk composition. Eighteen Holstein dairy cows (126 ± 5 DIM) were randomly assigned to a sequence of treatments in a 4x4 Latin square design with four treatments of betaine at 0, 25, 50, and 100 g/d, added to a standard lactation ration. Animals were fed individually using Calan gates, and feed intake and milk yield recorded daily. Each period lasted 16 d with milk sampled on the last day of each period. Milk composition was determined by a standard DHIA laboratory and milk fatty acids were determined by gas chromatography. Data were analyzed using the MIXED procedure in SAS and significance was determined at $P < 0.05$. Dry matter intake was altered (quadratic effect $P = 0.024$) by dietary betaine (18.8, 18.6, 18.4, 19.4 ± 0.98 kg/d for 0, 25, 50, and 100 g betaine/d, respectively). Further, milk yield was increased (quadratic effect $P < 0.001$) by supplemental betaine (22.6, 22.9, 22.4, 24.0 ± 0.89 kg/d for 0, 25, 50, and 100 g betaine /d, respectively). However, no significant effect of dietary betaine was detected on body weight or condition score ($P > 0.08$ for both). Percentages of milk fat, lactose, SNF, and SCC were not altered ($P > 0.29$ for all) whereas milk true protein content was decreased (quadratic effect $P = 0.025$) by betaine supplementation (3.35, 3.27, 3.27, and 3.28 ± 0.07% for 0, 25, 50, and 100 g betaine/d, respectively). Daily yields of milk protein, fat, or lactose did not differ with betaine supplementation ($P > 0.13$ for all). Further, no significant effect of dietary betaine was detected on milk fatty acid composition. Overall, inclusion of dietary betaine at 100 g/d increased dry matter intake and milk yield but decreased milk protein percent (at all levels of inclusion), whereas milk fatty acid profile remained unaltered. Further studies are needed to determine the optimum rate of supplemental betaine for dairy cows.

Key Words: betaine, milk yield, milk composition

W415 The effect of forage level and lipid supplement on selected strains of rumen bacteria in continuous culture fermenters. P. Gudla*[1], A. Ishlak[1], A. A. AbuGhazaleh[1], D. Hastings[1], K. Jones[1], E. Gastal[1], J. Trushenski[1], and S. Ibrahim[2], [1]*Southern Illinois University*, *Carbondale,* [2]*North Carolina A&T University*, *Greensboro*.

Previous studies have shown that trans fatty acids production in the rumen are influenced by lipid supplements and forage levels. The objective of this study was to evaluate the effects of forage level and lipid supplement on selected strains of rumen bacteria believed to be involved in biohydrogenation. A single-flow continuous culture system consisting of four fermenters was used in a 4 × 4 Latin square design with a factorial arrangement of treatments, with four 10 d consecutive periods. Treatment diets were: 1) high forage diet (70:30 forage to concentrate; HF), 2) high forage plus lipid supplement (HFL), 3) low forage diet (30:70 forage to concentrate; LF), and 4) low forage plus lipid supplement (LFL). The lipid supplement was a blend of fish oil and soybean oil added at 1 and 2 g/100g DM, respectively. The forage source was alfalfa pellets. During 10-d incubations, fermenters were fed treatment diets three times daily (45g/d, divided equally between three feedings) as TMR diet. Samples collected at 3 h post morning feeding on d 10 were used for quantitative PCR analysis. Data were analyzed with the PROC MIXED procedure of SAS. The DNA concentrations of *Anaerovibrio lipolytica* and *Butyrivibrio fibrisolvens* vaccenic acid subgroup (Butyrivibrio VA) were affected ($P < 0.05$) by forage level but not lipid supplement. The DNA concentrations of *Anaerovibrio lipolytica* (1.668, 2.597, 0.045 and 0.093 pg/40 ng of total DNA for treatments 1 to 4, respectively) and Butyrivibrio VA (0.324, 0.296, 0.011 and 0.014 pg/10 ng of total DNA) were significantly lower with the low forage diets. The DNA concentrations of *Butyrivibrio fibrisolvens* stearic acid producer subgroup (Butyrivibrio SA) were not affected ($P > 0.05$) by forage level or lipid supplement (149.4, 136.3, 123.2 and 158.3 pg/10 ng of total DNA). In conclusion, lipid supplement had no effects on the tested rumen bacteria and forage level affected both Butyrivibrio VA and *Anaerovibrio lipolytica*.

Key Words: forage level, lipid supplement, bacteria

W416 Changes in the parameter estimates for the linear relationships of milk and milk component yields with dry matter intake of dairy cows during the last decade. J. S. Lee*[1], S. Y. Lee[1,2], K. S. Ki[3], H. S. Kim[3], and S. Seo[1], [1]*Department of Animal Biosystem Sciences, Chungnam National University*, *Daejeon, South Korea*, [2]*Institute of Agricultural Science, Chungnam National University*, *Daejeon, South Korea*, [3]*Dairy Science Division, National Institute of Animal Science, RDA*, *Cheonan, South Korea*.

The parameter estimates from a meta-analysis is heavily dependent on the database used. Due to genetic improvement and changes in management of dairy cows, the parameter estimates of variables may vary with different time frames. The objective of this study is thus to compare the parameter estimates for linear relationships of milk and milk component yields with DMI obtained using data from two different time frames. For the parameter estimates of dairy cows before the year of 2000, previous published equations by others were used. For the data after the year 2007, we developed a database containing experimental observations for DMI and milk yield of dairy cows from the research articles published in the *Journal of Dairy Science (JDS)* from Dec. 2007 until Feb. 2010 (volumes 90 through 93). The database is composed of a total of 427 treatment means from 114 studies. The mean (±SD) DMI, BW, milk yield, milk fat yield (MFY), and milk protein yield (MPY) were 22.36 (±3.54), 637.76 (±52.49), 34.51 (±6.88), 1.22 (±0.26) and 1.07 (±0.21) kg, respectively. Using a simple linear regression, MY = 5.875 (±1.601) + 1.281 (±0.071) DMI ($R^2 = 0.436$) was obtained. Compared to a previous published equation based on the data published in *JDS* (from volumes 1 through 82), no significant difference was observed for the slope (1.281 vs. 1.378), but the intercept was significantly different (5.875 vs. −1.022; $P < 0.05$). Linear relationships of milk and milk component yields with DMI were also estimated using a random coefficient model with study as a random effect: MY = 12.678 (±2.382) + 0.998 (±0.106) DMI, MFY = 0.348 (±0.112) + 0.039 (±0.005) DMI, and MPY = 0.387 (±0.084) + 0.031 (±0.004) DMI. Compared to the previous parameter estimates using a similar approach with data published in *JDS* (volumes 73 through 83), no significant differences in the estimates of slope and intercept were observed. The results from this study suggest that average milk yield from dairy cows has been significantly increased during the last decade even though response of milk production to an increase in DMI has not been improved.

Key Words: milk yield, dry matter intake, dairy cows

W417 Effects of chemical treatment of whole barley grain with sodium hydroxide on nutrient intake and digestibility in midlactation of Holstein dairy cows. M. Khorashadizadeh*, A. A. Naserian, and R. Valizadeh, *Ferdowsi University of Mashhad, Excellence Center for Animal Science, Faculty of Agriculture, Mashhad, Khorasan Razavi, Iran*.

Nine multiparous midlactation Holstein cows (131.44±9.32 DIM, 30.2±5.14 kg daily milk yield) were fed a total mixed ration supplemented with ground barley grain (control), or whole barley grain treated with sodium hydroxide (10%) and dried in different periods including: dried immediately (0h) or after 48h storage in plastic bags (48h). Sodium hydroxide was used at the level of 3.5% (DM). Each period lasted 3 week; experimental analyses were restricted to the last week of each period. Diets were formulated according to NRC 2001. Cows were housed in tie stalls and fed the TMR two times a day to allow 5 to 10% orts (as-fed basis), and dry matter intake (DMI) was recorded at the last week of each period. Data were analyzed as a 3 × 3 Latin square using the GLM procedure of SAS (2001). The model included effects of diet, period and cow. Least squares means are reported throughout and significance was declared at $P < 0.05$. Diets had no effects on DMI (21.49, 22.35 and 20.19 ± 0.67 kg/d for control, 0h and 48h respectively), CP intake (3.4, 3.55 and 3.41± 0.16 kg/d for control, 0h and 48h respectively), NDF intake (7.69, 8.25 and 7.32 kg/d for control, 0h and 48h respectively) but OM intake (20.52, 19.78 and 18.45 ±0.56 kg/d for control, 0h and 48h respectively) and ADF intake (5.24, 5.65 and 4.63 kg/d for control, 0h and 48h respectively) decreased in 48h diet. The digestibility of DM (67.66, 69.22 and 67.77±1.7% for control, 0h and 48h respectively), OM (68.66, 70.22 and 69.22±1.6% for control, 0h and 48h respectively), NDF (59.44, 60.66 and 58.33 ±2.4% for control, 0h and 48h respectively) and CP (68.44, 70.11 and 69.89±1.9% for control, 0h and 48h respectively) were similar between diets, but ADF digestibility (57, 64.77 and 51.44±3.5% for control, 0h and 48h respectively) decreased in 48h diet in comparison with 0h diet; however 0h diet had more NDF digestibility than control diet. The results of the current experiment reveals that chemical treatment of whole barley grain with sodium hydroxide for 48h had negative effects on ADF intake and digestibility

Key Words: sodium hydroxide, whole barley grain, dairy cows

W418 Effect of glucogenic and ketogenic feeding strategies on metabolic status in postpartum transition cows. M. Larsen* and N. B. Kristensen, *Faculty of Agricultural Sciences, Aarhus University*, *Tjele, Denmark*.

We have previously found that abomasal glucose infusion in postpartum transition cows prevented the characteristic fall in glucose and insulin concentrations. Nine Holstein second lactation cows implanted with permanent indwelling catheters in the major splanchnic blood vessels were used to study the effect of glucogenic and ketogenic feeding strategies on metabolic status in postpartum transition cows. At calving, cows were assigned to 1 of 3 feeding strategies: a glucogenic strategy (GLUCO; 56.5% NaOH treated wheat, 25.8% grass-clover silage and 17.7% concentrate mix), a ketogenic strategy (KETO; 40.5% fodder beets, 25.8% grass-clover silage, 15% NaOH treated wheat and 18.7% concentrate mix) or a keto-glucogenic strategy (MIXED) with 100% alfalfa haylage at the calving day followed by a 6 day gradual shift to the glucogenic diet. Eight hourly sets of arterial, portal vein, and hepatic vein samples were collected starting 30 min before morning feeding at 12 ± 4 days before calving as well as 4, 15, 29 days in milk (DIM). The statistical model included treatment, DIM and treatment × DIM, where DIM within cow was considered as a repeated measure. All treatments were associated with decreasing ($P < 0.01$) arterial concentrations of glucose and insulin from prepartum to 4 DIM, whereas the β-OH-butyrate concentration did not change ($P = 0.12$). The arterial insulin concentration decreased more ($P = 0.04$) from prepartum to 4 DIM with MIXED as compared to KETO. Concomitantly, the arterial glycerol concentration increased more ($P \leq 0.05$) from prepartum to 4 DIM with MIXED as compared to the other treatments. The portal-arterial (P-A) glucose concentration difference increased ($P < 0.01$) from negative prepartum to positive at 4 DIM with all treatments; however, the positive P-A concentrations difference with KETO at 4 DIM tended ($P \leq 0.10$) to be lower than with the other treatments. In conclusion, the tested feeding strategies induced relatively modest changes in metabolic status in the very early postpartum phase. Thus, the potential for effectively manipulating the metabolic status using farm applicable feeding strategies seems limited.

Key Words: transition, glucose, metabolism

W419 Ruminal degradation dynamics of barley protein meal, corn distiller grains and soybean meal. S. Arriola*, C. Blatcher, M. McGilliard, and M. D. Hanigan, *Virginia Polytechnic Institute and State University*, *Blacksburg*.

The aim of this study was to determine the ruminal degradation dynamics of barley protein meal (BPM), corn distiller grains (CDG) and soybean meal (SBM). Three ruminally cannulated lactating cows were housed in individual stalls and fed a diet formulated to meet NRC nutrient requirements during a 15 d adaptation period. Five grams of BPM, CDG or SBM were ground through a 2 mm screen, sealed in Dacron bags, dried overnight at 60° C, and weighed. Forty-eight, 24, 16, 8, 4, 2, and 0 h before simultaneous removal, two bags with each feedstuff were placed in the rumen of each of the cows. After removal from the rumen, bags were washed, dried, and analyzed for dry matter (DM), N, and amino acid (AA) content. Ruminal degradation parameters for DM, crude protein (CP) and AA were estimated using the NLIN procedure of SAS. Resulting parameter estimates were analyzed using the MIXED procedure. BPM had the greatest soluble DM and CP fractions (64.8% DM and 76.8% CP), CDG was intermediate (45.1% DM and 40.1% CP), and SBM the lowest (31.8% DM and 13.9% CP). Degradation rates of DM were the greatest for SBM intermediate for BPM and the slowest for CDG. The CP degradation rates were similar between SBM and BPM, but lower for CDG. Finally, rumen undegraded DM was the lowest for BPM (23.9%). Ruminally undegraded DM was lower for SBM (27.4%) than CDG (40.4%). The same pattern was observed for the CP fraction, with BPM having the lowest undegraded CP (11.8%), SBM intermediate values (34.4%) and CDG the greatest (39.3%). In accord with DM and CP, the predicted essential AA percent remaining in the undegraded fraction was the lowest for BPM, as compared to SBM and CDG. These results show that BPM was not as good of a ruminal bypass protein source as SBM and CDG. The high solubility of the BPM was likely due to addition of the solubles to the product and drying conditions used in the pilot plant. The final commercial product may have different characteristics.

Key Words: barley meal, rumen degradation, protein

W420 Effects of storage temperature and pre-mixing on yeast cell viability. M. L. Sullivan*[1], W. K. Sanchez[2], I. Yoon[2], and B. J. Bradford[1], [1]*Kansas State University*, *Manhattan,* [2]*Diamond V Mills, Inc*, *Cedar Rapids, IA*.

Active dry yeast (ADY) products are commonly fed in the dairy industry, but little research has been done regarding quality control for such products. The objectives of this study were to measure the effects of

short-term high temperature storage on ADY viability and determine the impact on viability when storing yeast mixed with a vitamin/trace mineral pre-mix (VTM). Commercially available ADY products (n=5) were acquired through normal distribution channels, stored at 4°C upon receipt, and shipped to Medallion Labs for analysis of yeast colony forming units (CFU). ADY were mixed in duplicate with ground corn or VTM to achieve a targeted concentration of 2.2×10^8 CFU/g. One product was omitted due to its low CFU concentration. For each product, samples mixed in corn and VTM were stored at ambient temperature (22°C) while replicates were stored in an incubator at 40°C for 2 wk. Of the 5 products sampled, 2 arrived with CFU concentrations below the product guarantees. Products were mixed based on actual CFU concentration, and mixed samples met the targeted CFU concentration. There were no differences in CFU concentrations between corn and VTM samples immediately after mixing or after storage at ambient temperature. However, high-temperature storage significantly decreased CFU concentration ($P < 0.001$). There was also an interaction ($P = 0.02$) of pre-mix substrate and storage temperature, with VTM maintaining higher CFU concentrations than corn when subjected to high-temperature storage (7.4 vs. 7.1 $\log_{10}$ CFU/g). This could be the result of minerals, such as zinc, that sustained cell wall viability, antioxidant vitamins present in the VTM, or the difference in water activity of the substrates (Corn = 0.51; VTM = 0.45). Results indicated that yeast viability in ADY products was greatly diminished when stored at 40°C for 2 wk, but the reduction was less severe when mixed with a VTM premix.

Key Words: trace mineral, viability, yeast

W421 Replacement of high moisture corn or soy hulls by soy molasses in dairy cow diets. L. L. Bitencourt[1], N. M. Lopes[1], V. A. Silveira[1], G. Pessoa Júnior[1], O. F. Zacaroni[1], G. S. Dias Júnior[1], C. O. Faria[4], J. R. M. Silva[3], R. A. N. Pereira[2], and M. N. Pereira*[1], [1]*Universidade Federal de Lavras*, *Lavras, Brazil*, [2]*Empresa de Pesquisa Agropecuária de Minas Gerais*, *Lavras, Brazil*, [3]*Instituto Federal de Educação Ciência e Tecnologia do Norte de Minas Gerais*, *Januária, Brazil*, [4]*Better Nature Research*, *Ijaci, Brazil*.

Soy molasses (SM) is the by-product of protein isolation from defatted soy flakes. Two experiments evaluated strategies of feeding SM to dairy cows. The composition of SM (Sementes Selecta SA, Goiânia, Brazil) was (% of DM): 7.9 CP, 0 NDF, 4.1 EE and 10.8 ash. The DM content was 69.5% of as fed. Trial 1 evaluated SM as a replacement for high moisture corn (HMC). Treatments were (% of diet DM): Control with 21.5 HMC, SM1 with 17.2 HMC and 4.5 SM, and SM2 with 12.8 HMC and 9.1 SM. Diets also contained 41.8% corn silage, 5.4% tifton, 19.9% soybean meal, 8.3% whole cottonseed, 16.6% CP, 31.5% NDF, and 6.1% EE. Twenty-four Holsteins were paired blocked based on parity and yield and assigned to a treatment for 28 days, following a standardization period. Data obtained at the end of the standardization was used as covariate in the statistical model. Response variables were measured on the fourth week. Daily milk protein yield was 0.903 kg for Control, 0.871 kg for SM1, and 0.772 kg for SM2 ($P = 0.01$ linear), and milk yield was 30.2, 27.7 and 26.9 kg, respectively ($P = 0.04$ linear). There were no detectable treatment effects upon fat yield ($P = 0.80$), DMI ($P = 0.96$), MUN ($P = 0.97$), plasma glucose ($P = 0.72$), daily excretion of allantoin in urine ($P = 0.55$), and total tract digestibility ($P > 0.54$). Trial 2 evaluated the replacement of soy hulls (SH) by SM. This trial also used 24 cows, in a covariate adjusted randomized block design, with response evaluated on the fourth week after a standardization period. The Control treatment had 11.6% of SH on diet DM. The SM treatment contained 8.4% of SH and 3.3% of SM. Diets also contained 42.2% corn silage, 4.1% tifton, 20.6% soybean meal, 6.9% whole cottonseed, and 11.7% HMC. Milk yield was 27.6 kg for Control and 27.8 kg for the SM treatment ($P = 0.91$). There were no detectable treatment effects on DMI, milk solids content, solids production, MUN, feed efficiency, and milk energy secretion ($P > 0.28$). Replacing HMC with SM did not improve cow performance and replacing SH with SM, in a constant corn starch diet, had no effect on cow performance.

Key Words: soy molasses, sugars, byproducts

W422 Abomasal oligofructose infusion induced hindgut acidosis in Holstein steers. S. R. Mainardi*, B. A. Hengst, S. J. Nebzydoski, L. M. Nemec, and T. F. Gressley, *University of Delaware*, *Newark*.

Excessive microbial fermentation of carbohydrates in the large intestine of dairy cattle can result in post-ruminal acidosis which can negatively impact animal health and performance. This study evaluated whether abomasal infusion of a fermentable carbohydrate could be used to induce hindgut acidosis. Six ruminally cannulated Holstein steers were used in a crossover design study with 14-d treatment periods. Steers were fed a lactating cow ration ad libitum. On d 13 steers were treated with 0 (Control) or 1 (Oligo) g/kg BW oligofructose (Beneo P95, Orafti Active Food Ingredients, Tienen, Belgium) pulse-dosed into the abomasum in 1 L water. Fecal samples, blood samples, rectal temperature, heart rate, and respiratory rate were taken at 0, 3, 6, 9, 12, 24, and 48 h relative to the abomasal infusion. Fecal samples were used to determine dry matter (DM) percentage, pH, consistency score (1=liquid to 5=coarse), and volatile fatty acid (VFA) concentrations. Plasma or serum concentrations of metabolites (β-hydroxybutyric acid, blood urea nitrogen, and non-esterified fatty acids) and inflammatory markers (copper, serum amyloid A, and haptoglobin) were determined. There was no effect of treatment on DM intake, rectal temperature, heart rate, respiratory rate, or blood measures ($P > 0.10$). Fecal pH tended to be lower for Oligo than Control steers (6.76 vs. 7.02, $P = 0.06$). Treatment by time interactions were found for fecal score, DM, lactate and acetate ($P < 0.05$), and tended to occur for fecal propionate and butyrate ($P < 0.10$). Fecal score was lower for Oligo than Control steers at 6 and 9 h ($P < 0.01$). Compared to Control steers, fecal DM was reduced in Oligo steers at 6 h but was increased at 9 and 12 h ($P < 0.05$). The greatest difference for all VFAs occurred at 12 h, when concentrations of lactate, acetate, propionate, and butyrate were 0.5, 47, 11, and 4.0 m*M* in Control steers and 5.2, 76, 15, and 6.8 m*M* in Oligo steers, respectively. In conclusion, abomasal infusion of 1 g/kg BW oligofructose induced excessive microbial fermentation in the hindgut of steers without causing an acute inflammatory response.

Key Words: acidosis, hindgut, oligofructose

W423 Effect of processing of corn grain on mean particle size, particle distribution and ruminal starch degradability. S. Emanuele*[1], L. Carver[1], L. Davis[1], D. Lundquist[1], and J. Firkins[2], [1]*Quality Liquid Feed*, *Dodgeville, WI,* [2]*Ohio State University*, *Columbus*.

The objective of this trial was to determine the variability in rumen degradable starch (RDS) among corn samples and develop a regression equation to predict ruminal starch degradability. Eighty-seven corn samples were collected from 60 dairy operations in 11 states. Corn samples consisted of dry, high moisture and steam-flaked corn. Dry corn samples consisted of whole, rolled, crimped or ground samples and high moisture corn consisted of whole, rolled or ground samples. Steam-flaked corn was either rolled or flaked. Samples were collected from October 2008 to February 2009. Samples were analyzed, as-received, by Dairyland Labs, Arcadia, WI for in vitro ruminal and total tract dry matter and starch disappearance. Ruminal dry matter and starch

degradability was measured by a 12-h fermentation in rumen fluid. Total tract dry matter and starch degradability was measured by an 8 h digestion in acid pepsin and lipase enzymes which followed the 12-h ruminal fermentation. The median for RDS was 67.2% with a range of 25.4% to 91.6%. The median for total tract starch degradability was 74.4% with a range of 50.8% to 91.4%. The 12-h RDS was influenced by processing method ($P < 0.07$), being greatest for steam-flaked corn (71.2%) and ground dry corn (66.5%). RDS was influenced by particle size within processing method ($P < 0.05$). RDS varied from 53% to 67% for high moisture corn. The distribution of particle sizes also influenced starch degradability. Samples with a greater percentage of very fine particles tended to have greater starch degradability. RDS for dry corn varied from 50% to 73%. A 12-h ruminal starch degradability for fine ground dry corn can be estimated from mean particle size by the regression equation: Y = (76.1) + MPS X (−0.0073). Based on this data set, ruminal starch degradability is highly variable and influenced by processing method and particle size within processing method. This may lead to an over-estimation of rumen degradable starch (RDS) in the diet if processing method and particle size are not used in equations to predict ruminal starch degradability of corn samples.

Table 1. Effect of corn source and particle size on starch degradability

Item	Dry Corn	Dry Corn	Dry Corn	HM Corn	HM Corn	HM Corn	SF-Corn	SF-Corn	P-value
Processing Method	Crimped	Rolled	Ground	Whole	Rolled	Ground	Flaked	Rolled	
Particle Size	Coarse	Medium	Fine	Coarse	Medium	Fine	Medium	Medium	
12-hr Starch Degradability	48.5b	56.8ab	66.5ab	60.1ab	58.1ab	62.1ab	63.5ab	71.2a	0.05
SE	10.7	5.4	4.0	5.4	2.4	2.8	3.1	5.4	

LS means with common letter are not different.

Key Words: starch degradability, corn particle size

W424 Comparison of the effects of several nutrients on dairy cow milk fat content. G. Maxin*[1], F. Glasser[2], and H. Rulquin[1], [1]*INRA-Agrocampus ouest*, *Rennes, France*, [2]*INRA*, *Theix, Saint-Genes-Champanelle, France*.

Dietary changes can alter dairy cow milk fat production through modifications in the supply of nutrients. Indeed, several nutrients act as precursors or inhibitors of mammary fat synthesis, and they vary simultaneously following dietary changes. This meta-analysis aims to compare the effects of these nutrients on milk fat content (MFC). The effects of six nutrients were compared: acetate (C2), propionate (C3), butyrate (C4), glucose, trans10,cis12-CLA (CLA) and long-chain fatty acids (LCFA). A database was compiled from the studies involving digestive infusions (or rumen-protected forms) of these nutrients in dairy cows. It contained 142 comparisons between a nutrient infusion and a control. Response models of MFC (in g/100g milk) to the supply of each nutrient (in kg/d) were established. The nutrients differed in their effects on MFC: C2, C4 and LCFA increased MFC whereas C3, glucose and CLA decreased it. To compare the effects of these nutrients on MFC, we had to adjust the response models to in vivo variations in the nutrient supplies, observed following dietary changes. From published data, we estimated the maximal variations in the supply of these nutrients following dietary changes: 1.0 kg/d for C2, 1.0 kg/d for C3, 0.5 kg/d for C4, 1.5 kg/d for glucose, 1.5 g/d for CLA and 1.3 kg/d for LCFA. By applying the response models to these values, we estimated the maximal in vivo responses of MFC (g/100g milk) to the nutrients: +0.25 for C2, −0.48 for C3, +0.40 for C4, −0.43 for glucose, −0.36 for CLA, and +0.56 for LCFA. The individual responses of the nutrients were moderate and had the same magnitude. These results suggest that several of these nutrients could contribute to the changes in MFC observed following dietary changes.

Key Words: milk fat content, dairy cows, nutrients

W425 Phosphorus feeding for primiparous cows. V. R. Moreira*[1], L. K. Zeringue[1], C. Leonardi[2], and M. E. McCormick[1], [1]*Louisiana State University Agricultural Center*, *Franklinton,* [2]*Louisiana State University*, *Baton Rouge*.

The objective of this study was to evaluate production performance of two groups of 20 primiparous cows fed diets containing either 0.35% or 0.39% ± 0.01% P (DM basis) from 3 to 45 DIM (treatment period). Both groups of cows were fed 0.39% ± 0.01% P thereafter until 110 DIM (carry-over period). Both treatment diets contained 17.7% ± 0.35% CP, 26.8% ± 0.92% NDF, 16.6% ± 0.46% ADF, and 0.76% ± 0.05% Ca as analyzed (average ± standard deviation), and 1.61 Mcal/kg DM as estimated by the NRC (2001) model. Pregnant heifers were brought to the barn at least 20 days before expected calving. Cows were housed in a free-stall barn fit with electronic gates. Close-up TMR containing 0.33% ± 0.03% Ca and 0.28% ± 0.004% P (DM basis) was fed until two days after calving date. Treatments were randomly assigned to cows before the beginning of the experiment. Intake and milk yield were recorded daily. Weekly averages during treatment period (week 3 to 6) and carry-over period (week 7 to 15) were analyzed as repeated measurements using the Mixed procedure (SAS, version 9.2). Dry matter intake was 17.7 and 18.9 kg/cow/d (SEM = 0.45 kg/cow/d) for cows fed 0.35% P and 0.39% P respectively during the treatment period ($P = 0.08$). This difference increased slightly (21.6 vs. 22.9 kg/cow/d, SEM = 0.48 kg/cow/d) during carry-over period ($P = 0.06$). Milk yield was not significantly different, but differences between the two groups were similar to those observed in DMI during both periods (≈ 1.2 kg/cow/d). That was probably a result of greater variability in milk yield (SEM = 1.29 kg/cow/d) than in DMI. Milk yield of cows fed 0.35% P in the diet DM peaked on week 13, 2 weeks later than those cows fed 0.39% P (35.9 vs. 37 kg/cow/d, respectively). Cows from both treatments peaked intake at 14 weeks post-partum with 22.4 and 24 kg/cow/d for diets containing 0.35% P and 0.39% P, respectively. Cow performance was not significantly different between the two levels of P fed during this trial, however, the narrow difference in dietary P between treatments (0.04 percentage units) may warrant further investigation, given the tendency in higher DMI resulted in 1.2 kg/cow/d numerically higher milk yield with 0.39% vs. 0.35% P.

Key Words: phosphorus, dairy, primiparous

W426 Milk production and components of Holstein dairy cows fed diet supplemented with whole barley grain treated with sodium hydroxide. M. Khorashadizadeh*, A. A. Naserian, and R. Valizadeh, *Ferdowsi University of Mashhad, Excellence Center for Animal Science, Faculty of Agriculture, Mashhad, Khorasan Razavi, Iran*.

To examine the effects of chemical treatments of whole barley grain on milk production and components of dairy cows, 9 multiparous cows (131.44 ± 9.32 DIM, 30.2 ± 5.14 kg daily milk yield) fed a total mixed ration supplemented with ground barley grain (control), or whole barley grain treated with sodium hydroxide (10%) and dried in different periods including: dried immediately (0h) or after 48h storage in plastic bags (48h). Sodium hydroxide was used at the level of 3.5% (DM) of barley grain. Each period lasted 3 week; experimental analyses were restricted to the last week of each period. Diets were formulated according to NRC

2001. Cows were housed in tie stalls and fed the TMR 2 times a day to allow 5 to 10% orts (as-fed basis). Milk production was recorded at the last week of each period and milk samples were collected at the last 2 d of each period. Data were analyzed as a 3 × 3 Latin square using the GLM procedure of SAS (2001). The model included effects of diet, period and cow. Least squares means are reported throughout and significance was declared at $P < 0.05$. Table 1 shows the results of milk production and components. Chemical treatments of whole barley grain increase milk production, but the concentration of fat, protein, lactose, solid not fat (SNF) and milk urea nitrogen (MUN) did not change in diets. The results of the current experiment reveals that chemical treatment of whole barley grain with sodium hydroxide had no significant effects on milk components, but milk production increased when treated whole barley grain included in diets.

Table 1. Effects of chemical treatments of whole barley grain with sodium hydroxide on milk production and components

	Treatments				
parameter	control	0h	48h	P-value	SE
Milk (kg/d)	26.69a	27.58ab	28.16b	0.04	0.37
4% FCM 1(kg/d)	23.84a	24.38ab	25.47b	0.02	0.39
components					
Fat (%)	3.3	3.24	3.36	0.66	0.09
Protein (%)	3.01	2.96	2.99	0.93	0.05
Lactose (%)	4.27	4.3	4.23	0.74	0.05
SNF (%)	7.33	7.34	7.23	0.77	0.08
MUN (mg/dL)	15.99	15.44	15.98	0.72	0.48

[1] Fat-corrected milk = 0.4× [milk yield (kg)]+15×[fat yield(kg)].

Key Words: milk production, whole barley grain, dairy cows

W427 Effects of dietary cobalt supplementation and vitamin B_{12} injection on lactation performance by dairy cows. M. S. Akins*[1], S. J. Bertics[1], M. T. Socha[2], and R. D. Shaver[1], [1]*University of Wisconsin*, *Madison*, [2]*Zinpro Corporation*, *Eden Prairie, MN*.

The objective of this study was to determine lactation performance of primi- and multiparous dairy cows fed different levels and sources (inorganic and organic) of Co or given weekly vitamin B_{12} injections. Forty-five primi- and multiparous cows 60 d prepartum were blocked by parity (1 or >1) and expected calving date, then randomly assigned to 1 of 5 treatments in a randomized complete block design. The treatments were: no supplemental Co (Control), 25 mg Co from Co carbonate (CoCarb), 25 mg (LCoGH) or 75 mg (HCoGH) Co from Co glucoheptonate, and Control plus weekly 10 mg vitamin B_{12} injections (IB12). Cows were on trial until 150 days in milk. Cobalt (ppm DM) in the lactation diet was 1.0, 1.9, 2.3, and 5.2 for Control, CoCarb, LCoGH, and HCoGH, respectively. Far-off, close-up, and lactating diets were 13.8, 15.1, and 18.0% CP and 48.8, 40.2, and 32.9% NDF (DM basis), respectively. Intake was not affected ($P > 0.10$) by treatment and was 19.4 ± 0.5 and 23.1 ± 0.8 kg DM/d for primi- and multiparous cows, respectively. Fat-corrected milk (FCM) was not affected ($P > 0.10$) by treatment for primiparous cows (35.4 ± 1.4 kg/d), but for multiparous cows, CoCarb (42.4 ± 1.7 kg/d) produced less ($P = 0.04$) than LCoGH (47.5 ± 1.8 kg/d). Multiparous cows on IB12 tended to have lower FCM than the mean of LCoGH and HCoGH ($P = 0.10$). Milk yield for primi- ($P = 0.85$) and multiparous cows ($P = 0.21$) on Control did not differ from the mean of CoCarb, LCoGH, and HCoGH. Milk fat percent ($P = 0.048$) and milk urea nitrogen ($P = 0.005$) were greater for primiparous cows on CoCarb than LCoGH. Multiparous cows on IB12 tended ($P = 0.10$) to have higher milk protein percent than the mean of LCoGH and HCoGH, but protein yield did not differ ($P = 0.73$). Body weight and condition score and calculated energy balance were not affected by treatment ($P > 0.10$). Addition of Co above requirements or vitamin B_{12} injections did not improve lactation performance, because vitamin B_{12} status was likely adequate.

Key Words: cobalt, vitamin B_{12}, dairy cow

W428 Carry-over effects reveal that late lactation dairy cows require longer than 30 d to respond to Diamond V Original XP. W. K. Sanchez*[1], C. S. Dei[1], J. Miller[1], G. Poppy[1], and N. St-Pierre[2], [1]*Diamond V*, *Cedar Rapids, IA*, [2]*The Ohio State University*, *Columbus*.

Objectives were to evaluate responses to Diamond V Original XP Yeast Culture (XP) in late lactation dairy cows on commercial farms. Eight Holstein herds in Central California were used to study the effects of feeding a TMR supplemented with 56 g/d XP compared to an unsupplemented Control TMR (C). Herds were paired by test day and milking frequency to form 4 Latin squares with 3 periods of 30 d each, with the extra (final) period being used to estimate carryover effects. A total of 28,690 cows in 37 pens averaging 275 DIM were used in the study. Data were analyzed using a mixed model with the random effects of pair, dairy(pair), dairy × pair × treatment × prior and residual, and the fixed effects of dietary treatments and carryover. Pen was the experimental unit. Carryover effects were evident for milk ($P = 0.0005$), 3.5% FCM ($P = 0.0006$), and milk/DMI ($P = 0.01$). This means that the treatment the herd was on in the prior 30 d affected milk, FCM and milk/DMI response in the subsequent 30 d. Differences in least squares means showed advantages for XP vs. C in milk (31.2 vs. 29.1 kg; $P < 0.05$), FCM (31.4 vs. 30.1; $P = 0.11$), and milk/DMI (1.35 vs. 1.28; $P = 0.12$). No differences in DMI, milk fat % and SCC were observed. The significant carryover effect indicates that XP should be fed longer than 30 d to observe effects in late lactation and cross-over designs used to study the effects of XP (and possibly other rumen modifiers) should have longer than 30-d periods. The biological explanation of this delayed effect is not clear, but results are consistent with other research and field experiences that show a delay in the response of either adding or removing a rumen modifier from the diet.

Key Words: Diamond V XP, lactation, dairy nutrition

W429 Effect of dietary OmniGen-AF on milk somatic cell count and the ability of isolated blood neutrophils to kill pathogens. C. R. Rill*[1], T. Lu[1], J. E. Williams[1], B. Hatch[1], B. Shafii[1], P. Rezamand[1], J. Chapman[2], and M. A. McGuire[1], [1]*The University of Idaho*, *Moscow,* [2]*Prince Agri. Products Inc.*, *Quincy, IL*.

Mastitis results from the invasion of pathogens into mammary tissue and is characterized by inflammation and elevated milk somatic cell counts (SCC). Neutrophils are the primary innate defense mechanism for mammary tissue. The purpose of this study was to examine the effect of feeding a commercially available feed additive on SCC and neutrophil killing ability. Sixteen lactating dairy cattle (59-177 DIM; mean 100 ± 10 SEM) were randomly blocked by treatments based on parity, DIM, and milk production. Diets fed were identical with the exception of an experimental mix fed at 227 g/d containing carrier only or carrier plus OmniGen-AF at 56 g/d. Milk samples were collected 3 d before through d 17 of feeding and submitted to a certified lab for milk SCC analysis. Neutrophils from each animal were isolated from blood after 48 d of feeding and evaluated in vitro for their ability to kill three common mastitis causing microorganisms. Somatic cell data were log transformed, and mean differences were analyzed during d 5 through d

17 of initiation to feeding using ANOVA procedures on a relative basis to d −3 through d 4 of feeding. Neutrophil killing differences on d 48 of feeding were also assessed via ANOVA. Daily milk weights were not affected ($P = 0.24$) by OmniGen-AF feeding (31 vs. 35 kg; SEM = 1.84). Mean relative log SCC score was less ($P = 0.0349$) for OmniGen-AF treatment vs. control (0.85 vs. 1.31, respectively; SEM = 0.22). No differences were detected for the ability of neutrophils from control vs. OmniGen-AF fed animals to kill *Staphylococcus aureus* (35 vs 41%) or *Escherichia coli* (98 vs. 97%). However, killing of *Streptococcus uberis* was improved (15 vs. 73%; $P < 0.0001$). These results indicate the feeding of OmniGen-AF to enhance immune function may warrant further investigation.

Key Words: immunity, mastitis, feed additive

W430 Effects of two processed grain sources in preparturient diets on health and performance of Holstein dairy cows during transition period. E. Qashqayi*, H. Amanlou, D. Zahmatkesh, F. Niazi, and N. Aghaziarati, *Zanjan University*, *Zanjan, Iran*.

In order to evaluate the effect of two processed grain sources on health and performance in the periparturient period, thirty two multiparous Holstein cows averaging 719 ± 31.8 kg body weight (BW) were used in a randomized complete block design and randomly assigned to 1 of 2 treatments. The experimental diets were 1) 13.06% extruded branless wheat (EBW) on a DM basis and 2) 13.06% steam flaked barley (SFB) on a DM basis. The diets were fed as total mixed ration (TMR) and feeding started on average 21 ± 4.06 d prior to expected parturition. After parturition animals received the same lactation diet until 21 d. The results showed that prepartum dry matter intake was higher in cows fed diet 1 (EBW) than in cows fed diet 2 (SFB) (13.7 vs. 11.3 kg, $P < 0.001$) and was also higher in postpartum period (17.46 vs. 16.13 kg, $P < 0.001$). There were no differences in urinary pH and fecal pH, but fecal score in cows fed EBW was higher compared with cows fed SFB during last wk prepartum (3.43 vs. 3.19, $P < 0.05$). BW and body condition score (BCS) were not affected by treatments during periparturient period. Although there were no significant differences between treatments, cows fed the EBW had greater milk yield at 3 week (30.2 vs. 28.4, $P < 0.16$), 1 month (32.7 vs. 30.7, $P < 0.14$) and 2 month (44.2 vs. 44.1, $P < 0.96$). The treatments did not influence serum concentration of glucose, non-esterified fatty acid (NEFA), cholesterol, total protein, albumin, globulin, urea nitrogen, calcium and phosphorous in periparturient cows. Postpartum incidence of retained placenta, milk fever, ketosis, mastitis, dystocia, and metritis were not affected by prepartum diets. There was no effect on parturition condition, calf birth weight and calf condition. Considering higher dry matter intake and performance in EBW group, it appears that feeding extruded branless wheat can be useful in adaptation from gestation to lactation in transition Holstein cows.

Key Words: grain processing, transition period, productivity

W431 Influence of inoculation and storage time on in vitro gas production of high moisture corn. P. C. Hoffman[1], N. M. Esser*[1], R. D. Shaver[1], W. K. Coblentz[2], M. P. Scott[3], A. L. Bodnar[3], R. Schmidt[4], and B. Charley[4], [1]*University of Wisconsin*, *Madison,* [2]*US Dairy Forage Research Center*, *Marshfield, WI*, [3]*Iowa State University*, *Ames,* [4]*Lallemand Inc.*, *Milwaukee, WI*.

The hydrophobic prolamin (zein) proteins, which encapsulate high moisture corn (HMC) starch, are altered by genetic-maturity origin and fermentation. The effect of protein alteration on in vitro digestibility of HMC has not been thoroughly investigated. To assess influences of protein alteration, as effected by inoculation and storage time, on in vitro gas production of HMC, quadruplicate samples of two random HMCs (A and B) containing 25.7 and 29.3% moisture were ground (± 900 um), inoculated (I) with or without 600,000 cfu/g of LB 40788 (Lallemand Inc., Milwaukee, WI), ensiled, and stored for 0, 15, 30, 60, 120 and 240 d. The HMCs were re-ground through a 4-mm screen, inoculated with rumen fluid from two cannulated cows fed 35% concentrate. Samples were incubated for 36 h in an in vitro gas production (GP) system fit with wireless transponders. Total, 0-12, 12-24, and 24-36 h GP was evaluated with lag (h) and fractional rate (h^{-1}) estimated using a segmented non-linear model. Total GP of A, AI, B and BI were modestly altered by storage time and HMC (A vs. B). Larger alterations of 0-12 h GP (% of total) were observed for A, AI, B and BI, with 0 and 240 d GP at 52.0, 52.0, 59.4, 59.5 and 58.6, 60.2, 71.9 and 71.6%, respectively. Fractional rates of digestion were faster for corn B, and increased with storage time but were not affected by inoculation. Fractional rates were best correlated (r = −0.64, 0.58, 0.62, −0.70, 0.64) to pH, acetate, lactate, prolamin and NH_3-N contents of HMC and 0-12 h GP was best correlated (r = −0.73, 0.77, 0.72) to pH, lactate and NH_3-N. Lag times were shorter (1 h) for HMC B but lag time was not influenced by storage time or inoculation. Gas production pools, fractional rates and lag time were poorly correlated to ADF, NDF, ADF-CP and NDF-CP. Data suggest genetic-maturity origin and storage time alter in vitro gas production of HMC.

Key Words: high moisture corn, gas production, inoculant

W432 Comparing a 60-d dry period with far-off and close-up diets with a 40-d dry period with a single diet on milk production and body condition score. J. C. Plaizier*, L. Lippins, M. L. Connor, and D. O. Krause, *Department of Animal Science, University of Manitoba*, *Winnipeg, MB, Canada*.

It has been suggested that reducing the dry period from 60 d to 40 d and feeding a single diet during a short dry period, instead of separate far-off and close-up diets, do not reduce or can increase milk production in the subsequent lactation. This was tested in an experiment with 11 blocks of 2 Holstein dairy cows. Cows were either dried off 60 d or 40 d before the expected calving date. Cows with the 60-d dry period received a far-off diet until 21 d before the expected calving date, and a close-up diet from that day onwards until calving. Cows with the 40-d dry period received the close-up diet during the entire dry period. After calving, all cows received the same lactation diet. On average, the far-off diet contained 1.29 Mcal/kg of Net Energy for Lactation, 12.4% crude protein, and 42.9% neutral detergent fiber. On average the close-up diet contained 1.42 Mcal/kg of net energy for lactation, 12.9% crude protein, and 41.7% neutral detergent fiber. The diet fed to lactating cows contained, on average, 1.71 Mcal/kg of Net Energy for Lactation, 18.1% crude protein, and 33.9% neutral detergent fiber. Diet compositions are on a dry matter basis. Cows with the 40-d dry period had lower milk yields (41.7 vs. 45.0 kg/d), higher milk fat (4.16 vs. 3.80%), and lower milk protein yields (1.34 vs. 1.45 kg/d) during the first 3 mo of lactation than cows with the 60-d dry period. During this period, milk protein content and milk fat yield were not affected by the dry cow management, and averaged 3.40% and 1.75 kg/d, respectively, across treatments. The dry cow management had no effect on body condition scores (1 to 5 scale), which were, on average, 3.45, 3.25, 2.99, 2.79, and 2.76, at drying-off, calving, 3 wk after calving, 6 wk after calving, and 9 wk after calving, respectively. The current study did not show beneficial effects of reducing the dry period from 60 to 40 d and feeding a single diet during the 40-d dry period.

Key Words: dry period, milk production, body condition score

W433 Influence of inoculation and storage time on alteration of the starch-protein matrix in high moisture corn. P. C. Hoffman*[1], N. M. Esser[1], R. D. Shaver[1], W. K. Coblentz[2], M. P. Scott[3], A. L. Bodnar[3], R. Schmidt[4], and B. Charley[4], [1]*University of Wisconsin*, *Madison,* [2]*US Dairy Forage Research Center*, *Marshfield, WI*, [3]*Iowa State University*, *Ames,* [4]*Lallemand, Inc*, *Milwaukee, WI.*

The fates of hydrophobic prolamin (zein) proteins, which encapsulate corn starch creating vitreous endosperm, have not been investigated in high moisture corn (HMC). To assess influences of inoculation and storage time on hydrophobic proteins in HMC, quadruplicate samples of two random corns (A and B), containing 25.7 and 29.3% moisture were ground (± 900 um), inoculated (I) with or without 600,000 cfu/g of LB 40788 (Lallemand Inc., Milwaukee, WI), ensiled, and stored for 0, 15, 30, 60, 120 and 240 d. Nutrient composition (CP, prolamin, starch, ADF, NDF), fermentation (pH, lactate, acetate) and protein degradation markers (buffer-soluble CP, NH_3-N) were evaluated. At 0 and 240 d, α, β, γ and δ zein regions were profiled using HPLC. Data were evaluated as a split-split plot using the PROC MIXED procedures of SAS. Inoculation and storage time reduced pH, and altered lactate and acetate contents of HMC. Lactate and acetate contents of A, AI, B and BI at 240 d were 0.40, 0.32, 1.11, 0.73 and 0, 0.35, 0.30 and 0.87% of DM, respectively. Buffer-soluble CP of HMCs increased from 1.5-2.0% of DM at 0 d to > 4.0% of DM at 240 d. Inoculation had no effect on buffer-soluble CP, but increased NH_3-N content of HMC. Corn A contained more prolamin (5.8 vs 4.6 g of prolamin/100 g starch) than corn B. Peak areas for 6 α, γ and δ zein regions were higher for corn A and fermentation (0 vs 240 d) reduced all zein subunits with the exception of 2 α and 1 δ region. Fermentation reduced (>50%) 27 kDa γ zein which cross links and lies peripheral to α zein. Despite altering lactate and acetate contents, inoculation had no effect on hydrophobic proteins in HMC endosperm. Data suggest altering fermentation acids via inoculation has a minimal effect on hydrophobic proteins in HMC, but hydrophobic proteins in HMC are highly influenced by origin and storage time (proteolysis).

Key Words: high moisture corn, prolamins, inoculant

W434 Amylopectin to amylose ratio in hulless barley in relation to intestinally absorbed protein supply to dairy cattle: A preliminary study. P. Yu*, Z. Niu, and D. Damiran, *Department of Animal and Poultry Science, College of Agriculture and Bioresources, University of Saskatchewan*, *Saskatoon, SK, Canada*.

The objectives of this study were to investigate the relationship between the amylopectin to amylose ratio in hulless barley and intestinally absorbed protein supply to dairy cattle. The total intestinally absorbed protein supply to dairy cattle was determined according to the DVE/OEB system. The total intestinally absorbed protein supply was contributed from (1) the absorbable fraction of microbial crude protein (AMCP); (2) the absorbable fraction of ruminally undegraded feed protein (ARUP); and a correction factor for endogenous protein lost during the digestion process (ENDP). The results showed that the amylopectin to amylose ratio had no correlation with AMCP (R = −0.2928; $P = 0.4816$) and ENDP (R = 0.1952; $P = 0.6432$), but it has significant correlation with ARUP (R = −0.9759; $P < 0.0001$). The total intestinally absorbed protein supply from hulless barley has significant and negative correlation with the amylopectin to amylose ratio with R = −0.7807 ($P = 0.0222$). These results indicated that the amylopectin to amylose ratio in starch granule not only affects starch fermentation and utilization, but also affect protein value in hulless barley.

Key Words: amylopectin to amylose ratio, intestinally absorbed protein supply, hulless barley

W435 Effect of flax hulls in the diet and infusion of flax oil in the abomasum on absorption of the mammalian lignan enterolactone in dairy cows. H. V. Petit*[1], C. Côrtes[1], R. Kazama[2], D. da Silva-Kazama[2], G. T. D. Santos[2], L. M. Zeoula[2], N. Gagnon[1], and C. Benchaar[1], [1]*Dairy and Swine R & D Centre*, *Agriculture and Agri-Food Canada, Sherbrooke, QC, Canada*, [2]*Departamento de Zootecnia*, *Universidade Estadual de Maringa, Maringa, Brazil*.

Six rumen fistulated lactating cows were used in a 6 × 6 Latin square design to investigate the effects of abomasal infusion of flax oil on absorption of the mammalian lignan enterolactone (EL) in cows supplemented or not with plant lignans. The activity of β-glucuronidase was determined in ruminal fluid, urine, plasma, and milk. Treatments were: flax hulls supplementation (without: CON vs. with 15.9% in the DM: FHU) and 3 amounts of flax oil infused in the abomasum (0, 250 and 500 g/d). Experimental periods consisted of 21 d with 14 d of adaptation. Milk samples were collected twice daily on week 3 and pooled for EL assay. Blood was withdrawn from the jugular vein 6 h postfeeding on d 20. Rumen contents were sampled on d 21 before feeding and 2, 4, and 6 h postfeeding and urine samples were taken 2 h postfeeding. Concentration of EL in ruminal fluid was determined at 0 h (baseline) and on samples pooled for 2, 4, and 6 h. All data were analyzed using the MIXED procedure of SAS according to a 6 × 6 Latin square design with repeated measurements for enzyme activity. Concentrations of EL in urine, milk, ruminal fluid, and plasma were significantly higher ($P < 0.001$) for cows fed flax hulls while the abomasal infusion of flax oil had no effect ($P > 0.05$). Cows fed FHU tended ($P = 0.06$) to have higher fecal β-glucuronidase activity than those fed CON and flax oil infusion had no effect ($P > 0.10$). There was an interaction ($P < 0.05$) between hulls and oil for β-glucuronidase activity in ruminal fluid before and post-feeding. Cows fed the CON diet with no flax oil had higher ruminal β-glucuronidase activity before feeding than those fed flax hulls with no flax oil and there was no difference among the other treatments. This study suggests that the lower activity of β-glucuronidase in the rumen of cows fed FHU than in that of cows fed CON may result of an inhibitory effect of oil present in flax hulls on the microbial population involved in the absorption of mammalian lignans. Moreover, these data suggest that β-glucuronidase activity in the small intestine is not inhibited by the presence of flax oil.

Key Words: enterolactone, lignans, flax

W436 Evaluating various meal criteria methods for analyzing chewing data. D. D. Maulfair*, G. I. Zanton, and A. J. Heinrichs, *The Pennsylvania State University*, *University Park*.

When analyzing chewing data collected from cows housed in tie-stalls it is necessary to separate eating bouts into meals using an inter-meal interval or meal criteria. The objective of this study was to improve the existing method of calculating meal criteria by 1) fitting the data with a nonlinear mixed model, which acknowledges that period, treatment, and animal effects are common across the nonlinear profiles and should be accounted for at the time of fitting the nonlinear model and in addition to being used to calculate LSMEANS in proc mixed; 2) producing a meal criterion specific to each treatment at the time of fitting the nonlinear model; 3) making use of as much of the raw data as possible to limit the impact of the choice of bin width. In this study 3 different meal criteria were used to evaluate chewing behavior in lactating dairy cattle; 5 min, 7 min, and a calculated meal criterion based on the chewing data of the study. Eight multiparous, Holstein cows (90 ± 32 days in milk; 4 rumen cannulated) were randomly assigned to replicated 4 × 4 Latin squares. Cows were fed diets that varied in chop length of dry grass hay. Diet forages and their percentage of diet DM were: corn silage (29.4), hay-

lage (17.6), and grass hay (11.8). Observed meal criteria for the short, medium, long, and extra long diets were 7.6, 13.8, 10.5, and 11.2 min; the interval for the short treatment was less than for the other diets ($P < 0.05$). Eating and chewing time per day and per kg of DMI increased by up to 25.3 min/d and 1.0 min/kg DMI as meal criteria increased, but this did not affect any conclusions about differences between treatments. Number of meals/d decreased by as much as 3.4 as meal criteria increased, but there were no differences between diets in the number of meals/d for any of the meal criteria. It appears that the meal criteria value is not essential to obtain accurate conclusions about ration changes from chewing data collected in tie-stalls, but it does impact the values recorded for treatment means.

Key Words: chewing, meal criteria, particle size

W437 The effect of rumen-protected methionine and choline on reproductive performance of Holstein dairy cows. M. Ardalan*, K. Rezayazdi, and M. Dehghan-Banadaky, *Department of Animal Science, University College of Agriculture and Natural Resources, University of Tehran*, *Karaj, Iran*.

The objective of this study was to investigate the effect of feeding ruminally protected sources of methionine and choline on the reproductive indices of Holstein dairy cows. Forty Holstein dairy cows (10 cows per treatment= 6 cows in 1st lactation and 4 cows in 2nd lactation) in their first and second lactation were used from 4-week prepartum through 20-week postpartum and randomly assigned to receive one of the following treatments: 18 g/d of rumen protected methionine (RPM), 60 g/d of rumen protected choline (RPC), 18 g/d of RPM + 60 g/d of RPC, and neither supplement (control). Cows were housed in individual tie stalls and cared for under experimental procedures and protocols approved by the veterinary organization of Iran. The forage was 57% of the total DM of dry period diet and 44% of the total DM of lactation diet. Reproductive data were recorded, including days open, days to first estrus, number of pregnant cows and number of services per conception. Statistical analysis of reproductive data was performed using the general linear models procedure (Proc GLM) of SAS and the statistical model included the effects of treatment, parity, and treatment × parity. The treatments significantly affected services per conception and open days of lactating dairy cows ($P < 0.05$), but did not affect significantly on days to first estrus and number of pregnant cows. RPM+RPC-fed cows had the lowest open days, days to first estrus and services per conception compared with other groups ($P < 0.05$). Parity and treatment × parity had not significant effects on the reproductive indices of dairy cows. Results indicate that the supplementation of RPM and RPC can improve reproductive performance of Holstein dairy cows.

Key Words: rumen-protected methionine, rumen-protected choline, reproductive performance

W438 Effects of the source and amount of sulfur in prepartum diets on performance of periparturient Holstein cows. E. Manidari, H. Amanlou, M. Frozanmehr, H. R. Mirzaei Alamouti*, and E. Mahjoubi, *University of Zanjan*, *Zanjan, Iran*.

Twenty four multiparous Holstein cows (body weight (BW), 687.9 ± 32.33 kg) were used in a completely randomized design and assigned to 3 diets: 1) 0.21% sulfur (control, without sulfur supplementation), 2) 0.41% sulfur (with 0.79% magnesium sulfate) and 3) 0.41% sulfur (with 0.57% magnesium sulfate + rumen protected methionine (25 g/d, Mepron, Degussa Corp., Kennesaw, GA)). Cows were individually fed the total mixed ration with similar net energy for lactation (1.58 Mcal/kg dry matter), crude protein (13.3%) and dietary cation-anion difference (−32 meq/kg dry matter) from 21.9 ± 2.47 d relative to expected calving until calving. After calving, all cows received the same lactation diet until 21 d in milk. Colostrum production and composition were determined until 12 h after calving. Milk production and composition were determined 3 times per day until 21 d in milk. Data were analyzed using MIXED Procedure from SAS and cows nested in the diets were as random effects. Different variance-covariance error structures were tested for data measured over time as repeated measures. Diet with 0.41% sulfur from magnesium sulfate (diet 2) compared with diets 1 and 3 significantly decreased dry matter intake at periparturient period (8.7 vs. 7.4 and 9.7 ± 0.36 at prepartum and 10.7 vs. 8.1 and 10.9 ± 0.65 kg/d at postpartum, for the diets 1, 2,and 3, respectively). Colostrum production was lower ($P < 0.01$) for the diet 2 compared with the others (11 vs. 18 and 16.3 ± 2.45 kg, for the diets 1 and 3, respectively). The Diet 3 significantly increased protein and ash content in colostrum but fat content was not affected. Cows fed the diet 2 had lower ($P < 0.01$) milk yield (19.7 vs. 24.5 and 24.9 ± 1.15 kg/d) and milk components yield compared those fed diets 1 and 3, but milk components concentration were not affected. Cows fed the diet 2 significantly lost BW and body condition score. In summary, increasing sulfur concentration (0.41% of DM) using magnesium sulfate in close-up diets compared with other diets used in this study depressed performance of periparturient cows.

Key Words: sulfur, prepartum diet, periparturient Holstein cows

Small Ruminant: Sheep Production 2

W439 The effects of high dietary protein levels in Afshari ewes during late gestation. H. Amanlou, A. Karimi, and E. Mahjoubi*, *Zanjan University*, *Zanjan, Iran*.

It has been shown that due to declining DM intake during prelambing period, protein intake can be compromised unless dietary crude protein (CP) levels are increased. However results on the impacts of increasing the dietary CP level in prelambing ewes are contradictory. Thus, the aim of current study was to investigate the effects of dietary crude protein (CP) level in late pregnancy on colostrum production, colostrum components and lamb survival. Forty-one Afshari ewes were randomly assigned to three treatment groups in a completely randomized design since 3 weeks before lambing. The experimental diets were isoenergetic and included: 1) 120 g CP/kg DM (n = 14), 2) 140 g CP/kg DM (n = 13), and 3) 160 g CP/kg DM (n = 14). The offering high CP level did not influence dry matter intake (DMI) between treatments during last 3 weeks before lambing (1.81 ± 0.14, 1.77 ± 0.26 and 1.83 ± 0.21, treatments 1 to 3, respectively; $P > 0.05$). Increasing dietary CP did not affect colostrum volume (1379.2 ± 79.38, 1398.2 ± 43.85 and 1410.3 ± 67.2 kg, respectively; $P > 0.05$), however, significantly increased crude protein content of colostrum (118.8 ± 10.6, 121.5 ± 14.5 and 142.3 ± 12.7 g/kg, respectively; $P < 0.05$). Fat, lactose and SNF content of colostrum were not affected by treatments. It also decreased lamb birth weight (4.85, 4.61 and 4.11 kg, respectively; $P < 0.05$). Although increasing CP level had no effect on lamb survival rate from birth to weaning, it was numerically lower for treatment groups 2 and 3 (100, 95.23 and 86.66%, respectively). A tendency was detected for lower BW at weaning (34.6, 32.7 and 29.4 kg, respectively; $P < 0.12$) with added CP level. In general, because of the adverse effect of high dietary protein nutrition during late gestation on lamb birth weight and expense of protein in diet, feeding high protein diet to pregnant ewes with aim to increase colostrum production and lamb survival rate in Afshari ewes is not recommended.

Key Words: prelambing, Afshari ewe, CP level

W440 Fertility and prolificity of primiparous Suffolk ewes bred by fixed-timed artificial insemination or artificial insemination at detected estrus. G. Jasso-Diaz[1], O. Mejia[2], J. I. Aguilera-Soto*[1], F. Mendez[1], M. A. Lopez-Carlos[1], R. Rincon[1], and C. F. Arechiga[1], [1]*Universidad Autonoma de Zacatecas*, *Zacatecas, Mexico*, [2]*Universidad Nacional Autonoma de Mexico*, *Mexico, D.F.*

The purpose of the present study was to determine and compare fertility in Suffolk female sheep (n = 29) exposed to two different insemination procedures: 1) timed-artificial insemination (TAI) or 2) artificial insemination by detection of estrus (AIDE). In both treatments: 1) Timed artificial insemination sheep (n = 15) were treated with an intravaginal sponge containing 20 mg of fluorogestone acetate (FGA) from d −12 to 0, followed by an eCG intramuscular injection on day of sponge removal. Fixed-time intrauterine insemination was performed 56 h after intravaginal sponge removal at d 0 (without detection of estrus). 2) Insemination based on detection of estrus (AIDE; n = 14), female sheep were inseminated based on detection performed at 24 and 36 h after intravaginal sponge removal and eCG injection and inseminated at 48 h. Pregnancy diagnosis was determined firstly by non return to estrus (TAI= 93.3%; 14/15 ewes vs. AIDE=72.7%; 8/11 ewes), with non-significant differences within treatments ($P > 0.05$). Pregnancy diagnosis was performed at 45 d post-insemination by real time ultrasonography (5Mhz) confirming previous pregnancy diagnosis (93.3% vs. 72.7% for TAI and AIDE, respectively). Prolificity was not affected by insemination procedure (1.42 vs. 1.25, for TAI and AIDE, respectively). In conclusion, use of timed insemination did not compromise pregnancy, neither prolificity in Suffolk female ewes.

Key Words: sheep, artificial insemination, estrus detection

W441 Intake and performance of sheep supplemented with brewer waste (ensiled and dried) grazing under the rainy season of tropical. F. P. Portilho*, S. L. S. Cabral Filho, H. Louvandini, and B. A. O. Macedo, *University of Brasilia*, *Brasilia, DF, Brazil*.

At reduced costs industrial wastes enable usage of protein mineral mixtures as ingredients in the formulation to improve the productive capacity. The protein supplementation with residue of brewery provide rapid weight gain in the finishing phase on pasture, avoiding a possible protein deficiency in the case of high stocking rates and lower availability of fodder. The objectives of this study were to evaluate the dry matter intake and performance of finishing sheep in pasture during the rainy season and to evaluate replacement of traditional protein source (soybeans meal) by sources of low degradability in the rumen like cotton meal and brewery waste (dried and ensiled). We used forty male sheep of Santa Inês breed, with average weight of 22.04 ± 3.14 kg, grazing on Aruana grass (*Panicum maximum*), receiving supplementation of 100 g / animal / day for four treatments, plus a control without supplementation. Treatments were represented by supplementation offered for sheep grazing at the end of the rainy season during 30 days (between March and April). The treatments were composed as follows: T1) mostly of dried brewer grain (RDC), T2) by silage of waste brewery (SRC), T3) by cotton meal (FA), T4) by soybean meal (FS) and T5) without supplement (control–FSM). The experimental design was randomized blocks. Differences were observed for final weight between treatments evaluated ($P < 0.01$). The dry matter intake and weight gain varied among the treatments and there were differences ($P < 0.05$) in weight gain while comparing supplements (RDC, SRC, FA and FS) and control (FSM), with 0.131, 0.123, 0.101, 0.082 and 0.022 kg / day respectively. The feed efficiency had better trend for RDC and the worst one for the control animals (FSM). However, there were no differences ($P > 0.05$) among the treatments for feed efficiency. Therefore, the use of brewer waste in the diet of lambs at the end of the wet season can be an economical alternative as a substitute for soybean meal and yield good performances, as well as additional intake effects.

Key Words: brewer grains, supplementation, sheep

W442 Intake and performance of sheep supplemented with dried brewer grains, cottonseed meal and soybean meal grazing under tropic rainy season. F. P. Portilho* and S. L. S. Cabral Filho, *University of Brasilia*, *Brasilia, DF, Brazil*.

The usage of supplements in the rainy season provides benefits to the plants and animals. The objective of this study was to evaluate the DMI and performance of lambs during the rainy season, kept in the Tifton 85 pasture, and supplemented with different mixtures (energy and protein) with high (soybean meal) and low rumen degradable protein (dried brewery waste and cottonseed meal). Between March and April of 2007, 32 Santa Inês ewes, with average BW of 26.4 ± 4.9 kg, were kept on pasture forage of *Cynodon dactylon* cv. Tifton 85 and received supplementation of 100 g /ewe/ day. Treatments consisted of 2 formulations of protein supplements with dried brewery waste (DBW) and cottonseed meal

(CM), an one energy supplement with soybean and maize meal (SMM), and a control test with only a mineral mix (MM). The experimental design was completely randomized. We observed differences in DMI (% BW), which decreased for treatments in the following order: DBW > CM > SMM > MM (P <0.05). The results of ADG were higher for the energetic supplementation (SMM) with 149.16 g / d compared with CM and MM at 69.58 and 62.08 g / d, respectively (P <0.01), and without changes for RDC (103.75 g / day). For the feed efficiency, there were significant differences (P <0.05), with better results for SMM with 12.09 and the worst for CM, with an average of 19.18 among all treatments. We observed an increase of pasture consumption (CP) of 0.456 and 0.336 kg / day for DBW and CM having an additional effect of stimulating consumption of grass from these supplements and mild increase of 0.025 kg / day for SMM, causing a substitution effect with stimulus. Therefore, by not existing different performance between SMM and the DBW, it becomes economically viable the usage of DBW.

Key Words: brewer grains, cotton meal, soybean meal

W443 Evaluation of rhizoma peanut hay (*Arachis glabrata*) in sheep diets: Chemical composition, in vitro degradability, intake, and digestibility. A. A. Rodríguez*, G. Emmanuelli, W. González, and P. Randel, *University of Puerto Rico*, *Mayaguez*.

The effects of inclusion of *Arachis glabrata* (AG) on the chemical composition, in vitro degradability, and intake and digestibility by sheep of tropical grass hay (TGH) was determined. The legume was harvested, sun dried, and manually mixed with TGH at three different proportions: 100:0, 50:50, and 0:100 w/w. Triplicate samples from each combination were analyzed to determine OM, inorganic matter (IM), CP, ADIN, available CP (ACP), NDF, ADF, and lignin (L) content. IVDMD and in vitro NDF (IVNDFD) degradability were determined after 48 h of incubation. Data were analyzed using the GLM procedure of SAS in a randomized complete design and means separated with Bonferroni t-test. To determine forage consumption and digestibility a 3 by 3 Latin square experiment was conducted using crossbred lambs as experimental units. Lambs were assigned to the three diets. Each experiment period consisted of a 7-day diet adjustment and 5 d of data collection. OM content was lower and IM content was higher ($P < 0.05$) in mixtures containing 100% AG than 50% or 0%. CP, ACP, ADIN, ADF, and L increased as percentage of AG increased in the mixtures, but NDF content decreased. IVDMD also increased ($P < 0.05$) as proportion of AG increased, but IVNDFD decreased ($P < 0.05$). Forage consumption was similar ($P < 0.05$) in lambs fed 100% and 50%AG (1020 vs. 1056 g/d, respectively), however, while animals fed TGH alone had the lowest DM consumption (956 g/d). Daily consumption as % of animal body weight was lower ($P < 0.05$) in lambs fed TGH alone (3.17%) than those fed 50 (3.46%) or 100% AG (3.33%). Sheep fed diets containing increasing levels of AG had higher ($P < 0.05$) DMD (100% AG =62.7%, 50% AG=58.1%), CPD (100% AG=65.7%, 50% AG=62.8%) and NDFD (100% AG=57.7%, 50% AG= 53.1%) than animals fed TGH alone (DMD=54.4%, CPD=58.7%, NDFD=46.9%). In summary, CP, NDF contents and IVDMD were improved as percentage of AG increased in TGH:AG mixtures. Inclusion of AG at 50% of the total forage offered in TGH-based diets increased forage dry matter intake in sheep, while DM, CP and NDF digestibilities increased at both higher levels of AG.

Key Words: legumes, *Arachis glabrata*, sheep

W444 Metabolic profile in pregnant ewes fed oat straw-based diets supplemented with wheat hydroponic forage. E. Herrera-Torres[1], M. Cerrillo-Soto*[1,4], A. Juárez-Reyes[1,4], H. Bernal-Barragan[2,4], F. Ríos-Rincón[3,4], O. Reyes-Estrada[1], M. Murillo-Ortiz[1,4], G. Névarez-Carrasco[1,4], and M. Guerrero-Cervantes[1,4], [1]*Universidad Juárez del Estado de Durango*, *Durango, Dgo., México*, [2]*Universidad Autónoma de Nuevo León*, *Monterrey, Nuevo León, México*, [3]*Universidad Autónoma de Sinaloa*, *Culiacán, Sinaloa, México*, [4]*Red Internacional de Nutrición y Alimentación en Rumiantes*.

A study was conducted to determine the effect of supplementing wheat hydroponic forage (WHF) to pregnant ewes fed oat straw-based diets on serum glucose, non-esterified fatty acids (NEFA) and blood urea N (BUN) at late gestation. Thirty-nine primiparous Katahdin ewes (T1 = 43.8 ± 4.8, T2 = 39.2 ± 1.4, T3 = 38.1 ± 3.0 kg BW) were randomly assigned to 3 experimental dietary treatments: T1: 72% oat straw (OS), 28% WHF, T2: 64% OS, 13% WHF, 5% cotton seed meal (CSM) and 18% rolled corn (RC), and T3: 70% OS, 8% CSM and 20% RC. Diets were calculated to meet ewes requirements according to the Intestinal Digestible Protein French System (T1 = 85, T2 = 76 and T3 = 76g/d of metabolizable protein, respectively). Jugular blood samples were collected in vacutainer tubes early in the morning before feeding monthly. Glucose, NEFA and BUN were quantified with colorimetric procedures. Statistical analysis was based on a completely randomized design for repeated measurements. Highly significant interactions ($P < 0.001$) between month and treatment were registered in serum glucose and NEFA concentrations. Ewes fed diets with more WHF (T1) had less serum glucose concentrations during the third month of pregnancy ($P < 0.05$) than ewes fed T2 and T3. Values for NEFA were similar ($P > 0.05$) between treatments; nonetheless, a numerical increment in serum NEFA was observed in ewes fed T1 in the fifth month of pregnancy. No interactions ($P > 0.05$) between month and treatment were registered in BUN, therefore, just the means of concentrations of the BUN are presented and they were: 10.2, 10.2 and 11.3 (mMol/L) for T1, T2 and T3, respectively. The observed plasma levels of glucose, urea, and NEFA indicated that an increased intake of energy may be outlined mainly for ewes fed T1 to ensure an adequate nutritional status of the animals during late pregnancy.

Table 1. Least squares means of the concentrations of blood metabolites in pregnant ewes (mMol/L)

Month of gestation	T1	T2	T3	SE±
		Glucose		
3	2.9[b]	3.6[a]	4.2[a]	0.18
4	2.9[a]	3.2[a]	3.3[a]	0.18
5	2.2[a]	2.3[a]	2.5[a]	0.18
		NEFA		
3	0.38[a]	0.36[a]	0.46[a]	0.13
4	0.47[a]	0.54[a]	0.41[a]	0.13
5	1.07[a]	0.88[a]	0.74[a]	0.13

[ab]Means within rows with different superscript differ (P<0.05).

Key Words: metabolites, wheat hydroponic forage, pregnant ewes

W445 Performance and voluntary intake of ewe lambs in integrated crop livestock systems in the dry season. S. L. S. C. Filho*[1], B. A. O. Macedo[1], F. P. Portilho[2], H. Lovandini[1], and C. M. Pimentel[1], [1]*University of Brasilia*, *Brasília, Distrito Federal, Brazil*, [2]*EMBRAPA CERRADO*, *Brasília, Distrito Federal, Brazil*.

The objective of this study was to evaluate the performance of lambs at pasture, comparing nutritional quality of pastures that were reserved (set aside) during the raining season with those that were grazed after silage

or grain production. Four treatments were tested: *Brachiaria humidicula* with corn (BC), reserved *Brachiaria humidicula* pasture (RB), *Panicum maximum* cv. Aruana with corn (AC) and reserved *Panicum maximum* cv. Aruana pasture (RA). Thirty two crossbred Santa Inês × Ille de France ewe lambs aged from three to six months and weighing 22 ± 4.47 kg were used. The experimental design was completely randomized with two replicates per treatment, using eight experimental units (0.25ha), with four ewe lambs (testers) each. Voluntary intake and digestibility were measured with Cr_2O_3 and indigestibility ADF markers. The corn grain yield was 5.9 ± 1.1 t/ha and 4.1 ± 0.7 t/ha for BC and AC, respectively, with estimated silage yield for these treatments being 33.8 ± 6.0 t/ha and 31.3± 6.0 t/ha, respectively. There was no difference between the treatments ($P > 0.05$) in terms of CP, NDF and ADF of the pasture over the experimental period. The availability of dry matter before grazing was 3191, 3562, 3048 and 6565 kg/ha for the treatments BC, RB, AC and RA, respectively with daily weight gain being 108.5 ± 28.9; 38.5 ± 18.9; 89.5 ± 30.4 and 37.4 ± 4.5 g/day, respectively. The treatments with corn showed improved performance compared to the reserved pastures ($P < 0.05$). No significant differences were found between treatments for voluntary intake ($P > 0.05$), the average being 591.8 ± 175.44 g DM/animal/day. The dry matter digestibility for BC and RB was 43.7 ± 9.2 and 44.9 ± 6.9%, and for AC and RA was 51.1 ± 8.4 and 37.4 ± 4.5%. The AC treatment showed higher digestibility than RA, and digestibility of these did not differ from BC and RB ($P < 0.05$). The integrated pasture-crop system promoted higher performance of ewe lambs in the dry season compared to reserved pasture management, as well as providing additional silage or grain for the sheep farm.

Key Words: integrated crop livestock systems, humidicula, dry season management

W446 The effect of persimmon (*Diospros kaki* L.) vinegar supplement on feed intake, digestibility, and ruminal fermentation indices in sheep. J. H. Shin[1,2], Y. D. Ko[1], and S. C. Kim*[1,3], [1]*Department of Animal Science, Gyeongsang National University*, *Jinju, South Korea*, [2]*Department of Animal Sciences, University of Florida*, *Gainesville,* [3]*Institute of Agriculture and Life Science, Gyeongsang National University*, *Jinju, South Korea*.

This study estimated the effect of fermented persimmon (Diospros kaki L.) extract (FPE) supplement on feed intake, digestibility, nitrogen (N) balance, and rumen fermentation indices in sheep. Five male sheep (Corriedale × Polwarth, BW = 48.6 kg) were housed at metabolism crates and assigned to a 5 × 5 Latin square design with consecutive five 20-d periods which consisted of 14-d of adaptation and 6-d of data collection. The sheep were fed a diet containing concentrate and rice straw in a 3:7 ratio ad libitum. The five treatments were FPE supplemented at 0 (Control), 5, 10, 20, and 30 g/kg of concentrate. Tukey test and polynomial contrasts were used to identify differences ($P < 0.05$) and estimate the effects of FPE supplement level, respectively. Intakes of DM, OM, NDF, ADF, and nitrogen free extract (NFE) increased quadratically ($P < 0.05$) with increasing intake of FPE supplement and maximized (828, 710, 418, and 288 g/d, respectively) at 10 g/kg FPE. The digestibilities of DM, OM and NFE increased quadratically ($P < 0.05$) by increasing amount of FPE supplement, and sheep fed 5 and 10 g/kg diets had greater (52 vs. 49%, 55 vs. 52%, 60 vs. 55%; $P < 0.05$) DM, OM, and NFE digestibilities than Controls. By increasing FPE supplement concentration, N intake and fecal N increased linearly ($P < 0.05$), whereas N digestibility, retained N, and retained N ratio increased quadratically ($P < 0.05$). Retained N was maximized ($P < 0.05$) in sheep fed 5 and 10 g/kg diets (2 and 1.7 g/d). There was a quadratic increase ($P < 0.05$) of mean rumen ammonia N concentration and a linear increase ($P < 0.01$) in mean rumen VFA and acetate concentrations. The mean concentration of rumen propionate in sheep fed all FPE supplemented diets was greater (2.2 vs. 1.78 mmol/dL; $P < 0.05$) than Control, but the mean ratio of rumen acetate to propionate in sheep fed 5 and 10 g/kg diets was lower (2.6 vs. 2.9; $P < 0.05$) than that of Control sheep. In conclusion, FPE supplemented at 5-10 g/kg of concentrate improved feed intake, digestibilities of DM, OM and NFE, N metabolism, and rumen fermentation indices of sheep.

Key Words: persimmon, digestibility, sheep

W447 Prediction of rumen pH and digestibility of diets containing soybean hulls fed to ram lambs by the Small Ruminant Nutrition System. R. S. Gentil*[1], I. Susin[1], A. Cannas[2], A. V. Pires[1], C. Q. Mendes[1], E. M. Ferreira[1], G. H. Rodrigues[1], A. S. Atzori[2], and L. O. Tedeschi[3], [1]*Escola Superior de Agricultura Luiz de Queiroz (ESALQ)/ University of São Paulo*, *Piracicaba, São Paulo, Brazil*, [2]*University of Sassari*, *Sassari, Sardinia, Italy*, [3]*Texas A&M University*, *College Station*.

The Small Ruminant Nutrition System (SRNS) predicts feed values based on carbohydrate and protein fractions and their digestion rates, forage, concentrate and liquid passage rates, microbial growth, and physically effective fiber (peNDF). Data from four experiments with lambs were used to compare observed OM digestibility (OMD), NDF digestibility (NDFD), and pH with predictions made by the SRNS model v. 1.8.7. All experiments were designed to study soybean hulls (SH), a byproduct that is rich in digestible fiber but poor in peNDF. SH substituted corn meal in experiments 1, 2 and 3 and coastcross hay in experiment 4. To compare OMD and NDFD estimates with measured values, two values of degradation rate of B2 carbohydrate fraction (potentially digestible NDF) of SH (kd = 8, as in the SRNS feed library, and 14%.h^{-1}) were used. In the SRNS the kd of B2 carbohydrate fraction is reduced if pH decreases below 6.2. Thus, OMD and NDFD were predicted by using the rumen pH predicted by the SRNS (pH = 5.425 + 0.04229 x peNDF) or a fixed value of 6.46. The digestibility predictions were more precise and accurate when kd was assumed to be 14%.h^{-1} and fixed pH were used (OMD: mean bias (i.e. observed-predicted values; MB) = 0.57%, $r^2 = 0.70$ and root of mean square prediction error (RMSPE) = 3.05%; and for NDFD: MB = 2.25%, $r^2 = 0.52$, RMSPE = 5.24%). Rumen pH was slightly overpredicted (MB = −0.03, $r^2 = 0.61$, RMSPE = 0.17%). Thus, the SRNS predictions had good precision and accuracy for rumen pH, while OMD and NDFD digestibility were correctly predicted only if the kd of the B2 carbohydrate fraction of SH was greater than that reported in the SRNS feed library and not reduced when pH decreased.

Key Words: digestibility, rumen pH, SRNS

W448 Okara as a protein supplement for early lactating ewes. L. B. Harthan* and D. J. C. Cherney, *Cornell University*, *Ithaca, NY.*

Livestock producers must use cost-efficient feedstuffs if they are to remain profitable in the face of decreasing market prices and increasing feed prices. The objective was to evaluate the feeding value of wet okara, waste pulp remaining after production of soy milk, as a protein supplement for lactating ewes with twin lambs. A 4 × 4 Latin square replicated twice was conducted to examine the influence of concentrate mix (okara or not) and type of forage (silage or hay) on ewe milk composition and growth of lactating lambs. Ewes (multiparous; 55 to 74.8 kg) were 12.5 ± 3.5 DIM, and were raising twins. The 4 diets were formulated to have the same TDN (% of DM).Treatment periods were 14 days (7 days adaptation and 7 days collection), and ewes were fed

1 of 4 diets: a wheat middling and corn concentrate with mixed grass hay (TSH), okara and corn with mixed grass hay (OSH), soybean and wheat middlings fed with hay crop silage (TSS), and okara and corn with hay crop silage (OSS). Forages were fed separately from concentrate mixes. Ewes fed hay diets (TSH and OS) had lower forage DM intakes than ewes fed hay crop silage (TSS and OSS; $P > 0.05$). Intake of okara supplement was much higher ($P < 0.05$) with OSH (3.64 kg/d) than with OSS (1.70 kg/d) possibly a result of the high moisture content of the okara. There was no difference in supplement intake between TSH and TSS. Despite differences in DMI, there were no differences among diets for either ewe daily gain or lamb daily gains. There were no differences in ewe milk compositions among the diets. Based on similar ewe growth efficiencies, and average weekly gain of lambs, okara is an effective source of protein for lactating ewes.

Key Words: okara, protein, lamb

W449 Use of pinto bean waste on finishing hair-type lambs. G. Villalobos, F. Castillo*, D. Dominguez, H. Castillo, and J. A. Ortega, *Universidad Autonoma de Chihuahua*, *Chihuahua, Chihuahua, Mexico*.

Feeds price increment has obliged sheep producers to look for new alternatives in animal feeding; one of them is waste pinto bean grain. The objective was to evaluate the effect of three waste pinto bean grain levels (in concentrate dry matter) on dry matter intake (DMI), average daily gain (ADG) and gain efficiency (GE) of finishing hair lambs. Treatments were: Control (C= 0%), low waste pinto bean (LWB= 12.5%) and high waste pinto bean (HWB= 25%). Seventy two crossbred hair lambs (Dorper × Pelibuey and Kathadyn × Pelibuey) were used (36 females and 36 males), all lambs being twins, with 18.69 ± 3.89 Kg initial body weight and 75 ± 6 d old. Lambs were fed ad libitum with isoenergetic and isonitrogenous (2.6 Mcal/Kg ME; 17.9% CP) diets (80:20 concentrate:forage ratio) during 70 d, with an adaptation period of 18 d. Lambs were assigned to blocks by initial body weight (3 lambs per block, 4 female blocks and 4 male blocks by treatment) and then randomly assigned to the treatments (C, LWB and HWB; n= 24 per treatment) and were weighted every 14 d for ADG. In the last 5 d of each period DMI was measured for each block and then GE was estimated. Data for DMI, ADG and GE was analyzed with PROC MIXED in a completely random block arrangement where the treatment, gender and their interaction effects were evaluated, likewise a tendency analysis was made for each variable. For DMI (Kg) a quadratic effect was found ($P < 0.05$), but treatments were not different ($P = 0.0657$) (C= 1.22, LWB= 1.14 and HWB= 1.05). Data for ADG (Kg) showed a quadratic response for each treatment ($P < 0.05$) (C=0.26, LWB=0.23 and HWB=0.21) during the test. Final body weight lsmeans (Kg) were C= 37.67, LWB= 34.22 and HWB= 33.27. For GE (Kg) a clear general tendency was not found, with no differences between treatments ($P = 0.6001$) during the test (C= 6.53, LWB= 6.94 y HWB= 6.94). Gender and its interaction treatment by gender effect were not found ($P > 0.05$) for any variable. The best productive performance of treatments in this research was found for C, so that the waste pinto bean grain use on finishing hair lambs is not a recommendable alternative for this productive stage.

Key Words: hair lambs, waste pinto bean grain, feedlot lambs

W450 Effect of cull-chickpeas on apparent digestibility and energy concentration of feed in growing Pelibuey sheep. A. Estrada-Angulo*[1,4], H. Bernal-Barragán[2,4], M. A. Cerrillo-Soto[3,4], E. Gutiérrez-Ornelas[2,4], A. S. Juárez-Reyes[3,4], J. F. Obregon[1,4], J. J. Portillo-Loera[1,4], and F. G. Rios[1,4], [1]*FMVZ-Universidad Autonoma de Sinaloa*, *Culiacan, Sinaloa, Mexico*, [2]*FA-Universidad Autonoma de Nuevo Leon*, *Monterrey, Nuevo Leon, Mexico*, [3]*FMVZ-Universidad Juárez del Estado de Durango*, *Durango, Durango, Mexico*, [4]*Red Internacional de Nutrición y Alimentación en Rumiantes*, *Culiacán, Sinaloa, Mexico*.

A study was performed to determine the effect of cull chickpeas (CCP) substituting corn-soybean meal on apparent digestibility and energy concentration in growing sheep. Five Pelibuey males (30.0 ± 1.1 kg BW) were used in a 5 × 5 Latin square design with 6-day adjustment and 4-day collection phases. Experimental diets consisted of: 1) control; Sudan hay (10%), whole corn grain (67.6%), soybean meal (13.1%), sugarcane molasses (6%), sodium bicarbonate (0.6%) and mineral premix (2.7%); 2) CCP15; CCP (15%), whole corn grain (58.1%), soybean meal (7.6%); 3) CCP30; CCP (30%), whole corn grain (48.5%), soybean meal (2.2%); 4) CCP45; CCP (45%), whole corn grain (35.7%); and 5) CCP60, CCP (60%), whole corn grain (20.7%). All diets were isoenergetic (3.60 Mcal of DE/kg). Crude protein content for treatments 1, 2 and 3 was 16.0% while CP content for treatments 4 and 5 was 17.2 and 19.3%, respectively. Dry matter intake was adjusted to 1000 g/head/day (500g at 0800; 500 g at 1500). Fecal and feed samples were oven dried and analyzed for DM, OM, CP, and apparent digestibility of DM. Digestible energy content (Kcal/kg) was calculated by: 43.97 (digestible DM %) - 94. Data were analyzed by ANOVA. No treatment effects ($P > 0.05$) were registered in DM fecal excretion (140.6, 139.7, 148.4, 150.3, and 150.3 g/d) or apparent DM digestibility (85.9, 86.0, 85.2, 85.0 and 85.0%) for Control, CCP15, CCP30, CCP45 and CCP60, respectively. Meanwhile, neither the DE concentration (3.68, 3.69, 3.65, 3.64 and 3.64 Mcal/kg DM) nor the observed/calculated DE ratio (1.02, 1.03, 1.01, 1.01, and 1.01) differed ($P > 0.05$) among treatments. Data suggested that a whole corn grain-soybean meal mixture can be substituted up to 60% with CCP without affecting apparent digestibility of DM and energy concentration in diets for growing Pelibuey sheep.

Key Words: hair sheep, cull chickpeas, apparent digestibility

W451 Fiber digestibility of a finishing lamb diet supplemented with Fibrozyme. D. Domínguez, J. E. Cruz*, G. Villalobos, H. Castillo, L. Durán, E. Santellano, and L. Carlos, *Universidad Autónoma de Chihuahua*, *Chihuahua, Chihuahua, México*.

Fibrolytic enzymes can enhance rumen microbial enzyme activity under low ruminal pH conditions improving fiber digestion. This study evaluated the effect of Fibrozyme addition on fiber digestion of a finishing lamb diet. Six crossbreed lambs (Charolais × Pelibuey; 30 ± 6.1 kg) fitted with ruminal cannula were individually housed and randomly assigned to three levels of Fibrozyme (Alltech Inc.): 0.0 (T-0.0), 0.1 (T-0.1) y 0.2 g/kg of body weight (T-0.2) added to concentrate. The experimental design was a replicated 3 ×3 Latin square. Lambs were fed ad libitum with a diet containing 2.9 Mcal ME/kg DM and 15.9% CP, based on 20% alfalfa hay and 80% concentrate (% DM). Each experimental period last 17 d, with an adaptation phase of 7 d. Dry matter intake (DMI) was determined daily and individually from 8th to 12th d. Ruminal pH was determined on 13th d at 0, 1, 2, 4, 8, 12, 18 and 24 h after morning feeding. Fecal samples were taken on 15th to 17th d, to determine fiber digestibility using indigestible ADF. Content of NDF and ADF were sequentially determined in period composite samples of forage, concentrate, and fecal grabs. Dry matter intake and digestibility data were analyzed with PROC GLM, while ruminal pH data were analyzed as repeated measurements on time using PROC MIXED. DMI was similar among treatments (1.44, 1.48 and 1.48 kg, respectively; $P > 0.05$). Rumen pH for all treatments was lower than 6.0 during 14 h (from 4th to 18th h after feeding). Dry matter digestibility was not affected by treatments (76.6, 75.1, and 77.6%, respectively; $P > 0.05$). However, NDF and ADF digestibility was higher for T-0.2 vs.

T-0.0 and T-0.1 (15.0 vs. 12.7 and 8.9%; and 17.3 vs. 11.2 and 13.3%, respectively; $P < 0.05$). Hemicellulose digestibility was similar among treatments (14.4, 8.8 and 14.7%, respectively; $P > 0.05$). Adding Fibrozyme at 0.2 g/kg of body weight to finishing lambs diet improved fiber digestibility.

Key Words: Fibrozyme, fiber digestibility, hair lambs

W452 Effect of variety and maturity state of oat hay on performance of ewe lambs. D. Domínguez[1], S. Ramírez*[1], J. J. Salmerón[2], R. González[2], G. Villalobos[1], J. A. Ortega[1], and L. Carlos[1], [1]*Universidad Autónoma de Chihuahua*, *Chihuahua, Chihuahua, México*, [2]*INIFAP*, *Cuauhtémoc, Chihuahua, México*.

Oat hay is an important forage source in the sheep industry of Chihuahua, México. This study evaluated the effect of genotype and maturity stage on nutritional value of oat hay and their effect on performance of ewe lambs. Karma (K), Cevamex (C) and Bachiniva (B) oat varieties were cultivated under non irrigated conditions and harvested at soft-dough (SDS) and hard grain stage (HGS). Ninety hair ewe lambs of commercial crosses with an initial average weight of 30.2 ± 2.5 kg were randomly assigned to six treatments (n=15, 5 pens and 3 lambs per pen) in a 3 × 2 factorial design. Animals were fed ad libitum a 80:20 forage:concentrate diet (% DM) containing 2.4 Mcal ME/kg DM and 16.0% CP. Production of DM per hectare (DM/ha), and content of CP, NDF, ADF, and ADL were determined for oat varieties. Dry matter intake (DMI) was determined daily per pen, while body weight, average daily gain (ADG) and gain efficiency (GE) were recorded individually every 14 d, and apparent digestibility of DM, CP and NDF at the final of the study. Data was analyzed as a complete random blocking design in a factorial arrangement, using PROC MIXED. There was no effect of oat variety on DM/ha, but it was higher for HGS (5,211 vs. 4,293 kg/ha; $P < 0.05$). Genotype and maturity stage did not affect chemical composition. Content of CP, NDF, ADF and ADL for SDS and HGS were: 11.5 and 10.2; 51.8 and 51.1; 28.4 and 27.7; and 2.75 and 2.90%, respectively. DMI, final body weight, ADG and GE were not affected by treatments, average for SDS and HGS were: 1.29 and 1.22; 36.4 and 35.5; 0.116 and 0.110 kg; and 14.2 and 14.3, respectively. Dry matter and NDF digestibility was higher ($P < 0.05$) for C-SDS (67.6 and 59.5%), while CP digestibility was similar among treatments. Harvesting and feeding oat hay at SDS showed small benefit on nutritive value of forage, but did not improve animal performance.

Key Words: oat variety, maturity stage, ewe lambs

W453 Influence of substitution of alfalfa hay for dried grape pomace on performance and carcass characteristics of growing sheep. Y. Petriz-Celaya*, J. F. Calderon-Cortes, C. Perez, M. F. Montaño, and A. Plascencia, *Instituto de Investigaciones en Ciencias Veterinarias, Universidad Autónoma de Baja California*, *Mexicali 21100, Baja California, México*.

The comparative feeding value of unfermented dried grape pomace (DGP; 1.09 Mcal/kg of DE, 12% CP) was evaluated in an 84-d feeding trial involving 16 individually fed ewe lambs (17.2 kg initial wt). In the experimental diets DGP replaced (DM basis) 0, 10, 20 or 30% of late bloom alfalfa hay. Lambs were allowed ad libitum access to feed and water. Feed intake and orts were recorded daily. Initial and final shrunk weights were obtained following a 12-h withdrawal of feed. The trial analyzed as a randomized block design experiment. Substitution of DGP for alfalfa hay did not affect ($P > 0.10$) ADG, DMI/ADG, hot carcass wt, and dressing %, however DMI was slightly higher with T2 (10%) and T4 (8%) than T1, and ribeye muscle area was 11% greater with T4 than with T1. We conclude that DGP can replace up to 30% of late bloom alfalfa hay in diets for lambs without adversely affecting animal growth and carcass characteristics.

Table 1. Effect of the substitution of alfalfa hay by dried grape pomace on growing sheep performance and carcass characteristics

Grape pomace, %	T1, 0	T2, 10	T3, 20	T4, 30	SEM
Final wt, kg	26.16	26.40	25.32	26.28	0.94
ADG, g	0.11	0.11	0.10	0.11	0.01
DMI, kg/d	1.15a	1.27b	1.12a	1.24b	0.03
DMI/ADG	10.85	11.66	11.63	11.62	0.55
Hot carcass wt, kg	11.5	13.5	12.5	13.3	0.74
Dressing, %	44.17	51.49	49.35	50.75	3.07
Ribeye muscle, cm2	4.09a	3.78a	3.84a	4.53b	0.19

[ab]Means in the same row that do not have a common superscript differ ($P < 0.05$).

Key Words: dried grape pomace, sheep, carcass characteristics

W454 Effect of a basal creep feed diet modification on the preferences in pre-weaning piglets. J. Figueroa*[1], D. Solà-Oriol[1], X. Manteca[1], C. Chetrit[2], and J. F. Pérez[1], [1]*Universitat Autònoma de Barcelona*, *Bellaterra, Barcelona, Spain*, [2]*Bioibérica SA*, *Barcelona, Spain*.

Oronasal and postingestive experience play an important role in creep feeding intake. The aim of the present trial was to study the effect of basal creep feed diet modifications on creep-feed preference in sucking piglets. A total of 80 litters (10-12 piglets/sow) were used in a 6-day double choice-feeding test (DCFT) (22 to 28d-old piglets). The preference for 4 different modified diets was compared with that for a simple diet (CT) by using a DCFT. The CT diet included corn, barley and wheat (54.7%), sweet whey (14.12%), soybean protein concentrate (16.6%) and spray dried porcine plasma (5%). The modified diets included the flavored commercial creep-feed diet (COM) commonly used on the farm, and 3 different modifications of the CT diet, based on the incorporation of garlic flavor (0.075%, GAR) or the replacement of soybean meal by porcine digestible peptides (1.5%, PDP, Palbio 50RD), and of soybean oil by a intestinal porcine fat (T1Fat). Choice feeding test was conducted in the farrowing pens by using two small creep-feeders containing the two diets (side by side). Feeds were offered ad libitum in mash form. Preference was calculated as the percentage contribution of the test diet to the total creep feed intake. Litters showed a total creep feed intake of 476 g/d (SD 267 g/d). Preference values for PDP diet (50.1%) or T1Fat diet (60.0%, $P = 0.074$) were not significantly different from CT. CT diet was significantly preferred to the GAR diet (40.9%, $P < 0.01$) and the current COM diet (36.1%, $P < 0.001$). Our results suggest that the addition of new flavors or ingredients may affect the palatability of piglet′s creep feed diets. Piglets showed a preference for simple diets and neophobia or innate aversion to new flavors.

Key Words: palatability, choice-feeding, creep feed

W455 Nutritional value of Brazilian crude glycerol and semi-purified glycerol on starting pigs diets. I. Moreira*, P. L. de Oliveira Carvalho, L. M. Piano, J. B. Toledo, A. C. Furlan, C. de L. C. Filho, and T. M. P. da Cruz, *Universidade Estadual de Maringá*, *Maringa, Paraná, Brazil*.

One experiment was carried out to determine the nutritional value of four different types of glycerol. Two different types of crude glycerol from soybean oil (CGS), and animal fat + soybean oil (CGA), and two different types of semi-purified glycerol from soybean oil (SPGS), and animal fat + soybean oil (SPGA) were used. Glycerol is the main co-products of biodiesel production (esterification technologies using vegetable oil or animal fat). Gross energy (kcal/kg) of CGS, CGA, SPGS, and SPGA (as-fed basis) were 5,247; 5,242; 3,760; and, 3,217 respectively. A digestibility trial using 56 crossbred barrows with 19.20 ± 1.52 kg of initial body weight was conducted. The trial consisted of a randomized experimental design (4 × 3 factorial scheme) with four different types of glycerol and three levels of glycerol in the diet. Four experimental units (one pig) per diet were used. Glycerol levels used in the digestibility trial were 4%, 8%, and 12% of the basal diet (corn + soybean based) calculated according to NRC (1998). The digestibility coefficient (%) values of four different types of glycerol were: dry matter (CGS = 93.10, CGA = 80.55, SPGS = 95.87, SPGA= 89.44); organic matter (CGS = 90.27, CGA = 89.05, SPGS = 106.87, SPGA = 100.89); gross energy (CGS = 96.60, CGA = 98.11, SPGS = 100.88, SPGA = 100.09); metabolization coefficient of gross energy (CGS = 87.54, CGA = 85.98, SPGS = 89.69, SPGA = 91.15). The digestible (DE) and metabolizable energy (ME) values of glycerol were estimated by regression (Adeola, 2001) of DE and ME intake vs. glycerol intake. The values (as-fed basis) of DE and ME (kcal/kg) obtained were: CGS = 5,070 and 4,593; CGA = 5,143 and 4,507; SPGS = 3,793 and 3,373; SPGA = 3,220 and 2,932, respectively. The results indicate that all types of Brazilian glycerol used in this study are highly available energy source for starting pigs feeding.
Financial support: CNPq (Brazil).

Key Words: co-product, digestibility, glycerine

W456 Prediction of carcass composition in crossbred pigs using the real-time ultrasound: Comparison of the interpreting results. L. L. Lo*, M. E. Tai, and C. C. Tsai, *Chinese Culture University*, *Taipei, 111 Taiwan, ROC*.

Efficient use of the real-time ultrasound to predict carcass composition is important. The objective of the study was to compare the interpreting results of the ultrasound images from the farm and laboratory when predicting backfat thickness and longissimus muscle area of the pigs. Ultrasound images were obtained from 147 three breed (Duroc, Yorkshire, and Landrace) terminal crossbred pigs (71 gilts and 76 barrows) using an Aloka SSD 500 real-time ultrasound. All pigs were raised under commercial farm environment, and slaughter at an average age of 205 days for an average weight of 117 kg. The day prior to slaughter, two transverse images at the tenth rib and the last rib were taken and interpreted from each pig, and the images also were taped to be interpret in the laboratory by a trained operator later on. Carcass backfat thickness and longissimus muscle area at the tenth and the last rib were measured at a commercial slaughter plant using the standard procedure. All data were analyzed using a linear model that included fixed effects of year, herd, sex, and method. Phenotypic correlations between ultrasonic and carcass measured backfat thickness at the tenth and the last rib ranged from 0.828 to 0.849 when interpreting the ultrasound data in the field, and ranged from 0.797 to 0.836 when interpreting that in the laboratory. Ultrasound and carcass measured longissimus muscle area were slightly lower correlated when interpreting the results in the laboratory (r = 0.646-0.719) with that in the field (r = 0.722-0.755). There were no significant differences between the two methods for backfat thickness and longissimus muscle area ($P > 0.10$). When including ultrasound backfat thickness and longissimus muscle area in the regression equation for predicting carcass lean, interpreting results from the farm and laboratory gave the similar accuracies. Therefore, obtaining the real-time ultrasound images from the farm and interpret in the laboratory can be an optimal way in application of the real-time ultrasound technology for swine.

Key Words: interpreter, real-time ultrasound, carcass composition

W457 The effect of type of housing during gestation on gilt farrowing and piglet performance. R. Muns*, J. L. Ruiz de la Torre, E. G. Manzanilla, X. Manteca, and J. Gasa, *SNiBA, Departament Ciència Animal i dels Aliments, Universitat Autònoma de Barcelona*, *Barcelona, Spain*.

The objective was to evaluate the impact of gestation housing on gilt farrowing and piglet performance. Fifty-three gilts from a commercial farm were randomly distributed to one of the following treatments: T1) pen-grouped gestation (10 gilts/pen with an automatic feeding system) or T2) stall-allocated gestation. Back fat (BF) was measured ultrasonically

4 days before and 20 days after farrowing. Farrowing was monitored and the interval from 1st to last piglet born recorded. Piglets were weighted on farrowing day (day 0), day 1, day 2 and day 20 of lactation and rectal temperature (RT) was measured at birth. On day 2, litters were fixed at 12 piglets. Mortality before and after day 2 were registered. Data was analyzed with a one-way ANOVA with type of housing as main effect using SAS program. T1 sows had more BF at the beginning (18.7 vs. 14.6mm ± 3.42; $P < 0.001$) and at the end of lactation (15.0 vs. 12.9mm ± 4.86; $P < 0.003$) together with a shorter farrowing duration (2.5 vs. 3.0h ± 0.93; $P = 0.077$). Piglets initial BW did not differ between groups (mean value of 1.29 ± 0.310kg; $P = 0.485$). T2 piglets had more RT at birth than T1 (38.7 vs. 37.5°C ± 1.34; $P < 0.001$) and had an increased BW gain on day 1 (58.7 vs. 41.6g ± 67.68; $P = 0.059$). T2 gilts weaned more piglets (11.73 vs. 11.37 ± 0.673; $P = 0.020$) with less piglet mortality from day 2 to 20 (0.21 vs. 0.56 piglet/litter ± 0.528; $P = 0.114$). Although T2 gilts had a 30 min. longer farrowing, their piglets were born with higher RT. This fact could help piglets to had a better colostrum intake resulting in higher energy and immunological status which may explain the enhanced surviving at weaning. According to our results, we conclude that for gilts, the transition from a pen-housing gestation to a stall-farrowing allocation may suppose a bigger stress compared to a transition from stall-housing gestation. That stress could have a negative repercussion on offspring body temperature at birth, compromising its colostrum intake.

Key Words: gilts, gestation housing, piglets

W458 Performance of starting pigs fed on crude glycerol in Brazil. I. Moreira*[1], P. L. de Oliveira Carvalho[1], L. M. Piano[1], J. B. Toledo[1], A. G. Gallego[2], and G. Moresco[1], [1]*Universidade Estadual de Maringá*, *Maringa, Paraná, Brazil*, [2]*Universidad Del Tolima*, *Ibagué, Tolima, Colombia*.

This experiment was carried out to investigate the utilization of two types of crude glycerol which were obtained from soybean oil (CGS), and animal fat + soybean oil (CGA) on starting pigs performance. Glycerol is the main co-products of biodiesel production (esterification technologies using vegetable oil or animal fat). In Brazil, the primary feedstock for glycerol production is soybean oil. Chemical composition (as-fed basis): CGS (DM = 97.46%; CP = 0.06%; GE = 5,247 kcal/kg and ash = 4.45%) and CGA (DM = 94.55%; CP = 0.05%; GE = 5,242 kcal/kg and ash = 4.26%). In the performance trial, 90 piglets (BW = 15.18±0.67 to 30.28±1.68 kg) were allotted in a completely randomized design in 2 × 4 factorial scheme, with different levels (3, 6, 9, and 12%) of two types of crude glycerol (CGS and CGA) in the diet. An additional control diet was formulated containing no glycerol (0%). Five pens with two pigs/pen for each treatment resulting in 10 observations per treatment. Experimental diets were formulated according to NRC (1998) as isoprotein and isoenergetic. Performance data of 0, 3, 6, 9, and 12% of CGS were, respectively: ADFI = 1.601, 1.650, 1.602, 1.532, and 1.572 kg; DWG = 0.889, 0.937, 0.901, 0.851, and 0.850 kg; F: G ratio: 1.81, 1.75, 1.78, 1.80, and 1.854, and, in the same way, performance data of CGA were, respectively: DFI = 1.601, 1.599, 1.645, 1.546, and 1.646 kg; DWG = 0.889, 0.851, 0.934, 0.855, and 0.929 kg; F: G ratio: 1.81, 1.88, 1.76, 1.82, and 1.77. There were no interaction among levels of CG and types of crude glycerol, and the regression analysis indicates no effects ($P \geq 0.05$) of crude glycerol inclusion on piglet performance (DFI, DWG and F: G ratio). The results suggest that it is feasible to use up to 12% of both sources of CG on starting piglet diet, without impairing performance.
Financial support: CNPq (Brazil).

Key Words: biodiesel, co-product, glycerine

W459 Fatty acid profile in different tissues of newborn piglets. M. Sini, M. G. Manca, A. Nudda, and G. Battacone*, *Dipartimento di Scienze Zootecniche, University of Sassari*, *Sassari, Italy*.

Objective of the present study was to investigate fatty acid deposition in different tissues of newborn piglets and its relationship with fatty acid composition of diet of gestating sows. Six Landrace × Large White sows in second or third parity were bred with semen from a Landrace boar. During gestation, sows were individually housed in crates and fed a concentrate for gestating sows and gilts administered according to feed requirements during periods of fetal development. Immediately after parturition, one piglet per litter was stunned, exsanguinated and dissected. Brain, liver, hearth, thigh muscle of piglets and sows were weighed and samples were taken for fatty acid profile. Content of each fatty acid in organs and feed was expressed as a percentage of total FAME. Data were analyzed with one-way ANOVA using tissue as the main effect. The fatty acid profile was significantly different between tissues. Particularly, the highest content of PUFA n-3 was observed in brain (8.68 g/100 g of FAME) . This result is probably due to the higher concentration of DHA (8.49 g/100 g of FAME) that actually represents 97% of total n-3 FA in the brain. The content of DHA is high also in liver where it represents about 85% of total n-3 fatty acid. The content of PUFA n-6 was higher in hearth (29.16 g/100 g of FAME) than other tissues, maybe due to the higher content of linoleic and arachidonic acid (13.13 and 15.24 g/100 g of FAME, respectively). High values of arachidonic acid were also observed in brain where it is about 93% of total n-6 fatty acid. The concentration of unsaturated fatty acid was higher in hearth where they account for 2/3 of total fatty acid, while saturated fatty acid were higher in brain and muscle (48.41 and 47.54 g/100g of FAME, respectively). The research highlighted differences in long chain fatty acid composition between tissues of newborn piglets, especially for FA synthesized ex-novo.

Key Words: fatty acid, piglets, tissues

W460 Effect of terminal sire genotype and gender on growth performance and carcass traits of European-Chinese pigs. J. Viguera[1], M. Sánchez*[1], S. Garrido[1], J. Peinado[1], F. Flamarique[2], and L. Alfonso[3], [1]*Imasde Agroalimentaria S.L.*, *Madrid, Spain*, [2]*Grupo AN*, *Navarra, Spain*, [3]*Universidad Pública de Navarra*, *Navarra, Spain*.

A total of 168 pigs (half castrated male and half female) of 25.4 ± 4.1 kg of initial BW from Youna crossbreds sows (Gene +, France) was used to evaluate the effect of two terminal sire genotypes (MUS vs. PIE) on performance and carcass traits. There were fourteen replicates of six pigs per treatment. Data were analyzed as a completely randomized design by GLM of SAS. The model included the terminal sire genotype and sex as main effects. All pigs were reared under similar environmental and nutritional conditions, and were slaughtered at 102.3 ± 8.65 kg BW. MUS pigs grew faster than PIE pigs (782 vs. 711 g/d; $P < 0.01$). No significant differences in feed intake were detected. Therefore, MUS pigs showed lower feed conversion than PIE pigs (2.81 vs. 3.07 g feed/g gain; $P < 0.01$). MUS pigs showed longer carcasses and hams than PIE pigs (80.9 vs. 78.7 cm and 50.6 vs. 49.5 cm, respectively; $P < 0.01$). However, PIE pigs showed higher shape factor (1.46 vs. 1.43; $P < 0.01$) and had greater carcass yield (77.8 vs. 77.1%; P = 0.04), ham yield (27.8 vs. 27.1%; $P < 0.01$), and loin yield (7.40 vs. 6.91%; $P < 0.01$) than MUS pigs. Castrated males grew faster (777 vs. 716 g/d; $P = 0.02$) and ate more feed (2.30 vs. 2.08 kg/d; $P<0.01$) than females. Likewise, castrated males had more backfat and fat thickness at Gluteus medius muscle (21.2 vs. 18.1 mm and 17.3 vs. 13.4 mm, respectively; $P < 0.01$) but lower ham yield (27.0 vs. 27.8%; $P < 0.01$) and loin yield (6.79 vs. 7.52%; $P < 0.01$) than females. Results showed that Youna

crossbreds with MUS pigs perform better but have lower primal cut yields than Youna crossbreds with PIE pigs.

Key Words: European-Chinese pigs, growth performance, carcass traits

W461 The effect of aeration on the slurry quality and microbial communities in liquid swine manure during the digestion. M. Heo*[1,2], K. H. Park[2], D. Y. Choi[2], H. S. Kang[2], and S. Oh[1], [1]*Division of Animal Science, Chonnam National University*, *Gwangju, South Korea*, [2]*Animal Environment & Systems Division, National Institute of Animal Science R.D.A.*, *Suwon, South Korea*.

Liquid swine manure can be converted to a liquid fertilizer by aeration. We examined the temporal changes in the microbial community and associated characteristics that occurred by aeration during the digestion. Liquid swine manure, collected from the swine barns of the National Institute of Animal Science (NIAS), was subjected to 2 treatments: one in which the manure was not aerated (the control sample) and the other in which the manure was aerated continuously at a rate of 3.0 $m^3 \bullet h^{-1} \bullet t^{-1}$ (the aerated sample). The study was conducted in an outdoor research field at NIAS for 20 weeks (May to September). In the aerated sample, the concentration of volatilized NO_3 decreased from the 6th week, with a concomitant steep increase in the NH_4^+-N and NO_3^--N concentrations. The pH increased for the first 4 weeks and then decreased, and the decline was sharp in the 6th week. In the control sample, the concentration of volatilized NH3 continuously increased from the beginning, and the NH_4^+-N concentration slowly decreased. Nitrate was barley detected, and the pH was stable. There was a decrease in the number of bacteria, including Lactic acid bacteria, *Actinomyces*, coliformic bacteria, and *Salmonella*, and in the number of fungi; *Salmonella* could not be detected from the 18th week. *Bacillus* sp., *Acinetobacter* sp., *Pseudomonas* sp. (*Pseudomonas putida*), *Alcaligenes* sp., *Sphingobacterium* sp., *Brevundimonas diminuta*, and *Aeromonas hydrophila* were found in the aerated sample, but not in the control. In the aerated sample, *Bacillus* sp. were predominantly found in the 1st week; *Bacillus cereus* and *Baciilus pumilus*, in the 5th week; and *Bacillus cereus* and *Bacillus subtilis*, in the 6th week. This indicates that aeration promotes the growth of bacteria that are effective in reducing ammonia, and that *Bacillus* sp. are the most effective. Further research on the optimal cultivation conditions for the identified bacteria species would help in increasing the application of liquid fertilizers prepared from liquid swine manure.

Key Words: slurry, swine manure, microbila community

W462 Growth performance of pigs finished on brewers-grade rice. O. J. Gekara* and T. V. Dunbar, *University of Arkansas at Pine Bluff*, *Pine Bluff*.

The objective of this study was to determine whether brewers-grade rice can replace corn or milo in finishing pig diets without compromising animal performance. Seventeen finishing pigs of Yorkshire × Duroc breeding were randomly assigned to either brewers-grade rice/soybean meal mixture (RSB) or corn/milo based control (CON). The pigs were 157 days old at the start of the experiment and weighed 87.9±3.4 kg. The experiment lasted 28 days and finished pigs weighed 119.0±3.2 kg. Variables determined included ADG, ADFI, F:G ratio, apparent DM digestibility, and back fat thickness. There was no ($P > 0.10$) treatment × sex interaction for all variables measured. Compared to CON pigs, RSB pigs gained faster (1.26 vs. 0.95 kg/d), had better F:G ratio (0.38 vs. 0.29), higher apparent DM digestibility (91.0 vs. 74.0%), and lower ($P < 0.001$) cost of gain (0.98 vs. 1.62 $/kg gain). Back fat thickness for the two layers, 1 and 2, was similar ($P > 0.10$) for both groups (11.6 vs. 22.7 mm, respectively). Results of this study suggest that brewers-grade rice can be a suitable alternative to corn or milo for finishing pigs with no adverse effects animal performance. In conclusion, hog producers in the Mississippi Delta (southeast Arkansas) where rice is abundant and relatively cheaper than corn or milo may derive substantial savings on feed costs with the use of brewers-grade rice as an energy source. However, more research is needed to determine the effect of growth performance on grade and carcass quality.

Key Words: brewers-grade rice, finishing pigs, pig performance

W463 Differential expression of porcine sperm microRNAs and their association with sperm morphology and motility. E. Curry*[1], T. J. Safranski[2], and S. L. Pratt[1], [1]*Clemson University*, *Clemson, SC,* [2]*University of Missouri*, *Columbia*.

Although miRNAs have been shown to alter translation in nearly every biological process examined to date, little is known as to the identity of miRNA in porcine gametes or their potential involvement in reproductive processes. Recent investigations have demonstrated that the miRNA synthesis pathway is necessary for differentiation of mature sperm in mice; however, the specific miRNAs responsible for spermatogenesis have not been identified. The objective of this study was to determine the identities and compare the expression levels of miRNAs in control porcine sperm samples which exhibited >75% motility and <15% poor morphology (C; n= 7), samples with >15% abnormal morphology (AB; n= 7), and samples exhibiting <68% motility (LM; n= 8). qRT-PCR was performed in quadruplicate on 10 ng sperm RNA using the mirVana qRT-PCR miRNA Detection Kit (Ambion, Austin, TX) to compare expression levels of 10 specific miRNAs that are predicted to target genes that code for proteins involved in spermatogenesis, sperm structure, motility, or metabolism. Statistical analysis was performed using REST-2005 software with significance at $P < 0.05$. Results showed increases in the expression of four miRNAs, let-7a, −7d, −7e, and miR-22, in the AB group while miR-15b was decreased compared to C ($P < 0.05$). Two miRNAs, let-7d and let-7e, were increased in the LM group when compared to C ($P < 0.05$). Although the precise role of miRNA in sperm remains to be determined, their presence alone denotes an essential biological function. It is feasible that they are remnants of spermatogenic processes, stored for a later role in fertilization, or are delivered to the oocyte to influence early embryonic development. While there is no single cause of male infertility, the identification of miRNAs associated with sperm motility, structural integrity, or metabolism could lead to the development of a microarray or real time-based diagnostic assay to provide an assessment of male fertility status.

Key Words: microRNA, sperm, porcine

W464 Prediction of carcass composition in crossbred pigs using the real-time ultrasound: Choices of probing and measuring sites. L. L. Lo*[1], C. C. Tsai[1], M. E. Tai[1], R. S. Lin[2], and T. H. Huang[3], [1]*Chinese Culture University*, *55 Hwa-Kang Road, Taipei, Taiwan, ROC*,[2]*National ILan University*, *ILan, Taiwan, 260 ROC*, [3]*Taiwan Farm Industry Co., Ltd.*, *Pingtung, 900 Taiwan, ROC*.

Development of an optimum method for predicting carcass composition is essential for improving pig carcass performance. Real-time ultrasound data of backfat thickness, and longissimus muscle area were obtained from 147 three breed (Duroc, Yorkshire, and Landrace) terminal crossbred pigs (71 gilts and 76 barrows) using an Aloka SSD 500 real-time ultrasound machine to find the optimum probing and measuring sites between ultrasound measurements at the tenth and the last ribs for predicting carcass composition. All pigs were raised under

the commercial farm environment, and slaughter at an average age of 205 days for an average weight of 117 kg. The day prior to slaughter, two transverse images were taken at the tenth rib and the last rib from each pig. The backfat at two points, 1/2 and 3/4 the lateral length of the loin muscle perpendicular to the skin surface were measured. The correlation between ultrasonic and carcass measured fat thickness at the last rib were similar to those of the tenth rib at 1/2 and 3/4 point locations (r = 0.828-0.859). Ultrasonic and carcass measured longissimus muscle area was slightly higher correlated at the 10th rib compared with that of last rib. The best correlations between carcass lean percentage and ultrasound measurements were obtained with 3/4 point fat thickness at the tenth rib (r = −0.45) and with longissimus muscle area at the last rib (r = 0.47). When predicting carcass lean yield, the regression equation included the tenth rib ultrasound backfat measured at 3/4 point location and the tenth rib longissimus muscle area, gave the highest accuracy (R^2 = 0.892). Results from this study indicated that the tenth rib site and 3/4 point of the lateral length of the loin muscle can serve as the probing and measuring sites for prediction of carcass lean yield.

Key Words: ultrasound, carcass composition, pig

W465 Association between lactation feed intake and wean to service interval of sows. L. Anil*[1], S. S. Anil[2], and S. K. Baidoo[1], [1]*Southern Research and Outreach Center, University of Minnesota*, *Waseca,* [2]*Veterinary Population Medicine, University of Minnesota*, *St Paul.*

Previous studies have indicated the effect of inadequate lactation feed intake on subsequent reproductive performance of sows in breeding herds. However, most of them have used average feed consumption during the entire lactation, ignoring the effect of stage of lactation. The number of days of inadequate feed intake could be a better indicator of inadequate lactation feed intake. Factors such as parity, body condition of the sow at the end of gestation and litter size influence the quantity of feed consumed during lactation. The objective of the present study was to determine the association of number of days of <3 kg of feed consumption during the first 14 days of lactation with wean to service interval (WSI), accounting for the effects of parity and body condition of the sow prior to farrowing. This study involved 504 sows (289 sows housed in pens with electronic sow feeders and 215 sows in gestation stalls). Data with 990 parities of these sows with one or two farrowings, collected from the PigCHAMP database of the research unit were used for the analysis (Poisson regression, Proc genmod, SAS v 9.1). The average lactation feed intake and average WSI in the database were 6.0 kg and 7 days respectively. The number of days of 0 kg feed consumption increased by 4% ($P < 0.05$) with every day increase in WSI suggesting the negative relationship between daily lactation feed intake and WSI. The number of days of <0.5, <1.0, <1.5, <2.0, <2.5 and <3.0 kg of feed consumption within the first 14 days of lactation increased by 4.0, 3.1, 1.7, 1.9, 1.6 and 0.8% respectively ($P < 0.05$ all) for every day increase in WSI. This study confirms the negative relationship between lactation feed intake and WSI and indicates the need to ensure adequate lactation feed intake on all days during early lactation to prevent prolongation of wean to service interval.

Key Words: lactation feed intake, wean-to- service interval, sows

W466 Effect of terminal sire genotype and gender on growth performance and carcass traits of European-Chinese pigs destined to the dry-cured industry. M. Sánchez*[1], J. Viguera[1], C. Carrasco[1], J. Peinado[1], F. Flamarique[2], and L. Alfonso[3], [1]*Imasde Agroalimentaria S.L.*, *Madrid, Spain*, [2]*Grupo AN*, *Navarra, Spain*, [3]*Universidad Pública de Navarra*, *Navarra, Spain*.

A total of 160 pigs (half castrated male and half female) of 23.7 ± 5.0 kg of initial BW from Youna crossbreds sows (Gene+, France) was used to evaluate the effect of Duroc boar terminal sire (T line, fatter vs. P line, leaner) on performance and carcass and meat quality traits. There were eight replicates of ten pigs per treatment. All pigs received a common diet based on cereals and soybean meal ad libitum, and were slaughtered at the same age (177 d of age) with 116.5 ± 10.4 kg of final BW. Data were analyzed as a completely randomized design by GLM of SAS. The model included the boar terminal sire and sex as main effects. The slaughter weight was used as a covariate for carcass quality traits. Pigs from P sire line had lower feed conversion (2.85 vs. 2.98 g feed/g gain; $P < 0.05$) than pigs from T sire line. Ham yield tended to be higher in the P line pigs (26.73 vs. 26.46%; $P = 0.07$). However, no significant differences between P and T sire line pigs were found for backfat. Also, loins from T line pigs had higher redness value than those from P line pigs (4.16 vs. 3.52; $P = 0.04$), but no significant differences were observed between genotypes for lightness and yellowness of loin. Castrated males ate more feed (2.63 vs. 2.36 kg/d; $P < 0.01$), showed higher feed conversion (3.05 vs. 2.78 g feed/g gain; $P < 0.01$) and fatter carcasses (21.3 vs. 18.7 mm; $P < 0.01$) than females. Besides, females had higher carcass yield (76.19 vs. 75.35%; $P < 0.01$), ham yield (26.82 vs. 26.36%; $P < 0.01$), and loin yield than castrated males (7.98 vs. 7.99%; $P < 0.01$). It is concluded that Youna crossbreds with P sire line pigs perform better than T sire line pigs. However, no major differences were found between the male sire lines on carcass and meat quality traits of European-Chinese pigs destined to dry-cured product industry.

Key Words: European-Chinese pigs, pig performance, carcass quality

W467 Effect of hyperprolific Chinese sow genetic on sow performance. J. Viguera[1], M. Sánchez*[1], J. Sánchez[1], P. Medel[1], F. Flamarique[2], and L. Alfonso[3], [1]*Imasde Agroalimentaria S.L.*, *Madrid, Spain*, [2]*Grupo AN*, *Navarra, Spain*, [3]*Universidad Pública de Navarra*, *Navarra, Spain*.

A total of 58 primiparous sows was used to evaluate the effect of two hyperprolific Chinese genetics (Taizumu vs.Youli) on sow performance. All sows received ad libitum a common liquid diet from mating until weaning of piglets. Observations included body weight and fat depth at P2 at mating and every 4 weeks until weaning, feed intake during lactation, number of piglets born alive and weaned per sow and weight of litter at birth after cross-fostering and at weaning. Data were analyzed as a completely randomized design by GLM of SAS. At farrowing, Youli sows were heavier than Taizumu sows (88.8 vs. 81.2 kg; $P = 0.07$), a near significant trend. No other differences were detected on body weight or backfat during the experiment. Taizumu sows had a higher number of piglets born alive (13.84 vs. 10.87 piglets; $P < 0.01$), but with smaller body weight (1.24 vs. 1.41 kg; $P = 0.02$) and less uniformity (79.41 vs. 81.75%; $P = 0.02$) than Youli sows. However, Youli sows weaned a higher number (10.35 vs. 9.62 piglets; $P < 0.01$) of heavier piglets (7.22 vs. 6.71 kg; $P = 0.01$) than Taizumu sows. Moreover, Youli sows ate more feed (289.6 vs. 272.2 g/d; $P = 0.04$) than Taizumu sows during lactation. Under our experimental conditions it can be concluded that Youli sows had higher number of piglets born alive, but Taizumu sows weaned a higher number of heavier piglets.

Key Words: hyperprolific Chinese sows, piglet performance

W468 Influence of crowding stress during the nursery period on growth performance of gilts and barrows. J. H. Cho*, H. J. Mon-

egue, M. D. Lindemann, and G. L. Cromwell, *University of Kentucky*, *Lexington*.

Stocking density and/or floor space allowance can influence pig performance and, consequently, profitability. The objective of this study was to determine the effects of stocking density and floor space allowance during the nursery period on growth performance of gilts compared to barrows. Gilts were then retained to examine continuing effects on growth with the intent of following them through reproduction. During a 6-wk crowding period, a total of 240 pigs (120 gilts and 120 barrows; mean age of 21 d; 6.8 ± 1.0 kg BW) were allotted to 3 space allowances (SA) in a 2 × 3 arrangement (sex [gilts vs barrows] and SA [SA1, 6 pigs in a full pen: 1.22 × 2.44 m^2, 0.50 m^2/pig; SA2, 12 pigs in a full pen: 0.25 m^2/pig; SA3, 6 pigs in a half pen: 1.22 × 1.22 m^2, 0.25 m^2/pig)]. Feeder space and water nipple availability was identical for each pig in all treatments; diets were nutritionally adequate (NRC, 1998). During the grow-finish period, gilts had adequate floor space (6 pigs in a pen; 0.93m^2/pig). For the 6-wk nursery period, crowding reduced ADG ($P < 0.01$) in gilts (577, 536, and 558 g/d for SA1, SA2, and SA3, respectively) and barrows (578, 539, and 527 g/d). While ADFI and F/G were not affected by stocking density or SA, there was a much larger change in ADFI among treatments (gilts: 907, 845, 884; barrows: 916, 891, 858 g/d) than there was in F/G. (gilts: 1.57, 1.58, 1.58; barrows: 1.58, 1.65, 1.63). There was no sex by SA interaction on performance measures. During the grow-finish period, when gilts were housed at the same density in pens with the same space, there were no differences ($P > 0.10$) in ADG (890, 864, and 891 g/d), ADFI (2,677, 2,559, and 2,636 g/d), or F/G (3.01, 2.96, and 2.96) based on previous nursery housing treatment. These results demonstrated that crowding stress during the nursery period negatively affected growth performance of both gilts and barrows during that period of stress, but a continued effect of that stress was not manifested in gilts when subsequently housed in adequate space during the grow-finish period.

Key Words: nursery pigs, crowding stress

W469 Feed intake of gilts following intracerebroventicular injection of the novel hypothalamic RFamide (RFa) neuropeptide, 26RFa. C. J. Rogers*[1], N. L. Heidorn[1], C. R. Barb[2], G. J. Hausman[2], M. J. Azain[1], R. Rekaya[1], and C. A. Lents[1], [1]*University of Georgia*, *Athens,* [2]*USDA-ARS Richard B. Russell Agriculture Research Center*, *Athens, GA*.

RFamide (RFa) peptides have been implicated in a broad spectrum of biological processes including energy expenditure and feed intake. 26RFa is a recently discovered hypothalamic neuropeptide that altered the release of pituitary hormones and stimulated feed intake via a NPY-specific mechanism in rats. Voluntary food intake in the pig is regulated by changes in NPY, and we speculate that 26RFa is involved in the process. Thus, we tested the hypothesis that 26RFa stimulates food intake in the domestic pig. Prepuberal gilts (73 ± 17 kg BW) were fitted with intracerebroventricular (i.c.v.) cannulas and housed in individual pens. Pigs were allowed ad libitum access to feed for 7 d prior to treatment to establish a base line for voluntary feed intake. On the day of the experiment, feeders were removed from all pens at 0900 h. Beginning at 1100 h, gilts received i.c.v injection of either 10 (n = 8), 50 (n = 7) or 100 μg (n = 7) of 26RFa in 0.9% saline. Control animals received either 100 μg of NPY (n = 5) or 0.9% saline alone (saline; n = 5). Feeders were placed in all pens immediately after the last i.c.v. injection (1200 h) and cumulative intake was determined at 4, 8 and 24 h. Treatment had no effect on feed intake at 4 h. Feed intake of saline treated gilts at 8 h was not different when compared with 26RFa treated animals. However, NPY treated pigs ate more at 8 h (1.64 ± 0.20 kg) than saline treated pigs (1.07 ± 0.20 kg; $P < 0.05$) or pig receiving either 10 μg (0.90 ± 0.16 kg; $P < 0.01$) or 50 μg (1.13 ± 0.16 kg; $P < 0.06$) of 26RFa. Feed intake at 8 h of pigs treated with 100 μg (1.27 ± 0.17 kg) of 26RFa was not different from either NPY or saline treated animals. There were no differences between treatments in feed intake at 24 h. We conclude that 26RFa is not an orexigenic neuropeptide in the pig. Further study is needed to determine the effects of i.c.v. injection of 26RFa on hormone release from the anterior pituitary gland of the gilt.

Key Words: feed intake, 26RFa, hypothalamus

W470 Increasing productivity and disease control on swine farms trough management tools: A field study. G. Rocha-Chavez*[1], J. Castañeda[2], A. Sepulveda[1], J. G. Michel-Parra[1], M. A. Pinto[2], O. Montañez[1], A. Martínez[1], and J. M. Tapia- Gonzalez[1], [1]*Universidad de Guadalajara*, *Cd Guzman, Jalisco, Mexico*, [2]*Private Practice*, *Tamazula, Jalisco, Mexico*.

Current swine production systems use genetic and other technological tools to increase effectivity and profitability, however, emergent and old diseases are always devastating potential capacity of swine business. The present paper discuss a field study that combine a series of management tools that increased competitiveness in a porcine farm. Although this model has been implemented in different swine production systems, we describe the field experience of a small farm located at the southern part of Jalisco state in Mexico. A Farrow-to-finish 200-sow farm was selected for the present study. The farm was PRRS and PCV positive with glasser disease and mycoplasm persistent outbreaks. A very low feed efficiency and kg/sold/sow/year was present at the farm before intervention as well as high production costs (see table for more parameters). The following tools were implemented for 2 years: (1) Closed herd: the genetic progress was achieved by means of artificial insemination with no live animal introduction whatsoever. (2) Close monitoring of reproduction management: Heat detection and insemination was priority number one on morning chores. (3) Autovaccination program: A professional and well controlled autogenous vaccination program was implemented using exclusively row material from the farm. (4) Employers management program: an incentive-based program was implemented on the premise of happy workers are efficient partners.

Table 1. Production parameters at a pig farm before or after implementing selected management tools

Production parameter	Before	After
Wean to finish mortality, %	7.3 [a]	1.9 [b]
Farrowing rate, %	78.3 [a]	87.7 [b]
Feed efficiency, (feed to gain ratio)	3.7 [a]	2.8 [b]
Veterinary Services/Medicine per Cwt, US$	9.27	6.32
Total Cost per Cwt of Pork Produced, $	164.00 [a]	117.00 [b]

Different letters in the same line are statistically different, $P < 0.05$).

Key Words: swine, profitability, management tools

Wednesday, July 14, 2010

SYMPOSIA AND ORAL PRESENTATIONS

Animal Health: Respiratory Health, Viruses

767 Newly received feedlot heifers managed with three respiratory disease protocols. J. L. Wahrmund*[1], D. B. Burken[1], B. K. Wilson[1], S. J. Terrill[1], D. L. Step[2], C. R. Krehbiel[1], C. L. Goad[3], and C. J. Richards[1], [1]*Oklahoma State University, Department of Animal Science*, *Stillwater,* [2]*Oklahoma State University, Department of Veterinary Clinical Sciences*, *Stillwater,* [3]*Oklahoma State University, Department of Statistics*, *Stillwater*.

Commingled heifers were purchased and administered ruminal temperature monitoring devices in LA (n = 180, BW = 248.7 ± 35.7 kg) and KY (n = 162, BW = 243.9 ± 21.4 kg). Within purchase group, heifers were allotted to 12 pens for 56 d. Pens were assigned to 3 bovine respiratory disease (BRD) management treatments with pulls based on: visual signs (CON, n = 110), visual signs and(or) elevated ruminal temperature (TEMP, n = 116), or visual signs after metaphylactic tulathromycin treatment (MET, n = 116). Antimicrobial treatments for BRD included tulathromycin, fluoroquinolone, and ceftiofur-HCl. Effects of management and number of BRD treatments required were analyzed using the MIXED procedure of SAS. Heifers on CON, TEMP, and MET treatments were treated 0.55, 1.47, and 1.27 times for BRD, respectively. Final BW of TEMP heifers was 5.3 kg greater ($P < 0.05$) than CON, and MET heifers gained 0.12 kg/d more than CON heifers ($P < 0.05$). Interactions of management × number of BRD treatments required were observed ($P < 0.05$) for final BW and overall ADG. Final BW of CON heifers requiring one or 2 BRD treatments were 12.9 kg and 38.6 kg less ($P < 0.05$), respectively, than those never treated. Final BW of MET heifers requiring no additional BRD treatment were 18.9 kg greater ($P < 0.05$) than those requiring 3 treatments. Final BW of TEMP heifers receiving 2 or less treatments were not different ($P > 0.05$); however, BW of those treated 3 times was 15.1 kg less ($P < 0.05$) than those treated once. CON heifers requiring zero or one treatment gained 0.58 kg/d more ($P < 0.05$) than heifers requiring 2. MET heifers receiving no additional treatments gained 0.23 kg/d more ($P < 0.05$) than those receiving 3. TEMP heifers treated once or twice gained 0.46 kg/d more ($P < 0.05$) than heifers treated 3 times. Of heifers treated once for BRD, MET heifers gained 0.16 kg/d more ($P < 0.05$) than CON heifers. Of heifers treated twice, MET and TEMP heifers gained 0.64 kg/d more ($P < 0.05$) than CON. Management did not affect ($P > 0.05$) ADG of heifers treated 3 times. Ruminal temperature monitoring and metaphylactic antimicrobial treatment have positive effects on feedlot health and performance.

Key Words: disease, performance, temperature

768 Muscle gene expression in an acute model of bovine respiratory disease. R. L. Mills*, L. Carlos-Valdez, L. O. Burciaga-Robles, D. Stein, D. L. Step, R. W. Fulton, U. DeSilva, and C. R. Krehbiel, *Oklahoma State University*, *Stillwater*.

Bovine respiratory disease (BRD) has been shown to negatively impact carcass characteristics by leading to lighter carcasses, decreased *longissimus dorsi* (LD) area, and poorer carcass quality. To understand the effects of BRD on muscle gene expression, 8 beef steers (284 ± 37.4 kg) were exposed to 2 calves persistently infected with bovine viral diarrhea virus type 1b (BVDV) for 72h followed by intratracheal inoculation with *Mannheimia hemolytica* (MH). Muscle biopsies were taken from the LD before exposure to pathogens (PRE) and 24 h (24H) following inoculation. Total RNA was extracted, reverse transcribed, and expression levels analyzed using quantitative PCR. Glutamine synthetase (GS) was induced (+8.12, $P < 0.001$) and regulatory factor X-associated ankyrin-containing protein (RFXANK) and a homolog of tropomyosin 4 (TPM4) tended to be upregulated (+2.61 and +1.48, respectively; $P < 0.10$) in the 24H group. Glutamine synthetase induction is a hallmark of muscle deterioration. RFXANK is a regulatory protein known to bind major histocompatibilty complex class II (MHCII) promoters inducing MHCII expression involved in antigen presentation. Tropomyosin 4 is an actin-binding protein shown to affect muscle contraction in striated and smooth muscle tissue in humans. Results indicate that muscle proteolysis is occurring based on GS expression. MHCII may be upregulated in muscle histiocytes as demonstrated by increased levels of RFXANK transcripts. Glutamine status has been shown to affect immune status; therefore, the induction of these 2 proteins may be indicative of cooperation between macrophages and myofibers. These results suggest that cattle challenged with BRD pathogens may experience acute cachexia within 24h post-infection with BVDV and MH. Such myopathy may partially explain lighter carcass weights associated with cattle treated for BRD.

Key Words: beef cattle, bovine respiratory disease, skeletal muscle

769 Bovine respiratory disease related metabolic fingerprints in beef steers. S. J. Terrill*, R. D. Madden, J. W. Dillwith, L. O. Burciaga-Robles, D. L. Step, R. W. Fulton, A. W. Confer, M. Montelongo, and C. R. Krehbiel, *Oklahoma State University*, *Stillwater*.

Bovine respiratory disease (BRD) is the most costly disease in North American feedlots; however, diagnosis is subjective. Metabolomics, or the study of the total metabolic profile of a biological tissue or fluid, may provide a way for objective diagnosis. The objective was to identify biomarkers of BRD using metabolomic techniques (i.e., GC/MS). Twenty-four Angus crossbred steers were divided into 4 treatment groups in a completely randomized design (n = 6). Treatments were: 1) exposure to 2 BVDV persistently infected (PI) steers for 72 h (BVDV); 2) exposure to the 2 PI-BVDV steers for 72 h and intratracheal challenge with *Mannheimia hemolytica* on d 0 (BVDV+MH); 3) intratracheal challenge with *M. hemolytica* on d 0 (MH); and 4) no challenge (CTRL). Blood samples were collected at −72, 12, 24, and 48 h of *M. hemolytica* challenge. Using a GC/MS platform, total metabolic fingerprints of plasma were obtained. Normalized abundance values were analyzed and means separated using Tukey's procedure (GeneSpring MS 1.2; Agilent Technologies, Santa Clara, CA), and metabolites were identified using the NIST '05 MS Database (NIST, Gaithersburg, MD). At 12 h after infection, glutamic acid was lower ($P = 0.003$) across all treatments compared with CTRL, whereas threonic acid was greater ($P = 0.04$). Citric acid was greater ($P < 0.001$) in BVDV+MH and BVDV steers compared with CTRL. BVDV+MH steers had greater ($P = 0.003$) levels of isoleucine than CTRL, but the MH treatment had lower ($P = 0.003$)

isoleucine. At 48 h after infection, valine and leucine were lower ($P < 0.01$) in BVDV+MH cattle compared with CTRL, but greater ($P < 0.01$) in BVDV steers. Phenylalanine was lower (P 0.006) in both BVDV+MH and MH steers compared with CTRL, but was greater ($P = 0.006$) in BVDV steers. Glycine was lower ($P = 0.02$) in both BVDV+MH and BVDV treatments. There were no significant changes detected at 24 h after infection. Results suggest significant changes in AA profiles at 12 and 48 h after BVDV exposure and *M. hemolytica* infection. GC/MS metabolic fingerprinting is a promising technique that may provide for better diagnosis and identification of BRD.

Key Words: amino acids, bovine respiratory disease, metabolomics

770 Evaluating timing of weaning stress on response to BVD2 vaccinations in Angus calves. E. D. Downey*[1], E. C. Conrad[1], J. F. Ridpath[2], R. G. Tait Jr.[1], and J. M. Reecy[1], [1]*Iowa State University*, *Ames,* [2]*National Animal Disease Center/ARS/USDA*, *Ames, IA*.

This study was designed to evaluate the impact of environmental factors and genetic controls on response to vaccination against bovine viral diarrhea virus type 2 (BVDV2) in Purebred American Angus beef cattle. This study utilized 362 Angus calves born in the spring (n = 211) and fall (n = 151) of 2007. Two doses of modified live Bovishield Gold-5 (initial and booster) were administered 3 weeks apart. The herd was managed with 2 calving seasons, fall and spring. Calves, from each season, were allotted to one of 2 weaning/vaccination management protocols based on dam management group. In protocol 1, calves were weaned at initial vaccination. In protocol 2, calves were weaned at the time of booster vaccination. Viral neutralizations were conducted using cytopathic BVDV2 to determine antibody titer at initial vaccination, at booster vaccination, and 3 weeks post booster vaccination. Titer levels at initial vaccination were significantly influenced by calf age ($P < 0.001$), calving season ($P < 0.001$), and gender ($P < 0.05$). There was no significant difference ($P = 0.219$) in the initial titer level between the 2 protocol groups. Response to initial vaccination was calculated by finding the difference between the booster titer score and the initial titer score; response to booster vaccination was the difference between the titer score 3 weeks post booster injection and at booster injection. The overall response was calculated as the titer score 3 weeks post booster injection minus initial titer score. Response to initial vaccination, response to booster vaccination and overall response were significantly ($P < 0.001$) affected by the titer level at the beginning of the specified response period. All 3 response variables were significantly ($P < 0.05$) different across the 2 weaning protocol. The interaction between weaning protocol and the respective titer level was significant ($P < 0.05$) or suggestive ($P < 0.10$) of an effect on all 3 response variables. Based on this preliminary data, management of weaning/vaccination stress in conjunction with titer level at initial vaccination can affect the antibody response developed in Angus calves.

Key Words: beef cattle, vaccination, weaning

771 Alterations in the somatotropic axis during an infectious bovine rhinotracheitis viral (IBRV) challenge in beef steers. S. M. Falkenberg*[1], T. B. Schmidt[1], D. H. Keisler[2], J. L. Sartin[4], J. O. Buntyn[1], and J. A. Carroll[3], [1]*Mississippi State University*, *Mississippi State*, [2]*University of Missouri*, *Columbia*, [3]*Livestock Issues Research Unit, USDA-ARS*, *Lubbock, TX*, [4]*Auburn University College of Veterinary Medicine*, *Auburn, AL*.

The objective of this trial was to identify the cytokine response following IBRV exposure and the impact on the somatotropic axis, 12 steers (228.82 ± 22.15 kg) were randomly assigned to a Control (CON) or an IBRV challenged group. Prior to the challenge steers were fitted with an indwelling rectal probe and a blood sample was obtained. On d 0, IBRV steers received an intra-nasal dose of IBRV (2 mL/nostril; Cooper strain, 1×10^7 PFU/mL) and CON steers received an intra-nasal dose of saline (2 mL/nostril). IBRV steers were placed in a paddock isolated from the CON cattle as well as all other cattle on the research farm. The first 48 h post-challenge, blood was collected via single jugular venipuncture. At 72 h post-challenge steers were fitted with indwelling jugular catheters, and then moved to individual stanchions. Blood samples were intensively collected on d 4–8 post-challenge. IBRV steers had elevated rectal temperatures as compared with CON steers ($P < 0.05$) starting on d 2, peaking on d 4 (40.8 ± 0.54 vs. 39.5 ± 0.54°C), and returning to baseline on d 6. The response patterns for cortisol (CORT), interferon-γ (IFN-γ), and growth hormone (GH) all followed a similar pattern for IBRV steers starting on approximately d 2, peaking on d 4, and tapering off on d 6. The peak concentration on d 4 for CORT (pg/mL; 136.96 ± 67.70 vs. 74.5 ± 45.76), IFN-γ (ng/mL; 133.41 ± 126.45 vs. 27.98 ± 10.38), and GH (ng/mL; 48.43 ± 7.66 vs. 32.74 ± 12.67) for the IBRV steers as compared with CON. While there was a difference ($P < 0.05$) in GH concentrations between the IBRV and CON steers, IGF-1 concentrations did not differ ($P > 0.05$) between the 2 groups. Collectively the data revealed alterations in the somatrotrophic axis that were not associated with a large increase in circulating concentrations of pro-inflammatory cytokines. We conclude that the low dose of the virus used in the present study, while sufficient to elicit a febrile response, it did not result in the calves becoming septicemic which would explain the lack of a detectable cytokine response.

Key Words: cattle, cortisol, cytokines

772 Identification of genetic regions associated with bovine viral diarrhea-persistently infected cattle. R. Zanella*[1], J. Wenz[1], E. Casas[2], J. S. Neibergs[1], D. Moore[1], and H. L. Neibergs[1], [1]*Washington State University*, *Pullman*, [2]*United States Meat Animal Research Center*, *Clay Center, NE*.

Bovine viral diarrhea virus (BVDV) is one of the etiologies involved in bovine respiratory disease (BRD). BVDV infection can also cause reproductive disorders and acute fatal hemorrhagic disease resulting in poor performance and economic losses to the cattle industry. Infection with BVDV can be transient or persistent. Transient infections are temporary and last until the animal builds immunity to the virus. Persistent infections (BVD-PI) occur when a cow and her fetus are infected with BVDV at approximately 40 to 140 d of gestation. BVD-PI animals shed virus throughout their lives. Previous studies have found bovine chromosomes (BTA) 2 and 26 to be linked to BRD. The objective of this research was to determine if these regions were associated with BVDV-PI infection. Ear notches of 8624 commercial beef calves were tested by qtRT-PCR for the presence of BVDV. Calves positive for BVDV were confirmed to be BVD-PI by ELISA at the Washington Animal Disease Laboratory. Sixty-five BVD-PI calves, their dams, and 60 contemporary calves (controls) from the same herd were genotyped for 6 microsatellites on BTA 2 and 7 microsatellites on BTA 26. Allele frequencies were compared between BVD-PI calves and controls, dams of BVD-PI calves and controls with a Fishers exact test. BTA 26 was associated with persistent infection when BVD-PI calves ($P = 0.01$) and dams of BVD-PI calves ($P = 2.8 \times 10^{-6}$) were compared with controls. Strong evidence for an association with BTA 2 and persistent infection was demonstrated for BVD-PI calves ($P = 1 \times 10^{-10}$) and the dams of BVD-PI calves ($P = 1 \times 10^{-13}$). These results are congruent with the BRD linkage results and suggest that BTA 2 and BTA 26 harbor loci that influence both BRD and BVD-PI.

Key Words: BVD-PI, loci, association

773 Economic analysis of persistently infected bovine viral diarrhea disease prevalence in Washington beef herds. J. S. Neibergs*, H. L. Neibergs, J. Wenz, and D. Moore, *Washington State University*, *Pullman*.

Studies have identified that bovine viral diarrhea virus (BVDV) causes economic losses throughout the beef production chain primarily through persistently infected (PI) calves. The purposes of this study were to identify BVDV-PI prevalence in Washington cow-calf herds, identify herd health management risk factors associated with positive PI prevalence, determine economic losses, and to evaluate the economic efficacy of disease management. A state-wide voluntary BVDV-PI testing program tested 8,624 calves from 60 herds, identifying 80 (0.92%) BVDV-PI calves in 8 herds (13.3%). Two herds had catastrophically high prevalence with 13% and 52% PI positive calves. Washington PI prevalence was substantially higher than comparable studies. Managers with positive herds were interviewed to collect production and economic performance data using NCBA SPA economic methods. Herd economic losses ranged from $1.34 to $236.75 per cow. Total ranch losses ranged from $482 to $20,124 reflecting differences in losses due to the proportion of BVDV-PI calves in the herd. Losses are the market value losses of removing PI calves from the commercial production chain and detected losses in reproduction efficiency through the SPA analysis. The presence of PI calves was due to poor bio-security practices in the 2 herds with catastrophic prevalence. Purchased replacements were not quarantined or BVDV-PI tested. Two PI cows produced PI calves among the other herds. Specific risk factors were not identified in the remaining herds. BVDV health management recommendations are: to test calves to determine herd prevalence, test replacements and quarantine new animals, and implement a BVDV vaccination program. Annual testing of all calves is not economically effective, because once a herd is determined to be BVD-PI free to eliminate production losses, the regional market does not provide a price premium for tested negative calves. New cost effective disease control methods such as genetic selection for disease resistance are needed to reduce BVDV-PI prevalence and its associated economic losses.

Key Words: BVD-PI, economics, prevalence

774 Pre-arrival management of newly received beef calves with or without exposure to a persistently infected bovine viral diarrhea virus type I calf affects health, performance, bovine viral diarrhea virus type I titers, and circulating leukocytes. J. T. Richeson* and E. B. Kegley, *University of Arkansas*, *Fayetteville*.

Calves persistently infected (PI) with bovine viral diarrhea virus (BVDV) are a major source of the virus; however, consequences of exposure to a PI-BVDV calf in preconditioned (PC) vs. auction market (AM) cattle may differ. Our objective was to compare treatments of PC or AM origin, with (PI) or without (CON) exposure to a PI-BVDV calf in a 2 × 2 factorial arrangement to evaluate effects on health and performance in a randomized block design using the MIXED procedure of SAS. Four sets (block) of PC steers (n = 236) from 3 ranches were selected randomly, weaned, dewormed, vaccinated, tested for PI-BVDV status, and kept on the ranch for ≥42 d. Subsequently, PC calves were transported to a stocker unit (SU), weighed (251 ± 2 kg), bled, and assigned randomly to treatment (PCPI or PCCON) with no additional processing. Simultaneously, 4 sets of AM calves (n = 292) were assembled for delivery to the SU within 24 h of PC arrival. The AM calves were weighed (245 ± 1.3 kg) and administered the same processing procedures as PC; however, bull calves were castrated, stratified by sex, and AM calves were assigned randomly to treatment (AMPI or AMCON). Calves were fed identically and followed the same antibiotic treatment protocol. Daily gain for the entire 42 d was greater ($P < 0.001$) for PC (1.2 kg) than AM (0.85 kg). There was an exposure effect ($P = 0.002$) on ADG from d 28 to 42; CON gained 1.12 kg vs. 0.90 kg for PI. Morbidity rate was greater ($P < 0.001$) in AM (70%) than PC (7%). Treatment with a third antibiotic occurred more often ($P = 0.04$) for PI, likewise the greatest number of chronic cattle were AMPI ($P = 0.06$). BVDV type I titer levels were greater on d 0 for PC (treatment × day, $P < 0.001$), and seroconversion to BVDV on d 0 was 100% for PC vs. 23% in AM. Neutrophil:lymphocyte was greater ($P < 0.001$) for AM on d 14 and 28. Results suggest that PC gain faster and require fewer antibiotic treatments; whereas, PI-BVDV exposure reduced gain and increased antibiotic treatment cost, particularly in AM.

Key Words: beef calves, preconditioned, BVDV

ASAS Western Section Symposium: Perinatal Programming of Offspring Quality 1: Basic Concepts and Experimental Evidence

775 Key principles of developmental programming of later life events: Observations in primate development. P. W. Nathanielsz*[1], L. Cox[1], T. McDonald[1], S. Ford[2], K. Mitsuya[1], and M. Nijland[1], [1]*Center for Pregnancy and Newborn Research, The University of Texas Health Science Center*, *San Antonio*, [2]*University of Wyoming*, *Laramie*.

Mammals pass more biological milestones before birth than the rest of life. Critical developmental phases are windows of potential susceptibility to adverse gene-environment epigenetic influences that may predispose to chronic later life diseases e.g., hypertension, obesity, and diabetes. Compelling human epidemiological and animal research studies clearly demonstrate that a suboptimal intrauterine environment alters the trajectory of development and epigenetically modifies cell function. The controlled animal studies to evaluate normal and abnormal fetal development have mostly been conducted in rodents or sheep. There are, however, considerable differences in pregnancy between primates and other species. Rodents are polytocous species delivering up to 16 altricial pups which with their placentas are a biomass equivalent to a woman delivering a sixty pound baby. Many fetal stages of development in precocial species occur postnatally in rodents when oxygenation, metabolic and hormonal status differ significantly. The developmental challenges most extensively investigated are poor maternal nutrition and maternal stress. Developmental programming represents a convergence of environmental influences on genotype. This presentation will focus on our studies in baboon fetal and postnatal life with offspring of control (CTR) ad lib fed baboons and baboons undergoing maternal nutrient reduction (MNR) that eat 70% of the global diet consumed by CTR females in pregnancy and lactation. At term, MNR reduces islet cell number and protein content of insulin and key growth factors such as IGF-I and IGF-II. Gene array studies show dysregulation of several pathways in the placenta, liver, kidney and brain – many of these pathways involve nutrient signaling and energy generation and utilization. These changes and epigenetic marks resulting from altered methylation will be discussed.

776 Epigenetic transgenerational actions of environmental factors on reproduction and disease: The ghosts in your genome. M. K. Skinner*, *Washington State University*, *Pullman*.

Transgenerational effects of environmental factors (e.g., nutrition and endocrine disruptors) significantly amplify the impact and health hazards of these factors. One of the most sensitive periods to exposure is during embryonic gonadal sex determination when the germ line is undergoing epigenetic programming and DNA re-methylation. A model endocrine disruptor tested was vinclozolin, which acts as an anti-androgenic compound. Previous studies have shown that this endocrine disruptor can effect embryonic testis development to subsequently cause an increase in spermatogenic cell apoptosis in the adult. Interestingly, this spermatogenic defect is transgenerational (F1, F2, F3 and F4 generations) and shown to be due in part to a permanent altered DNA methylation of the germ-line. This appears to involve the induction of new imprinted-like DNA methylation sites that regulate transcription distally. Differential DNA methylation regions were identified with ChIP-Chip analysis in F3 generation sperm. The impact of these epigenetic changes have on the genome used transcriptome analysis. The expression of hundreds of genes were found to be altered in the embryonic testis and surprisingly this altered transcriptome was similar for all generations (F1-F3). All tissues examined had a transgenerational transcriptome effect that was tissue specific. In addition to detection of the male testis disorder, as the animals age transgenerational effects on other disease states were observed including tumor development, prostate disease, kidney disease and immune abnormalities Therefore, the transgenerational epigenetic mechanism appears to involve the actions of an environmental compound at the time of sex determination to alter the epigenetic (i.e., DNA methylation) programming of the germ line permanently that then alters the transcriptomes of developing organs to induce disease development transgenerationally. Similar Transgenerational effects have now been observed with nutrition, BPA and phthalates. The suggestion that environmental factors can reprogram the germ line to induce epigenetic transgenerational disease is a new paradigm in disease etiology.

777 Even her uterus can't protect you. Stress in life: A multi-species review. D. C. Lay Jr.*, *USDA-Agricultural Research Service, Livestock Behavior Research Unit*, *West Lafayette, IN*.

All environments can pose challenges to animals which cause stress; they meet these challenges by making behavioral and physiologic adjustments. These adjustments include behavioral responses of fighting or hiding; and physiologic adjustments which include such processes as regulation of blood glucose, altered cardiac function and others that help the animal to react to the stress and to bring the body back to its normal state. However, when this occurs to animals which have developing ova, are pregnant, or caring for young; there is a potential for the stress to also influence the development of these individuals. Although the literature is not always consistent in how the individuals are affected, alterations due to early exposure to stress have been shown in mice, guinea pigs, poultry, swine, sheep, cattle, horses and humans, to name a few. It is clear that stress during these early developmental stages can alter how the animals respond to stressors later in life, with changes seen in both their behavior and physiologic responses to stressors. In mammals, the uterus is an affective barrier to many of the external threats to which the fetus may be exposed; however it is clear it is not full-proof. In avian species, stress responses can alter the hormonal content of the yolk which then later alter the development of the embryo. One theory suggest that alterations due to stress are adaptive, preparing the offspring for a stressful environment. The timing of such events during fetal and neonatal development is critical to the integrity and normal function of all animals. The observation that stress can alter the later responses of so many species of animals is profound. In addition, the fact that exposure to stress can have deleterious effects to all the livestock and poultry species which we raise, necessitates our complete understanding. It also may provide a mechanism with which we could facilitate animals' adaptation to environments in which they will be housed in the future.

Key Words: stress, development, programming

778 Fixed-time AI conception rates in beef cows resulting from reduced 2-shot prostaglandin intervals on day 5 of a 5-d CIDR-Co-synch estrus synchronization. J. L. Seabrook*, R. K. Peel, G. E. Seidel, and J. C. Whittier, *Colorado State University*, *Fort Collins*.

The objective of this study was to quantify fixed-time AI (TAI) pregnancy rates resulting from reduced intervals between 2 25 mg dinoprost tromethamine (PG) injections on d 5 of a 5-d CIDR-Co-synch estrus synchronization program. Angus and Angus-influenced commercial cows (n = 873) maintained on native pasture at 3 locations were randomly assigned to treatments, blocking for BCS and postpartum interval (PPI). On experimental d 0 all cows received 100 μg GnRH i.m. and a CIDR (1.38 g progesterone). On d 5, CIDRs were removed and cows were administered 2 injections of 25 mg PG i.m. either 2, 4 or 6 h ± 30 min apart. On d 8, 72 ± 3 h after the first PG injection, all cows received 100 μg GnRH i.m. and were TAI. Conception rates were determined by rectal ultrasonography 40 ± 2 d following TAI. The TAI conception rate was 59.7% for the 6 h interval group, 51.4% for the 4 h interval group ($P = 0.05$), and 50.6% for the 2 h interval group ($P = 0.04$). Body condition score ($P = 0.06$) was a marginally significant source of variation for TAI conception rate; shorter PPI intervals negatively affected pregnancy rate ($P = 0.02$). Reducing the interval between PG injections from 6 to 4 or 2 h resulted in a 9-percentage point (15%) reduction in TAI conception rates for cows in this 5-d CIDR-Co-synch estrus synchronization protocol.

Key Words: beef cow, CIDR Co-synch, prostaglandin interval

779 Effect of castration technique on beef calf performance and residual feed intake. T. M. Warnock*[1], T. A. Thrift[1], M. Irsik[1], M. J. Hersom[1], T. D. Maddock[2], and G. C. Lamb[2], [1]*University of Florida*, *Gainesville,* [2]*University of Florida*, *Marianna*.

The objective of this study was to examine whether castration method would alter daily feed and water intake, calf performance, and residual feed intake. Brangus (n = 45) and Angus (n = 30) male calves weighing 226 ± 34 kg (200 + 26 d of age) were placed in a GrowSafe 4000 feed intake facility 7 d post weaning (15 calves/pen; 7–8 calves/feed node). Body weight gain and DMI were recorded over an 84-d period. Calves were offered a mixed diet (TDN = 67.3% and CP = 12.2%, DM = 89%) ad libitum. Calves were adapted to the facility for 21 d before the start of the trial. Shrunk BW was recorded on d 0, 14, and 84; full BW was recorded on d 7, 28, 42, 56, and 70. On d 0 calves were assigned to one of 5 treatments (n = 15/treatment): 1) control steers were castrated surgically before weaning at an average age of 52 d (8–85 d) (CON); 2) intact bulls (BULL); 3) bulls castrated surgically (SUR); 4) bulls castrated by the Callicrate Bander (No-Bull Enterprises, LLC, St. Francis, KS; BAN); and 5) bulls castrated using the Henderson castration tool (Stone Mfg & Supply Co., Kansas City, MO; HEN). During the first 14 d post castration, BAN calves gained BW slower ($P = 0.009$) than CON calves (0.10 vs. 0.68 kg/d) and tended to gain BW slower ($P = 0.08$) than BULL calves (0.12 vs. 0.48 kg/d). Additionally, CON calves gained more BW ($P = 0.04$) than HEN and SUR calves, 0.68, 0.24, and 0.22 kg/d, respectively. DMI was similar ($P > 0.10$) among castration methods 14 d post castration. BAN calves had decreased ($P = 0.04$) average daily water intake compared with BULL, CON, and SUR calves (28.39 vs. 38.86, 45.20, and 39.18 L/d respectively) and tended to drink less ($P = 0.08$) than HEN calves (28.39 vs. 37.20 L/d). During the experiment, all treatments had similar ($P > 0.10$) ADG and residual feed intake. Our results suggest that method of castration did not have a long-term impact on performance or efficiency of weaned calves.

Key Words: beef cattle, castration, performance

780 Effect of preconditioning average daily gain on feedlot performance and carcass characteristics of beef cattle. J. D. Savell*, T. A. Thrift, and M. J. Hersom, *University of Florida*, *Gainesville*.

A study was conducted to evaluate the effect of preconditioning ADG (PCADG) on feedlot performance and subsequent carcass characteristics in beef cattle. Steers (n = 1,100, BW = 254 ± 28 kg) and heifers (n = 421, BW = 241 ± 25 kg) from a single ranch were shipped 370 km to be preconditioned in North Central Florida. Calves were preconditioned on 8 ha bermudagrass pastures and acclimated to a high energy starter ration with a DMI target of 3% of live BW. Calves were preconditioned for 43 ± 9 d and then shipped 2,365 km to a feedyard to be finished in Western Kansas that utilized the Micro Beef Technologies ACCU-TRAC Electronic Cattle Management system. The effect of increasing PCADG was evaluated against the dependent variables (feedlot ADG, feed efficiency, days on feed, cost of gain, HCW, quality grade, ribeye area (REA), REA/100 kg, and yield grade) and regression analysis was performed. Feedlot ADG was similar ($P = 0.54$) across varying levels of PCADG. Feedlot feed efficiency improved ($P < 0.05$) for both steers (0.62 kg of feed/kg of gain) and heifers (0.46 kg of feed/kg of gain) as PCADG increased. Days on feed decreased ($P < 0.01$) by 7.2 d for each 1.0 kg increase in PCADG. Cost of gain decreased ($P < 0.05$) 9.8 cents/kg for each 1.0 kg increase in PCADG. As PCADG increased by 1.0 kg/d, HCW increased ($P < 0.001$) by 19.5 kg. Quality grade ($P = 0.24$) and yield grade ($P = 0.29$) were not affected by PCADG. Calves that gained more during preconditioning had greater ($P < 0.001$) actual REA but smaller ($P < 0.01$) REA/100 kg value. Preconditioning ADG was not a good predictor of feedlot ADG. Improvements in feedlot feed efficiency associated with high gaining calves during preconditioning resulted in fewer days on feed and reduced cost of gain in the feedlot. As PCADG increased, HCW increased, REA increased, and REA/100 kg decreased. Quality grade and yield grade were minimally affected by PCADG.

Key Words: carcass, performance, preconditioning

781 Effect of estimated Brahman percentage on preconditioning performance, feedlot performance and carcass characteristics of beef cattle. J. D. Savell, T. A. Thrift, and M. J. Hersom*, *University of Florida*, *Gainesville*.

A study was conducted to evaluate the effect of Brahman percentage in beef calves on preconditioning and feedlot performance and subsequent carcass characteristics. Steers (n = 1,100, BW = 254 ± 28 kg) and heifers (n = 421, BW = 241 ± 25 kg) from a single ranch were shipped 370 km to be preconditioned in north central Florida. Upon arrival, Brahman percentage was estimated to be 0, 1/8, 1/4, or 3/8 Brahman influence by 2 evaluators, with a third evaluator resolving any discrepancies. Phenotypic evaluation of Brahman percentage was made based on the visual appearance of the underline and size of the hump. Length, shape, and orientation of the ear were also used to estimate Brahman percentage. Calves were preconditioned for 43 ± 9 d and shipped 2,365 km to a feedyard to be finished in Western Kansas that utilized the Micro Beef Technologies ACCU-TRAC Electronic Cattle Management system. The effect of increasing estimated Brahman percentage was evaluated

against the dependent variables (preconditioning ADG, feedlot ADG, G:F, days on feed, cost of gain, HCW, quality grade, ribeye area [REA], REA/100 kg, and yield grade) and regression analysis was performed. As Brahman percentage increased by 1/8, preconditioning ADG increased ($P < 0.05$) by 0.03 kg/d. Feedlot ADG was similar ($P = 0.12$) across varying levels of Brahman percentage. Days on feed, G:F, and cost of gain were similar across levels of Brahman percentage ($P > 0.05$). Hot carcass weight declined ($P < 0.001$) by 8.78 kg as Brahman percentage increased by 1/8. Quality grade also decreased ($P < 0.01$) as Brahman percentage increased. Actual REA decreased ($P < 0.01$) as Brahman percentage increased, but no differences in REA/100 kg were observed. Cattle that exhibited 1/8 Brahman influence had a greater decrease ($P < 0.05$) in numerical values for yield grade than those estimated to be 0 or 1/4 Brahman, and were similar ($P > 0.05$) to those estimated to be 3/8 Brahman. As Brahman percentage increased preconditioning ADG increased, feedlot performance was minimal impacted, and HCW and quality grade declined.

Key Words: Brahman, carcass, performance

782 Breed and winter nutrition effects on body weight, condition, and blood metabolite patterns of cows grazing bahiagrass pastures. S. W. Coleman*, M. J. Williams, C. C. Chase, and D. G. Riley, *USDA ARS Subtropical Agricultural Research Station*, *Brooksville, FL*.

Generally the largest economic costs for cattle production are for winter feed. This 2-yr study evaluated 2 winter nutrition programs on Angus, Brahman, and Romosinuano purebred cows (n = 298, aged 3 to 16 yr) rotationally grazing bahiagrass pastures at STARS. Treatments (TRT) began after weaning and were replicated (R) over 3 farms. Treatments were: TRT1) peanut/bahiagrass hay fed free choice from first frost and supplemented with heavy blackstrap molasses at 2.2 kg/hd/day from weaning until end of breeding (~June 15); and TRT2) bahiagrass hay supplemented with urea-fortified molasses (16% protein equivalent) at 2.2 kg/hd/d from weaning until Jan 15 and then 4.5kg/hd/d of 50% heavy blackstrap molasses and 50% soybean hulls until end of breeding. At monthly intervals, all cows were weighed (BW), scored for body condition (BCS), and blood samples were collected by jugular puncture (5 cows per breed-TRT-rep group) and analyzed for plasma urea N (PUN), glucose (GLU), and non-esterified fatty acids (NEFA). Data were analyzed on cows that calved using Proc Mixed of SAS. The statistical model included fixed effects of cow breed (BR), cowage, TRT, month (M) and R; year (Y) was random, and cow was a repeated effect. Three-way interactions (Y × TRT × M and Y × TRT × R) were significant ($P < 0.001$) for all responses, and the BR × TRT × M interaction was significant for BW, BCS, and NEFA. Important differences included: 1) cow BW was always lower for TRT2 than TRT1 (avg. 505 vs. 487 kg, $P < 0.002$), especially during winter when supplement was fed, yet PUN was higher ($P < 0.01$) for TRT2 in May, June and Sept-Dec for 2002, but no differences were noted in 2003 until Nov; and 2) Plasma levels of NEFA escalated to near 1 mEQ/L at calving and then declined to 0.40, except for Brahman cows who maintained higher (0.58 mEQ/L, $P < 0.01$) levels than the other breeds from 60 d postpartum until weaning, probably due to inadequate intake to support milk production.

Key Words: cow-calf, winter supplementation

783 Genetic mechanism underlying the effect of breed on fatty acid composition in Angus and Charolais finishing steers. A. K. Sexten*, J. W. Dillwith, D. R. Stein, C. R. Krehbiel, and R. G. Mateescu, *Oklahoma State University*, *Stillwater*.

Genetic variability in beef fatty acid composition consists of differences between breeds and between animals within breed. The effect of breed on fatty acid profile in beef was evaluated in longissimus muscle (LM) from Angus (n = 19) and Charolais (n = 14) feedlot finished steers. Steers were fed a total of 140 d before slaughter. Longissimus muscles were biopsied on d 127 of the finishing period between the 12th and 13th ribs and fatty acid composition was determined. Lipids were extracted in triplicate with a 2:1 (v/v) methanol:chloroform solution then acid and base derivatized before separation by gas chromatography on an Agilent 5890 gas chromatograph with 7673 autosampler. Percent composition of each fatty acid was calculated and the effect of breed was analyzed using the general linear model of SAS. Hot carcass weights did not differ, however, Angus steers had higher marbling scores ($P = 0.01$) and more backfat ($P = 0.01$) than Charolais steers. Although percent of saturated fatty acids did not differ between Angus (44.9%) and Charolais (44.0%) steers, Angus steers LM had a higher percent of monounsaturated fatty acids (43.7 vs. 39.4%; $P = 0.01$) and a lower percent of polyunsaturated fatty acids (11.1 vs. 16.3%; $P = 0.03$), omega-3 fatty acids (0.58 vs 0.82%; $P = 0.04$) and omega-6 fatty acids (10.5 vs. 15.5%; $P = 0.03$). Microarray analysis utilizing a long oligo bovine array was also performed. Preprocessing and normalization of data was accomplished using the R-project statistical environment with the Bioconductor and LIMMA package through the GenePix AutoProcessor (GPAP 3.2). Nine genes were found to be significantly ($P = 0.01$) differentially expressed (DE) between Angus and Charolais LM. Ontology analysis of the DE genes was carried out using GFINDer with KEGG analysis utilized to identify the most relevant biological pathways. These results provide insight into the challenge of developing and implementing a program to improve the healthfulness of beef utilizing existing natural genetic variation to manipulate fat composition through breed selection.

Key Words: beef, fatty acid, gene expression

Breeding and Genetics: Milk and Carcass Composition

784 Feasibility of a genetic evaluation for milk fatty acids in dairy cattle. H. Soyeurt*[1,2], V. M.-R. Arnould[1], S. Vanderick[1], and N. Gengler[1,2], [1]*University of Liege, Gembloux Agro-Bio Tech, Animal Science Unit*, *Gembloux, Namur, Belgium*, [2]*National Fund for Scientific Research*, *Brussels, Brussels, Belgium*.

Recent development of equations based on mid-infrared (MIR) spectrometry for the prediction of milk fatty acid (FA) contents allows their measurement on a large scale during performance recording. The objective was to show that a genetic evaluation for milk FA in dairy cattle is feasible in the Walloon region of Belgium and to report first results. Estimated breeding values (EBV) and associated reliabilities (REL) were computed using a multi-trait test-day animal model similar to the one used for the routine genetic evaluation for yield traits. Studied traits were first lactation test-day milk, fat and protein yields, fat (FAT) and protein contents, and content of saturated fatty acids in milk (g/100g of milk, SAT). More than 6,700,000 records were available for common production and content traits and 194,000 records were used for SAT. Used variance components were estimated using REML. The average SAT content was 2.79% with a standard deviation (SD) of 0.50%. A total of 1,707 Holstein bulls used in Walloon Region had REL superior to 0.49 for all studied traits. REL for SAT ranged from 0.53 to 0.99. A total of 1,217 bulls had REL superior to 0.74. SD of EBV for SAT was 0.20%. The maximum and minimum SAT EBV values were 0.89% and −0.69%, respectively. To have a direct measure of the part of FAT that is not due to SAT, a new trait (dSAT) was post-evaluated and defined as difference between expected SAT EBV for a given FAT EBV and the estimated EBV for SAT. This new trait can be assumed to be a direct predictor of the content of unsaturated fatty acids in fat. The interest is that this trait cannot be accurately predicted directly by MIR. The maximum and minimum EBV for dSAT for the 1,707 bulls were −0.28% and 0.24%, respectively. Based on these results, a genetic evaluation for milk fatty acids is feasible. In the bull population used recently, a genetic variability for dSAT exists and could be used to improve the milk fat composition.

Key Words: genetic parameter, milk, fatty acid

785 Heterogeneity of residuals variances of milk fatty acids in dairy cattle. V. M.-R. Arnould*[1], H. Soyeurt[1,2], S. Vanderick[1], and N. Gengler[1,2], [1]*University of Liège, Gembloux Agro-Bio Tech*, *Gembloux, Belgium*, [2]*National Fund for Scientific Research*, *Brussels, Belgium*.

Routine genetic evaluation for milk fatty acids is under development in the Walloon Region of Belgium. The objective of this study was to test the heterogeneity of residual variances and therefore indirectly the potential need to adjust for this heterogeneity if it exists. The residuals were computed as the difference between the observed and the estimated values using a multi-trait random regression test-day model, similar to the Walloon routine model, used for first lactation only milk yield, quantities and percentages of protein (PROT) and fat (FAT), content of saturated fatty acids in milk (g/100g of milk, SAT) and, content of monounsaturated fatty acids in milk (g/100g of milk, MONO). Residuals were considered homogeneous inside strata defined, among others, by weeks of lactation, by days in milk and by calendar months of test date. About 6,687,000 records were available for milk yield and for FAT and PROT parameters. For SAT and for MONO, about 184,000 records were available in this database. Means of residuals were stable and close to zero for all traits. Variances were more variable for MONO and SAT than for milk yield, for example. Daily and weekly variances tended to decrease at the end of the lactation (50%). When the variances were computed by month of test date, some variations were observed and some periods of year were more marked. In conclusion, the observed residual variances were less stable for MONO and SAT. We can conclude that introduction for heterogeneous residual variance is more important for the new traits (MONO, SAT) than it was for the old, traditional ones.

Key Words: routine genetic evaluation, heterogeneity of residual variances, milk fatty acids

786 Relationships between feedlot growth and carcass traits in Angus: Tri-County Steer Carcass Futurity. L. D. Leachman*, D. R. Notter, S. P. Greiner, and R. M. Lewis, *Virginia Tech*, *Blacksburg*.

The objective was to characterize growth and carcass traits and associated genetic parameters in 2,199 steers and 424 heifers sired by registered Angus bulls and evaluated under feedlot conditions in the 2002–2006 Iowa Tri-County Steer Carcass Futurity Program. Traits evaluated were initial (IBW) and slaughter BW (SBW; kg), and carcass backfat thickness (CFAT), marbling score (CMAR) and ribeye area (CREA). Univariate and bivariate sire models were fitted with ASReml3. Fixed effects included contemporary group (CG) and linear and quadratic effects of age at IBW nested within season and year of feedlot delivery. Random effects were sire and residual. The CG consisted of sex, pen, dam breed-type, owner, and feedlot. Delivery seasons were January–April, May–August and September–December. Data were edited to CG and sire families with at least 5 animals. Trait sample means (SD) for steers were: IBW, 289 (40.3) kg; SBW, 543 (46.4) kg; CFAT, 1.21 (0.33) cm; CREA, 79 (7.2) cm^2; and, CMAR 1057 (89.0). Heifers weighed less, had smaller CREA, and more fat. Phenotypic variances, heritabilities and correlations are shown in Table 1. All traits were moderately to highly heritable. Cattle with heavier IBW had heavier SBW and larger CREA at harvest. Heavier SBW was strongly associated with larger CREA and with a tendency for less CMAR. More CFAT was related moderately to smaller CREA. Given their heritabilities, and the size and direction of most correlations, feedlot traits are clearly amenable to selection.

Table 1. Phenotypic variances (P-var), heritabilities, and genetic and phenotypic correlations[1]

	IBW	SBW	CFAT	CREA	CMAR
P-var	711	1933	0.0918	50	6751
IBW	**0.50±0.11**	0.69±0.09	0.03±0.19	0.35±0.15	−0.07±0.16
SBW	0.58±0.02	**0.45±0.10**	0.04±0.20	0.63±0.12	0.25±0.17
CFAT	0.06±0.03	0.13±0.02	**0.27±0.08**	−0.34±0.18	−0.11±0.19
CREA	0.26±0.02	0.41±0.02	−0.12±0.02	**0.39±0.09**	0.23±0.18
CMAR	−0.09±0.03	0.07±0.03	0.12±0.02	−0.03±0.03	**0.46±0.10**

[1]Heritabilities in bold on diagonal; genetic and phenotypic correlations above and below the diagonal.

Key Words: feedlot, performance, cattle

787 Heritabilities, genetic and phenotypic correlations among Warner-Bratzler shear force and repeated objective measurements of temperament in fed cattle. R. L. Weaber[1], T. M. Taxis*[1], W. R. Shafer[2], L. L. Berger[3], D. B. Faulkner[4], M. M. Rolf[1], D. L. Dow[1], J. F. Taylor[1], and C. L. Lorenzen[1], [1]*University of Missouri*, *Columbia*, [2]*American Simmental Association*, *Bozeman, MT*, [3]*University of Nebraska*, *Lincoln*, [4]*University of Illinois*, *Urbana*.

Tenderness is a primary meat palatability attribute affecting consumer satisfaction of beef. Beef cattle temperament has been associated with a variety of performance measures. Performance data and pedigree records were provided by the American Simmental Association (ASA) to elucidate the relationship between temperament and tenderness in *Bos taurus* breeds. Data included WBSF records from ASA's carcass-merit program and a subset collected at the University of Illinois (UI). Exit velocities were recorded when cattle went on trial (EV1) and 42 d later (EV2). Single animal and single sire contemporary groups (CG) were removed from the data set leaving 2,819 WBSF, 917 EV1 and 976 EV2 phenotypes in 176 CG for evaluation. A pedigree was formed with 13,418 animals including 2,488 sires. Phenotypic means (SD) were 36.65 N (10.56 N) for WBSF, 1.74 m/s (0.76 m/s) for EV1 and 1.65 m/s (0.79 m/s) for EV2. A tri-variate animal model with CG, sire and dam breed composition as fixed effects and animal as random effect was fit to estimate variance components. Phenotypic correlations (SE) estimated between WBSF with EV1 and EV2 were −0.05 (0.05) and −0.03 (0.04), respectively, and between EV1 and EV2 was 0.59 (0.02). Heritabilities (SE) for WBSF, EV1 and EV2 were 0.19 (0.06), 0.30 (0.11) and 0.25 (0.10) respectively. Genetic correlations estimated between WBSF with EV1 and EV2 were 0.02 (0.38) and −0.30 (0.36) respectively. Given the high genetic correlation between EV1 and EV2 of 0.99 (0.07) a repeated records analysis was conducted for EV with an uncorrelated random effect for animal using the same fixed effects as before. A likelihood ratio test was used to determine that the repeated records model implemented provided a better fit ($P < 0.0001$) to the data than did the tri-variate model. Heritabilities were 0.19 (0.06) and 0.39 (0.08) for WBSF and EV, respectively, with a genetic correlation of −0.10 (0.20). The near zero genetic correlation and moderate heritabilities suggest producers can select to improve temperament and/or WBSF without substantial correlated response.

Key Words: heritability, beef temperament, tenderness

788 Development and validation of an Angus-specific IGENITY profile for marbling, backfat thickness, hot carcass weight, ribeye area, yearling weight, and heifer pregnancy rate based on a whole genome scan. B. W. Woodward*[1], D. J. Garrick[2], R. L. Fernando[2], S. Northcutt[3], B. Bowman[3], S. W. Bauck[1], R. D. Schnabel[4], and J. F. Taylor[4], [1]*Merial Limited*, *Duluth, GA*, [2]*Iowa State University*, *Ames*, [3]*American Angus Association*, *St. Joseph, MO*, [4]*University of Missouri*, *Columbia*.

Genomic markers are now being widely used in the selection of beef and dairy breeding animals via various commercial products with a wide range in price. The objective of this study was to develop a cost effective, yet informative low-density panel of SNPs derived from the Illumina Bovine SNP50 specifically for Angus cattle. Target traits were marbling, backfat thickness, hot carcass weight, ribeye area, yearling weight, and heifer pregnancy rate. Multiple methods were initially evaluated for SNP selection and the method of choice involved a 2-stage process combining Bayesian model averaging and semi-parametric models. There were 41,028 SNP genotypes for 1,710 bulls born between 1955 and 2003. Predictability was assessed as the correlation between genomic predictions and EPD in training and cross-validation sets of animals, and by validating on a new set of 275 younger bulls. EPD were from the American Angus Association. Correlations between molecular breeding values and EPD for marbling, backfat thickness, hot carcass weight, ribeye area, yearling weight, and heifer pregnancy rate in cross-validation bulls were 0.71, 0.68, 0.73, 0.68, 0.71, and 0.32, respectively. Corresponding correlations in the group of 275 bulls were 0.66, 0.38, 0.73, 0.68, 0.76, and 0.20. Therefore, correlations for both groups of validation bulls indicate this SNP panel derived from the SNP50 could provide a powerful tool for genomic selection.

Key Words: SNP, whole genome, selection

789 The economics of using DNA markers for beef bull selection in the seedstock sector. A. L. Van Eenennaam*[1], J. H. van der Werf[2], and M. E. Goddard[3,4], [1]*University of California*, *Davis,* [2]*University of New England*, *Armidale, NSW, Australia*, [3]*Victorian Department of Primary Industries*, *Bundoora, VIC, Australia*, [4]*University of Melbourne*, *Parkville, VIC, Australia*.

The objective of this study was to estimate the value derived from using DNA test information to increase the accuracy of beef sire selection in a closed seedstock nucleus herd. Breeding objectives for commercial production systems targeting 2 diverse markets, a domestic market where steers are finished on pasture, or a high value export market where steers are finished on concentrate rations and marbling has a high value, were examined considering both maternal (self-replacing) and terminal herds. Selection index theory was used to predict the response to conventional selection based on phenotypic performance records, and this was compared with including information from 2 hypothetical marker panels. In one case the marker panel explained a percentage of additive genetic variance equal to the heritability for all traits in the breeding objective, and in the other case to half this amount. Discounted gene flow methodology was used to calculate the value of DNA test information over that derived from conventional selection for the modeled seedstock herd. Results were ultimately calculated as discounted returns per DNA test purchased by the seedstock operator. DNA testing using these hypothetical marker panels increased the selection response between 33 and 171%. The value of this improvement relative to that obtained using traditional performance recording ranged from AU$156–681 per commercial bull, and AU$9,203–35,823 per stud bull. If the entire bull calf crop was tested to achieve these gains, the value of genetic gain derived from DNA testing ranged from AU$367–1,386 per test. These values assumed commercial producers were willing to pay a price premium for genetically superior bulls and some level of industry vertical integration such that market signals from the processor and feedlot were transferred up the chain to commercial and seedstock producers. All values were sensitive to index accuracy in the absence of DNA information. The development of selection indexes including DNA-based predictions of economically relevant traits not currently included in genetic evaluations will be required to assess the value of DNA information for the beef industry.

Key Words: DNA marker, beef bull, accuracy

790 Studies on the application of dielectric spectroscopy for the measurement of process cheese functionality. J. Amamcharla*[1], L. E. Metzger[1], O. Grace[2], and C. Jones[2], [1]*Midwest Dairy Foods Research Center, Dairy Science Department, South Dakota State University*, *Brookings,* [2]*Biosystems and Agricultural Engineering, Oklahoma State University*, *Stillwater*.

This study evaluated the potential of dielectric analysis of process cheese for prediction of the textural (hardness) and melting properties. Process cheeses (n = 24) with similar composition (fat, protein, moisture, and salt) were procured from a commercial manufacturer (Bongards' Creameries, MN). Dielectric properties (permittivity (ε′) and loss factor (ε″)) of the process cheeses were collected over the frequency range 0.2 – 3.2 GHz at a constant temperature (25°C). Dielectric measurements were made using an open-ended high temperature dielectric Probe (model: 8710–2036; Agilent Technologies, Englewood, CO) connected to a vector network analyzer (model: N5320A; Agilent Technologies). The system was calibrated using distilled water at 25°C, air and a short circuit mode. Dielectric spectra were collected in triplicate at 4 different locations on each sample. The replicates with a standard deviation less than 4% were selected and averaged to get a single dielectric spectrum for each sample. A decrease in the ε′ and ε″ was observed as the incident frequency increased for all process cheeses. Partial least square regression (PLSR) models were developed using the dielectric spectra of process cheeses to predict the hardness (gf), melting point (°C) and modified Schreiber melt diameter (mm) of process cheese. Penetrometer, dynamic stress rheometry (DSR), and modified Schreiber melt (MSM) test were used as respective reference methods. The PLSR models were validated using the full cross-validation method. Root mean square error of crossvalidation was found to be 1.41°C, 1.25 mm, and 11.64 gf for DSR melt point, MSM diameter, and hardness of process cheese, respectively. Correlation coefficients of 0.94, 0.91, and 0.91 were observed for process cheese functional parameter and the dielectric spectra. Practical utility of the calibration models were evaluated using the range error ratio (RER). The RER was found to be > 8 for the 3 functional properties, indicting a limited to good practical utility. Further validation of the results on a larger data set will be necessary.

Key Words: dielectric spectroscopy, process cheese, functional properties

791 The effect of NaCl/KCl substitution on Halloumi cheese during storage: Chemical composition, proteolysis, texture profile, and microstructure. M. M. Ayyash* and N. P. Shah, *Victoria University*, *Melbourne, VIC, Australia*.

The effect of partial substitution of NaCl with KCl on chemical composition, LAB count, organic acids profile, proteolytic pattern, texture profile, and microstructure of Halloumi cheese was investigated. Halloumi cheeses were made and kept in 4 different brine solutions (at 18%) including NaCl only (HA), 3NaCl:1KCl (HB), 1NaCl:1KCl (HC), and 1NaCl:3KCl (HD) and then stored at 4oC for 56 d. Chemical composition, proteolysis, texture profile and microstructure were analyzed. No significant ($P > 0.05$) effect was observed between control and experimental cheeses in terms of composition and LAB count and pH values at the same storage period. At same salting treatment, moisture content decreased significantly while LAB count significantly ($P < 0.05$) increased. There was a significant ($P < 0.05$) difference in ash, sodium and potassium contents among cheeses at the same storage period. However, these parameters increased ($P < 0.05$) during storage at same salt treatment. There was no significant ($P > 0.05$) difference in lactic and citric acid contents among cheeses. In contrary, there was a significant ($P > 0.05$) difference in acetic acid concentration among cheeses. There were no significant ($P > 0.05$) differences in WSN, TCA-SN, and PTA-SN of experimental cheeses at same storage period. However, these parameters increased ($P < 0.05$) during storage at same salt treatment. Peptide pattern and urea-PAGE also showed no significant difference among experimental cheeses. There was no significant difference in TPA parameters between cheeses at same storage period. At same salt treatment, hardness, and cohesiveness decreased ($P < 0.05$) and adhesiveness increased ($P < 0.05$) during storage period. ESEM images showed compact and closed texture in all experimental cheeses. Our results showed that Halloumi cheeses can be stored in brine solution partly substituted with KCl without any adverse effect on their quality.

Key Words: Halloumi cheese, NaCl/KCl, chemical composition

792 Influence of NaCl reduction on the properties of Cheddar cheese. K. V. Grant*[1], S. Govindasamy-Lucey[2], J. A. Lucey[1], J. J. Jaeggi[2], M. E. Johnson[2], and S. A. Rankin[1], [1]*University of Wisconsin*, *Madison*, [2]*Wisconsin Center for Dairy Research*, *Madison*.

Reducing sodium in processed foods is a current trend in the food industry. The goal of our research is to develop reduced NaCl Cheddar cheese with acceptable body and flavor. To better understand the many roles of NaCl in cheese we studied the properties of Cheddar cheese with 3 NaCl levels: normal (1.7%), reduced (1.2%), low (0.7%). Curds were prepared using traditional Cheddar manufacturing, then subdivided into 6 batches and salted at the 3 levels, each in duplicate. Analysis was performed at 4 d, 3 wk, 5 wk, 3 and 6 mo. Within the first 5 wks of ripening there were significant differences in cheeses. Differences in moisture content and water activity were found: 37.0% and 0.970; 36.2% and 0.959; and 34.1% and 0.955 in normal, reduced and low NaCl cheese, respectively. The starter culture numbers also differed by 5 wks of ripening: 1.49×10^9, 1.04×10^9, and 7.44×10^8 CFU/mL for normal, reduced, and low NaCl cheese, respectively. Texture profile analysis revealed a significantly softer ($P < 0.01$) texture of low NaCl Cheddar compared to reduced and normal NaCl cheeses at 3 and 5 wks. Rheological small amplitude oscillatory shear tests indicated differences in loss tangent (LT) values during heating. A LT value of 1 is often used as a melting point. At 5 wks of aging the temperature where LT=1 was 50.4, 48.4 and 47.4°C for normal, reduced and low NaCl cheeses. Sensory analysis of the cheese was performed using a trained sensory panel (n=16) after 5 wks of ripening. Panelists found the lower NaCl cheeses to be significantly more acidic ($P < 0.005$) with a higher total off-flavor intensity ($P < 0.05$) and lower Cheddar flavor acceptability ($P < 0.005$).
This work shows that reducing the NaCl level in Cheddar cheese impacted starter culture growth, texture, meltability and flavor acceptability. The wide-ranging impact of NaCl reduction on cheese suggests that a range of approaches, such as addition of flavor enhancers and antimicrobials will be needed to increase the acceptability of low NaCl cheeses. This study provides a benchmark for our ongoing work on approaches to improve low NaCl Cheddar cheese. Results for cheese aged 3 and 6 mo will be reported.

Key Words: low sodium, Cheddar cheese

793 Influence of sodium gluconate on flavor and microbiology of low fat Cheddar cheese. D. J. McMahon*[1], C. J. Oberg[2], L. Moyes[2], R. E. Miracle[3], and M. A. Drake[3], [1]*Western Dairy Center, Utah State University*, *Logan,* [2]*Microbiology Department, Weber State University*, *Ogden, UT,* [3]*Southeast Dairy Foods Research Center, North Carolina State University*, *Raleigh.*

Low fat cheese manufactured using *Lactococcus lactis* ssp. *lactis* generally develops a flavor profile during aging uncharacteristic of Cheddar cheese. Such cheeses can have rosey aroma and taste as well as a pronounced burnt-brothy-bitter taste. The objective of this research was to determine if sodium gluconate (SG) addition during cheesemaking could ameliorate low fat cheese flavor. Cheese (in duplicate) was made using 700 kg of milk using a stirred curd method with SG added during salting to produce 4 blocks that were about 6% fat, 53% to 54% moisture, 1.7% to 1.8% salt, pH 5.0 to 5.3, and SG addition levels of 0% (control), 0.8%, 1.6% and 2.4%. The cheese was stored at 6°C and analyzed monthly for total lactic acid bacteria (LAB), lactococci, and nonstarter LAB (NSLAB) (i.e., *Lactobacillus casei*-type bacteria) using selective media. Cheese was analyzed at 4 and 6 mo for flavor profile using descriptive sensory analysis (15-point scale) and for compounds suspected of contributing to rosey and burnt off-flavors in low fat cheese. Adding SG did not change the LAB, lactococcal or NSLAB populations. Irrespective of SG addition, lactococcal populations gradually decreased during the first 5 mo of storage to about 10^4 cfu/g while NSLAB increased from their initial low level to high levels (10^7 to 10^8 cfu/g) within 30 d and remained the dominant LAB throughout storage. At 4 mo, cheeses all had rosey and burnt flavors with no differences ($P > 0.05$) in flavor except for a slight trend ($P < 0.05$) for increased saltiness with SG (3.5 for 2.4% SG cheese compared with 3.2 for control). At 6 mo, similar results were obtained and some bitterness was detected (absent at 4 mo) with the 1.6% and 2.4% SG cheeses having less ($P < 0.05$) apparent bitterness than the control cheese (0.5 compared with 1.0). Phenyl ethanal, phenyl ethanol, sotolone, or furaneol varied between replicates but not between treatments ($P > 0.05$). Homofuraneol and phenyl acetic acid were lower ($P < 0.05$) in the cheeses with 1.6% and 2.4% SG than in the control or cheese with 0.8% SG. This suggests that adding SG might be masking the bitter taste associated with burnt flavor in low fat Cheddar cheese.

Key Words: low fat, burnt flavor, microflora

794 Optimization of the manufacture of a no-fat added reduced-sodium processed cheese (Requeijão cremoso). L. M. Spadoti, A. G. F. Van Dender, P. B. Zacarchenco*, F. K. H. S. Trento, A. T. S. Alves, T. Q. Mendes, R. C. S. C. Ormenese, M. A. Morgano, and K. Yotsuyanagi, *Instituto de Tecnologia de Alimentos-ITAL*, *Brazil*.

The increased incidence of cardiovascular diseases caused by hypertension and obesity have heightened consumer awareness of nutrition and healthy eating. Within this context, the demand for foods with reduced levels of fat and/or sodium has greatly increased. Requeijão cremoso is a genuinely Brazilian processed cheese with a mild flavor, clear and shiny in color, and a creamy and elastic texture forming long strings. However, as with most cheeses, it is a source of fat and salt (sodium chloride). In view of the high consumption of this cheese in Brazil, and the current demand for healthier foods, no–fat added reduced-sodium requeijão (NFARSR) similar to the traditional product as to the main characteristics of flavor, texture and composition would be an important alternative to meet the needs of the changing market. In this study, the fat in requeijão was replaced by whey protein concentrate (WPC34%), while sodium reduction was achieved by replacing 40% of the sodium chloride by potassium chloride and by partially replacing the traditional, sodium phosphate-based emulsifying salt (Joha S9) by a potassium phosphate-based emulsifying salt (Joha S9K). The objective of this study was to optimize the use of the emulsifying salt combination (JohaS9+JohaS9K) to reduce the sodium level of an existing no–fat requeijão developed at Tecnolat–ITAL. For this purpose, a 2^2 factorial design with 2 factors (JohaS9 and JohaS9K), 2 levels (+1, −1) with 3 repetitions at the central point was used, resulting in 11 experimental trails. The results were evaluated by the surface response method to assess physical–chemical, sensory and instrumental texture parameters. Analysis of the surface response graphs, and especially the comments made by sensory panelists regarding flavor and texture, showed that RB4 – made with a mixture of 1.0% JohaS9 and 0.8% Joha S9K – was the NFARSR formulation that best met the preset specifications.

Key Words: reduced-sodium, processed cheese, cheese

795 Consumer flavor preferences and level of aged Cheddar cheese flavor. D. J. McMahon* and R. Wadhwani, *Western Dairy Center, Utah State University*, *Logan.*

Development of new cheese products such as low fat cheeses often have the goal of duplicating the flavor of the full fat counterpart. Sensory panels involving untrained consumers are often used to determine if a desired flavor profile is obtained Four sets of cheeses were obtained that including cheeses from 2 different manufacturers (designated A and B) that were labeled as mild, medium, sharp or extra sharp were purchased locally. A second set of Cheddar cheeses (designated C and D) were obtained from Utah State University (USU) that were 3, 6 and 12 mo of age and designated as mild, medium and sharp. All cheeses were tested by a trained descriptive cheese panel to produce a flavor profile for each cheese. Then 2 different consumer sensory panels (n = 120 for each panel) were conducted in which consumers were asked about their cheese flavor preferences, their cheese buying frequency, the form of cheese they buy and how they use cheese. They were then presented with 2 sets of cheeses (one commercial and one USU cheese) for overall liking using a 9-point hedonic scale and for flavor, texture, chewiness, and level of sharpness using a 5-point Just About Right (JAR) scale with 1 being "too little," 3 being "just about right" and 5 being "too much" of the attribute. Panelist responses were recorded via computer keyboard using SIMS 2000 software. The cheese panelists were from 18 to 35 years of age, with >60% being frequent cheese consumers. The majority of the panelists stated that they preferred to buy medium Cheddar cheese followed by sharp aged, mild with extra sharp being the least preferred. The 4 sets of cheeses had different flavor profiles ($P < 0.05$) and their overall liking scores were significantly different ($P < 0.05$) and ranged from a high of 6.82 for cheese A-mild to 4.87 for cheese B-sharp. The other top-ranked cheeses were C-mild, D-mild, B-medium. The 4 sharp cheeses had the lowest scores ($P < 0.05$). On the JAR scale the cheese with scores closest to JAR were C-medium, D-medium, A-medium for flavor; C-medium. C-sharp, and A-sharp; while for chewiness it was A-mild, C-medium and C-sharp. JAR thus matched better with consumer stated preferences.

Key Words: Cheddar, flavor, sensory

796 Nutritional and organoleptic quality of Cheddar cheese prepared from goat and buffalo milk blends. M. Nasir*, H. Jabeen, M. Abdullah, M. A. Jabbar, and M. A. Ali, *University of Veterinary and Animal Sciences*, *Lahore, Punjab, Pakistan*.

The goat milk in developing countries like Pakistan is not usually processed and its value in human nutrition has so far received very little factual attention from researchers and manufacturers. Thus the present

research project was designed to assess the feasibility of buffalo milk replacement with goat milk for Cheddar cheese manufacturing. Goat and buffalo milk were blended at various levels (25:75, 50:50, 75:25; goat milk: buffalo milk) and used along with 100% buffalo and 100% goat milk for Cheddar cheese preparation. The cheese thus prepared was subjected to different physicochemical analysis i.e., fat, protein, lactose, ash, total solids, SNF, amino acids, fatty acids, organic acids, pH, acidity and sensory evaluation at 0, 30, 60, 90 and 120 d of storage intervals. The data thus obtained was analyzed through ANOVA technique by applying 2-way CRD and the level of significance was defined as $P \leq 0.05$. Buffalo milk contained significantly ($P \leq 0.05$) more total solids and fat and less protein content as compared with goat milk. Therefore the addition of goat milk resulted in decreased fat and total solids, however there was progressive increase in protein content in cheese with the level of goat milk. pH and acidity of the cheese were not affected by the milk type, however there was decrease in pH and increase in acidity with storage period. Although, there was significant ($P \leq 0.05$) change in various fatty acids, organic acids and amino acid with level of goat milk in cheese samples, yet it had non-significant ($P \geq 0.05$) effect on the overall sensory quality of the finished product except for the attributes of flavor and overall acceptability beyond 50% goat milk level in samples; having significantly ($P \leq 0.05$) lower scores. The highest scores for most of the sensory parameters were awarded to the samples at 90 d storage interval. Thus, it is concluded that the Cheddar cheese with good nutritional profile and high acceptable quality can be made with up to 50% replacement of buffalo milk with goat milk, and may be recommended for commercial application.

Key Words: goat milk, Cheddar cheese, sensory quality

797 Ability of Smart Nose to discriminate *tina* biofilms contributing to produce unique volatile compounds in inoculated milk. S. Carpino*[1], I. Stampelou[2], G. Belvedere[1], C. Pediliggieri[1], and G. Licitra[3,1], [1]*CoRFiLaC, Regione Siciliana*, *Ragusa, Italy*, [2]*Wageningen University*, *the Netherlands*, [3]*DACPA, University of Catania*, *Catania, Italy*.

Wooden equipment is used in the traditional cheese making process of PDO Ragusano cheese and no starters are added in the cow raw milk. A source of aromatic components in milk might be the biofilm microflora released from the traditional wooden vat called *tina*, used during cheese making, as well as the flora naturally present in raw milk. Thus, the objectives of this work were to investigate the potential role of the *tina* biofilm to generate aroma compounds when inoculated into milk and to assess the ability of a Smart Nose to discriminate them by analyzing the aroma profiles of the inoculated milks. Pasteurized milk was used to avoid the interference of aroma compounds generated by the natural microflora present in raw milk. In this study, *tina* biofilms isolated from 3 different farms were inoculated in milk and incubated at conditions simulating the ones of the real cheese making of Ragusano before brining. The inoculated milk samples were analyzed through Smart Nose and the data were statistically treated by Principal Component Analysis (PCA). The PCA results showed first of all a good separation of the inoculated milks from the blank one (non-inoculated milk), highlighting a significant influence of *tina* biofilm on the developed milk aroma profile. In addition, all inoculated milk samples showed a clear separation among them, thus showing that each *tina* biofilm had a different behavior regarding aroma releasing when inoculated into milk under certain conditions. Certain volatile compounds were detected by GC-MS analysis in all 3 inoculated samples while these were totally absent in the blank, showing that were produced by the biofilm. Moreover, it was observed that the microbiological composition of each *tina* biofilm gave respectively a different aroma contribution. In conclusion, it was shown that Smart Nose is able to discriminate quite well aromatic profiles attributed exclusively to the biofilm bacteria during the first steps of cheese making.

Key Words: *Tina* biofilm, aroma profile, Smart Nose

798 Segmentation of scanning electron microscopy images using incremental learning. G. Impoco[1], L. Tuminello[1], M. Caccamo*[1], and G. Licitra[1,2], [1]*CoRFiLaC, Regione Siciliana*, *Ragusa, Italy*, [2]*DACPA, University of Catania*, *Catania, Italy*.

This study tested a method for automatic quantification of digital micrographs based on statistical classification of pixels and incremental learning. Ten scanning electron microscope (SEM) images of Ragusano cheese were used as training set and the main microstructural features were gathered in 3 morphologically meaningful classes: fat globules, whey pockets, and protein matrix. A series of 10 numerical values (descriptor) was associated to each pixel. Images were partitioned into significant regions (segmentation) by clustering pixel descriptors using the k-means algorithm. According to the resulting clusters, an initial automatic classification associated each region to a specific microstructural feature. The classified images, used as reference labelings, were used to automatically learn a Bayesian statistical model which associates to each pixel its probability to belong to a certain feature class. This model was used to classify again input images. Output classifications were presented in color to a SEM specialized operator, who could select misclassified regions and associate them with a different, more appropriated label (re-labeling). New statistics obtained from the re-labeled regions were integrated into the model. The updated model was used to re-classify input images. This process of supervised re-labeling and automatic pixel classification was iterated until satisfactory results were obtained. We compared incremental learning to off-line image labeling, where the input images are manually labeled only for the initial training of the model, from a single reference data set. Experimental data showed that incremental learning gives better results than off-line learning. The training phase is less burdensome and time consuming for the user, and it can be adapted to new image samples without executing from scratch the long and tedious initial training.

Key Words: image analysis, SEM, cheese microstructure

799 Improvements and validation of mid-infrared predictions of milk fatty acid. H. Soyeurt*[1,2], S. McParland[3], D. Berry[3], E. Wall[4], N. Gengler[1,2], F. Dehareng[5], and P. Dardenne[5], [1]*University of Liege, Gembloux Agro-Bio Tech, Animal Science Unit*, *Gembloux, Namur, Belgium*, [2]*National Fund for Scientific Research*, *Brussels, Brussels, Belgium*, [3]*Teagasc Moorepark Dairy Production Research Centre*, *Fermoy, Cork, Ireland*, [4]*Sustainable Livestock Systems Group, Scottish Agricultural College*, *Penicuik, Midlothian, United Kingdom*, [5]*Agricultural Walloon Research Centre, Quality Department*, *Gembloux, Namur, Belgium*.

The development of mid-infrared equations to predict the milk fatty acid (FA) content of milk allows prompt analysis of large numbers of samples. The first aim was to improve these predictions by comparing 6 statistical approaches. The second one was to validate the new equations using an independent sample set. The calibration set contained 239 spectrally different Belgian milk samples collected for over 2 years from several cows and breeds. FA were quantified by gas chromatography (GC). Statistical approaches tested were 1) partial least squares regression (PLS), 2) PLS and first derivative, 3) PLS and repeatability file (RF), 4) PLS, first derivative and RF, 5) PLS, second derivative, and 6) PLS, second derivative and RF. This last file contained spectra obtained from the same samples using 5 spectrometers. Cross-validation (CV) used 20 groups from the calibration set. Methods were compared using the ratio of the standard deviation of GC values to the standard error of CV (RPD). An external validation permitted a second comparison and was done using 362 samples collected for one year from multiple breeds and cows in Belgium, Ireland, and Scotland. Different RPD values were obtained by the 6 methods. Generally the equations developed using method 4 gave better results suggesting the adaptation of the methodology to the studied FA. It confirms by the obtained validation coefficients of determination. Highest values were observed for the equations with the highest RPD values except for C18:0. The ability to predict FA using method 4 gave superior results to those shown in previous publications.

Key Words: mid-infrared, milk, fatty acid

800 Evaluation of a faster extraction and purification procedure for the analysis of vitamin D in fortified milk. T. C. Schoenfuss*[1] and O. Shimelis[2], [1]*University of Minnesota*, *St. Paul,* [2]*Sigma-Aldrich*, *Bellefonte, PA*.

Current methods to analyze vitamin D in milk require lengthy sample preparation steps to extract vitamin D before analysis by chromatographic methods like HPLC. The approved method from Standard Methods for the Examination of Dairy Products requires multiple days to accomplish and includes over-night saponification, liquid-liquid

extraction, dry down of over 135 mL of hexane under nitrogen, and solid phase extraction before HPLC. Various direct extraction techniques have been attempted but have not been adopted by the industry due to low extraction rates. The goal of this project was to develop a quicker, simpler method to quantify vitamin D in milk by combining new technologies. The method developed involved precipitating protein in 10 mL of milk with 10 mL of ethanol, sonicating for 1 min at 70% amplitude with a sonic horn immersed in the sample to break up complexes, and 2 liquid extractions with 15 mL hexane. The hexane extracted was dried down under nitrogen with a TurboVap LV Evaporator (Caliper LifeSciences, Hopkinton, MA) and reconstituted in 1 mL hexane. Solid phase extraction with an adsorbent designed for fatty acid methyl esters (Ag-Ion SPE tube, Sigma-Aldrich, Bellefonte, PA), and reverse phase HPLC of the eluent was done with several different columns and mobile phases that all allowed separation of D2 and D3. Vitamin D2 and D3 were observed to have different affinities for the solid phase extraction column, especially in the presence of fat, and the extraction rate from milk for D3 was up to 30% lower than D2. This extraction procedure can be completed in 1 d. This work highlights promising improvements for vitamin D analysis in milk that could reduce the time and solvents necessary.

Key Words: vitamin D, milk, extraction

801 Structural comparison of bovine and camel chymosin in relation to cheesemaking properties. K. B. Qvist*[1], J. L. Jensen[2], J.-C. N. Poulsen[2], M. Harboe[1], H. van den Brink[1], A. Mølgaard[2], and S. Larsen[2], [1]*Chr. Hansen*, *Hørsholm, Denmark*, [2]*Department of Chemistry, University of Copenhagen*, *Copenhagen, Denmark*.

By initiating milk coagulation, rennet enzymes are essential in cheesemaking. Bovine chymosin (BC) has long been considered the most suitable rennet, but recently it has been shown that *Camelus dromedarius* chymosin (CC) provides several benefits over bovine chymosin (BC), having a 7-fold higher ratio between milk clotting and general proteolytic activity. The objective of this work was to investigate the structural background for the improved selectivity of CC. Crystals of fermentation produced CC were grown with the hanging drop vapor diffusion technique. Data were collected by radiation with x-rays at 1.04 Å, and reduced with the XDS software, followed by flagging of reflections for free R-factor calculation, using the CCP4 suite. Molecular replacement was done with the Phenix software suite using the BC structure 1CMS as template. Cycles of manual fitting and refinement were done with Coot and Phenix, respectively. Validation was done with the WHAT IF package. The structure of CC, without the first 10 residues was obtained at 1.85 Å resolution, with a free R-factor of 0.21. The overall fold was similar to that of BC, but with notable differences in the details. L32V and E290D substitutions provide more space for bulky amino acids at the P1 and P1' positions, respectively. A further 7 substitutions in the extended binding region may contribute to selectivity differences. Also, in CC a surface patch, at positions 244–254, previously implicated in binding the positively charged sequence 98–102 of κ-casein (KC), was less negatively charged than in BC. This mirrors the fact that 98–102 in camel KC is more positively charged than in bovine KC. A patch near the edge of the cleft, at positions 289–300 was significantly more negative in CC. Finally, differences in the location of the N-terminal were observed. In conclusion, several structural differences likely to affect cheesemaking properties were identified.

Key Words: camel chymosin, 3-D structure, renneting

802 Detection of proteolysis in milk. A. S. Grandison*[1], L. M. Chove[2], and M. J. Lewis[1], [1]*University of Reading*, *Reading, Berkshire, UK*, [2]*Sokoine University*, *Morogoro, Tanzania*.

The quality of raw milk is affected by proteolysis during storage. It occurs through either bacterial or native proteases. Plasmin, the major protease occurring in milk, forms part of a complex system which hydrolyses the caseins and thus affects the quality of dairy products. These effects may be positive, as in cheese ripening; or negative as in the production of bitter off-flavors in dairy products or age-gelation in UHT milk. The enzyme system is very heat resistant and cannot be eliminated by pasteurization or even UHT processing. The aim of this study was to develop a simple method to detect protease activity in milk. Analysis of pH 4.6 or 6% trichloracetic acid (TCA) soluble extracts of milk by trinitrobenzene sulfonic acid (TNBS), reverse phase high performance liquid chromatography (RP-HPLC), gel electrophoresis and fluorescamine methods was carried out to determine their relative suitability for the detection of proteolysis in milk during storage for up to 7 days. Trypsin or plasmin were added to UHT sterilized milk at different levels to promote/accelerate proteolysis. This was due to the high cost of plasmin, hence trypsin was used for initial trials as it has a similar mode of action to plasmin. The TNBS, fluorescamine and RP-HPLC methods gave highly correlated results ($R^2 > 0.93$), clearly demonstrating increased proteolysis during storage. Gel electrophoresis revealed that the breakdown products from trypsin were similar to plasmin. The most obvious phenomenon was that γ-caseins, formed as a result of β-casein degradation, subsequently disappeared due to extensive proteolysis in the trypsin samples. Similar trends were found for both the pH 4.6 and 6% TCA soluble extracts. The amido methyl coumarin (AMC) method, which is specific for plasmin activity, was found to be very sensitive in the determination of proteolysis by plasmin, but is also very expensive. On balance, the TNBS method was recommended on the basis of accuracy, reliability, simplicity and cost.

Key Words: proteolysis, plasmin, trypsin

803 Genotyping of κ-casein and β-lactoglobulin genes in Chinese Holstein dairy cows, Jersey and water buffalo. D. X. Ren*[1], S. Y. Miao[1], Y. L. Chen[1], C. X. Zou[2], X. W. Liang[2], and J. X. Liu[1], [1]*Institute of Dairy Science, Zhejiang University*, *Hangzhou 310029, P. R. China*, [2]*Water Buffalo Institute, Chinese Academy of Agricultural Science*, *Nanning 530001, P. R. China*.

The present work is carried out to analyze the polymorphism of κ-casein and β-lactoglobulin genes in Chinese Holstein dairy cows, Jersey and water buffalo. The DNA was extracted from the blood samples of 82 Holstein, 56 Jersey and 48 buffalo. Identification and genotyping of κ-casein and β-lactoglobulin gene was conducted by PCR-RFLP assay. Different restriction endonucleases, *Hinf*I and *Hae*III, were used. The PCR product of the primer specific for κ-casein and β-lactoglobulin gave the specific band at size 379, and 252 bp, respectively. After digestion of PCR product with restriction enzymes, different genotypes of κ-casein and β-lactoglobulin were obtained, the fragment size of which is shown in Table 1. Among the examined Holstein cows, κ-casein genotype of AA, BB, and AB was 45.83, 8.34, and 45.83%, and corresponding genotype for β-lactoglobulin was 19.1, 20.6, and 60.3%, respectively. For Jersey, the κ-casein genotype of AA, BB, and AB was 0, 80, and 20%, and the corresponding value was 36.8, 22.8, and 40.4%for β-lactoglobulin, respectively. However, all buffalo samples were homozygous for the κ-casein and β-lactoglobulin, with all genotype as BB. In summary, allele of κ-casein gene was mainly A in Holstein dairy cows and B in Jersey, while β-lactoglobulin was mainly A in both Holstein cows and Jersey. However, water buffalo were monomorphic

for the κ-casein and β-lactoglobulin genes, possessing only allele B in homozygosis form.

Table 1. Fragment size corresponding to different genotypes of κ-casein and β-lactoglobulin after digestion of PCR product with restriction enzymes

Milk protein	Genotypes	Size of fragments from digestion of PCR product with restriction enzymes (bp)
κ-casein	AA	156, 132, 91
	BB	288, 91
	AB	288, 156, 132, 91
β-lactoglobulin	AA	144, 108
	BB	108, 74, 70
	AB	144, 108, 74, 70

Key Words: genetic polymorphism, κ-casein, β-lactoglobulin

804 Impact of plasmin hydrolysis of caseins on the minimum coagulation temperature observed for milk during renneting. B. Coude*, Y. Lu, and J. Lucey, *University of Madison*, *Madison, Wisconsin*.

The rennet coagulation of milk involves 2 different stages. The primary stage is the enzymatic phase in which rennet hydrolyzes κ-casein. The second stage is an aggregation of renneted micelles but this aggregation reaction is highly temperature dependent and does not occur at temperatures < 18°C. It is not clear why the aggregation reaction is so temperature dependent. We believe that at low temperature β-casein may protrude from the surface of casein micelles thereby, creating an additional barrier to aggregation. We hypothesized that removal of β-casein, that is close to the micelle surface, should allow rennet coagulation to occur at lower temperatures. We used plasmin enzyme to hydrolyze β-casein since it is more susceptible to hydrolysis than α-caseins while κ-casein is resistant to breakdown. We studied the impact of plasmin hydrolysis of caseins on the minimum temperature at which the rennet coagulation reaction could occur in milk. Human plasmin (0.01mg/ml) was added to reconstituted skim milk. Milk samples were incubated with plasmin at 37°C for 0.5 to 6 h. Hydrolysis was terminated by adding soybean trypsin inhibitor. The extent of degradation of caseins was determined with SDS-PAGE. Degradation of α- and β-caseins after incubation with plasmin for 0.5 to 6 h ranged for about 10 to 40%, and about 30 to 60%, respectively. Rennet was added to milk at different temperatures: 32, 25, 20, 15, 10 and 5°C. Coagulation was visually determined (Berridge method) as well as monitored by dynamic low amplitude oscillatory rheology. The minimum rennet coagulation temperature for control milk (without plasmin hydrolysis) was ~20°C. Milk that was hydrolyzed with plasmin at 37°C for 0.5 or 1 h could undergo rennet coagulation at ~15°C. Milk that was hydrolyzed with plasmin at 37°C for 2 h and up to 6 h could undergo rennet coagulation at temperatures as low as 5°C. In conclusion, these results support the hypothesis that at low temperature, β-casein on the micelle surface inhibits the aggregation of renneted micelles.

Key Words: plasmin, hydrolysis, rennet coagulation

805 Bilingual audiovisual technology improves dairy animal care and quality assurance. B. Butler*, S. Torres, J. Valles, C. D. Reinhardt, and D. U. Thomson, *Kansas State University*, *Manhattan*.

The Beef Cattle Institute at Kansas State University (BCI) has developed bilingual educational tools based on audiovisual technology to improve technical knowledge within livestock operations. The Dairy Animal Care and Quality Assurance (DACQA) program is available in a package of 36 multimedia modules with a total length of 2hrs and 42 min of training material to train animal care givers in areas of animal health, productivity and well-being. This quality assurance program promotes the best management practices for dairy animal care and husbandry through each area of the milk production operation, including proper management of feedstuffs and nutrition; pharmaceutical usage and administration; cattle handling guidelines; identification; record keeping and animal marketing decisions. The information in the modules is presented in a simple and colloquial communication to assure effective transmission of information. Two of the DACQA modules (one module addressing animal health practices and one module addressing animal handling) were presented to 10 professional dairy care workers who had a preference for learning in either English (n = 7) or Spanish (n = 3); a 10-question examination with questions relating to each specific module was given before and after viewing each of the modules. Test scores improved by 28% from pre-viewing to post-viewing ($P < 0.01$; pre-viewing score = 7/10; post-viewing score = 9/10); there was no effect of module or language preference or their interaction ($P > 0.37$). These results concur with previous data we have generated which demonstrated a 25% increase in knowledge of beef quality assurance best management practices following viewing of this type of module. With the audiovisual technology available, the industry not only addresses current topics related to producing safe and wholesome dairy products, but also supports a welfare-centered and economically sustainable dairy industry.

Key Words: bilingual, dairy, training

806 Impact of a practical dairy farm management training workshop on the knowledge level of participants. E. Ashraf*[1], Z. Hayat[1], M. Z. U. Khan[2], S. U. Ansari[1], I. Hussain[1], F. A. Atif[1], M. Arif[1], and M. Luqman[1], [1]*University College of Agriculture*, *University of Sargodha, Sargodha-40100, Pakistan*, [2]*University of Veterinary & Animal Sciences*, *Lahore, Pakistan*.

The dairy industry is an important part of the economy in developing countries. There is a dire need for trained human resources for the development of this sector. Five d training workshop was organized for demonstration of dairy management practices. Participants (n = 36) were randomly selected across the country. The objectives were to evaluate the knowledge level of participants after making them aware of the latest feeding and management techniques practiced in the dairy industry, and to identify factors that are directly related to their learning. The pre and post test each comprising of 20 multiple choice questions was given to the participants at the start and end of the training. There was a significant improvement in the knowledge level after attending the training since the Mean = 5.03, $t = 9.39$, SE = 3.21 with p-value <0.1. On average there was a 25% increase in the marks of the participants. Complete regression model was run with the independent variables of age, experience, and education on the difference of the pre and post tests and model was statistically significant $F(3, 32) = 2.75$ $P < 0.1$. Age was the only significant predictor in the model and showed negative effect on the difference of marks of the participants, and explains 20% of the total variance. This explained the phenomenon that as age increases the impact of training on the knowledge level decreases. Another regression model was run on the marks after the training. The model was statistically significant $F(3, 32) = 4.20$ $P < 0.1$. It was revealed that education level plays a central role in the knowledge improvement and was a good predictor which explained 28% of the total variance in the data. Correlation of the variables also confirmed the results and showed that only education is positively significantly correlated with the marks of the participants after completing training. The other 2 variables, age and experience, showed a negative relationship with the marks of the participants. It is concluded that older participants with lower education levels could not perform well in short training programs and need separate extensive and long-term training sessions.

Key Words: training, knowledge, dairy

807 A stochastic evaluation of reproductive management programs for dairy herds. J. O. Giordano*, P. M. Fricke, M. C. Wiltbank, and V. E. Cabrera, *University of Wisconsin*, *Madison*.

A Markov-chain simulation model was developed to compare the net present value (NPV, $/cow/d) generated by different reproductive management programs (RP) in a dairy herd. The daily NPV of a specific RP was calculated by adding the discounted expected monetary values (DEMV) of that proportion of cows that become pregnant at each successive AI service until a maximum predefined DIM plus the DEMV of that proportion of cows not becoming pregnant to the RP. The DEMV for a lactation defined by DIM at pregnancy was calculated based on the value of milk produced, feed cost, expected value of a new born calf, and cost of culling. Economic, productive, and reproductive values were user–defined for each RP evaluated. The model sequentially estimated the percentage of cows eligible for breeding, becoming pregnant, and not becoming pregnant at each AI service based on the service rate (SR) and conception rate (CR) of each RP. Total AI service cost including pregnancy diagnosis (PD) was applied to all cows until pregnancy or culling for reproductive failure. For synchronized AI services, total cost was calculated by adding the individual cost of: treatments, labor, AI, and PD. Total cost for estrous services was calculated by adding the individual cost of heat detection, AI, and PD. A decision tree then compared the NPV for different RPs. A comparison among commonly used programs with typical reproductive values (Table 1) indicated that a Presynch–Ovsynch (PS–Ov) protocol with 100% TAI (A) for 1st service was stochastically dominant over RP (B) and (C). Utilization of this model by commercial dairy herds may facilitate selection of economically optimal RP based on farm-specific parameters.

Table 1. Net present value for commonly used reproductive programs

	1st AI					
	ES		TAI			
	(%)		(%)		NPV ($/cow/d)	NPV ($/1000-cow/y)
Program	SR[2]	CR[2]	SR[2]	CR[2]	Mean±SD (Range)	Difference from maximum
(A)100% TAI PS-Ov & Ovsynch	-	-	100	[36,43,50]	6.93±0.03(6.87–6.99)	Max
(B)ES[1] + TAI PS-Ov & Ovsynch	[26,49,55]	[30,35,39]	[74,51,45]	[20,30,41]	6.83±0.03(6.76–6.89)	−36,500
(C)100% ES[1]	[45,55,65]	[28,33,36]	-	-	6.81±0.02(6.77–6.84)	−43,800

[1]ES = estrous service, [2]Triangular distribution [min, most likely, max].

Key Words: economics, simulation, stochastic

808 Optimization of insemination and replacement decisions under herd constraints. A. De Vries*, *University of Florida*, *Gainesville*.

Existence of herd constraints such as a limited number of replacement heifers or a milk quota implies that optimal insemination and replacement decisions for individual animals are not independent. Historically, calculation of such optimal decisions has shown to be difficult. A linear programming model was developed to evaluate optimal replacement and insemination decisions for dairy heifers and cows considering herd constraints. The model considered 3 semen types (for example sexed dairy, conventional dairy, conventional beef), 5 levels of milk production, and 10 parities including heifers. Each parity had 20 voluntary culling opportunities for non-pregnant animals. Heifers and cows were allowed a maximum of 18 insemination opportunities. Time step between insemination decisions depended on service rate. Time step for culling decisions include the start of the parity and before each insemination opportunity. The model contained 3,700 decision variables. Genetic value of heifer calves was a function of service sire net merit, age of the dam, and level of milk yield of the dam. Inputs were lactation curves, milk price, feed costs, insemination costs, service rates, conception rates, dystocia costs, involuntary culling risks, and other variable and fixed costs. To illustrate, profit/cow per yr in a closed herd with choice from 3 semen types was $368. Conventional semen was used in 13% of the heifer inseminations and 47% of the cow inseminations. Sexed semen was used in 74% of the heifer inseminations and 11% of the cow inseminations. Average milk yield was 32 kg/cow per d. Setting the milk quota to 30 kg/cow per d resulted in $293 profit/cow per yr with 97% of all slots filled. The optimum insemination mix included less conventional semen, more beef semen, more sexed semen in cows but less in heifers. The linear programming model formulation allows for exploring realistic optimal replacement and insemination decisions when herd constraints need to be considered.

Key Words: culling, insemination, herd constraint

809 Animals and Food Security: Blending land-grant missions through international engagement in Romania. P. D. Ebner* and M. A. Russell, *Purdue University*, *West Lafayette, IN*.

This international service-learning course works in villages with Heifer Project Romania and uses extension activities to enhance the capabilities of US land grant universities to better conduct their missions domestically and abroad. Students work in bi-national teams across agricultural and community disciplines to apply their knowledge and experience to make a difference. This course builds upon established collaborations with Heifer Project Romania and 3 agricultural sciences and veterinary medical universities in Romania to develop intercultural competencies. Extension educators have the expertise to facilitate the organization of local associations to better prepare the community for the future. Funding agencies around the globe seek to serve private or public organizations that have the capacity to implement their projects. Through these activities, teams bring home the ideas and technologies of other countries and develop international networks to make our domestic clientele competitive in the future. The authors have conducted similar courses and experiences in Paraguay and Ecuador.
Students develop an ability to effectively communicate with others regardless of culture and backgrounds, the capacity to work effectively as part of bi-national, problem-solving teams, and the capability to apply social, economic, political, and environmental principles to serve in an international rural village or their own county. With focus on environmental stewardship and protection systems, participants learn and apply topics of large scale composting (with manure), swine and poultry nutrition, ruminant nutrition, livestock diseases, livestock care standards, and environmental regulations for livestock production (European Union). Students develop experience in designing smaller-scale management systems and facilities that provide more flexibility to their livestock owners in their home counties. We will share both qualitative and quantitative methods of assessing learning and the development of intercultural competencies as well as the agronomic practices.

Key Words: international extension, environmental protection, intercultural competencies

810 Avian embryology posters as a teaching aid. T. A. Hess*[1], J. P. Blake[2], W. D. Berry[2], and R. A. Voitle[2], [1]*School of Forestry and Wildlife Sciences*, *Auburn, AL*, [2]*Auburn University, Poultry Science Department*, *Auburn, AL*.

A project was undertaken that documented the embryonic development of both chickens and game birds (bobwhite quail and ringneck pheasants). There is a vast amount of information about the developmental stages of avian embryos (due primarily to the ability to incubate eggs away from the dam); this project condensed an enormous amount of knowledge into a readily accessible visual source for educational purposes. After incubating eggs in a staggered schedule, embryos were extracted from the shells at specific stages of development. Embryos were collected for each day of incubation for each species (chicken, bobwhite quail, ringneck pheasant). Pictures were taken of the embryos (Nikon D70S Camera; AF Micro Nikkor 60mm lens; Nikon SBR200 ring flash; CS920 Photographic Copy Stand). Posters were developed commercially incorporating photography and text describing the physiological changes, to stand as representations of the developmental stages. These posters were then provided to meet the educational needs of the poultry industry, game bird producers, and educational systems (middle through high schools) across Alabama. Knowing the many stages of avian embryonic development is useful information for both the seasoned poultry producer as well as those studying embryology. Game bird producers, often an underserved portion of the poultry community, can use these posters to train hatchery personnel or to provide game bird-based embryological training to local schools.

Key Words: embryology, chicken, game birds

811 Alternative fuel demonstrations on Pennsylvania turkey, broiler and duck farms burning poultry litter, wood pellets and wood chips vs. propane. P. H. Patterson*, R. M. Hulet, and D. E. Buffington, *The Pennsylvania State University*, *University Park*.

Propane costs, grower profitability and concerns about combustion gases (CO2, H2O) and litter quality were instrumental in establishing 4 poultry farm fossil fuel alternative demonstrations. Two turkey houses, 15.2 × 183m with 17,000 birds/house were originally fitted with 30 brooders/house. A 586kW (2 mill BTU/hr) boiler made by Bio-Fuel Technologies www.Bio-FuelTechnologiesLLC.com was installed between the houses with 8 ceiling mounted heat exchangers/house. The chain grate fuel delivery allows this farm to burn spent turkey litter. We are currently monitoring propane and litter consumption, litter and air quality and bird performance. On 2 broiler farms a FarmTek 234kW (800,000 BTU/hr) hot air furnace http://www.farmtek.com/farm/supplies/cat1a;ft1_heaters_accessories.html was installed in the middle of one house with 2 61cm air tubes and fans pushing heat to both ends. The furnaces are fueled by hardwood pellets from Energex Pellet Fuel, Inc. www.energex.com. One house per farm has the 234kW furnace, while the other has

the original propane equipment to compare fuel consumption and bird performance. Farm A houses are 14.6 × 152m with 30,000 birds each and 11 radiant tube heaters/house. Farm B houses are 13.4 × 152m with 27,000 birds each and 4 wall mount space heaters. A duck farm with 2 houses 13.7 × 137m upgraded the original 6 propane space heaters/house with 12 hot water heat exchangers and a 264kW (900,000 BTU/hr) boiler made by Total Energy Solutions LLC www.gototalenergy.com. The fuel is a course hardwood chip. The farm broods 9400 birds in the first 45.7m to 18d, and finishes at 39d in the remaining 91m. They grow 13 flocks/house/yr, and finish birds at 3.3kg. Monitoring continues and outreach has included 3 field days and 2 presentations to state government and sponsors. An overview of the farms, their installations and YouTube videos are planned for our extension webpage http://poultryextension.psu.edu/. Further descriptions of the alternative fuel systems and their performance will be submitted for publication and presented at in-state meetings.

Key Words: alternative fuel, demonstrations, poultry performance

812 Equine rotational grazing demonstration: Field observations and extension program impact. A. O. Burk*, N. M. Fiorellino, K. M. Wilson, T. A. Shellem, and M. E. Dwyer, *University of Maryland*, *College Park*.

An equine rotational grazing demonstration site was constructed to temporally assess performance of the vegetation and horses within the rotational system and to train horse farm operators to adopt environmental protection best management practices (BMPs). Four Thoroughbred geldings (initial BW 476.4 ± 5.4 kg; initial BCS 4.9 ± 0.9 units) were rotationally grazed between April 2009 and January 2010 using 4 0.49 ha mixed grass/legume pastures, one 0.08 ha mixed grass heavy use paddock, and one 0.04 ha sacrifice area. Mean pasture vegetative cover over the observational period was 78 ± 3% with the majority represented by grasses (69%), and to a lesser extent legumes (6%) and weeds (3%). Horses spent an average of 80.1 ± 6.5% of days grazing pasture with June and July having the most days grazing (100%) and December and January having the least days grazing (38.8% and 51.6%, respectively). Horse were moved onto and off of pasture when grass height averaged 11.1 ± 1.1 and 6.9 ± 1.3 in, respectively. Horse BW peaked in November ($P = 0.009$) while BCS remained unchanged. Assuming 2% DM intake, pasture or supplemental hay met nutritional requirements for horses at maintenance, with the exception of sodium, zinc and copper. Amount of hay offered when horses were housed in the sacrifice lot was highest during May, December, and January. In regards to extension education, 3 2 h events were held at the site in April, June, and August drawing 141 participants. After attending the events, the majority of participants (≥51%) indicated a significant to very significant increase in their knowledge of 9 of 16 topics related to environmental protection BMPs. More than 80% of participants indicated they would adopt 12 of 15 BMPs with lowest rates observed for maintaining a stocking density of 0.6 ha horse $^{-1}$ (58.1%), applying herbicides as needed (69.8%), and use of heavy use pads in muddy areas (79.5%). Use of the equine rotational grazing demonstration site has been a valuable tool to increase our knowledge of the performance of a rotational grazing system for horses and in increasing the adoption of environmental protection BMPs by horse farm operators.

Key Words: extension, horse, environment

813 Milk production and feed efficiency in dairy cows fed corn silage hybrids varying in fiber digestibility. L. E. Chase*, *Cornell University*, *Ithaca, NY*.

A trial with lactating dairy cows was conducted to examine the relationships between corn silage hybrid fiber digestibility, milk production, dry matter intake and feed efficiency. Brown midrib (BMR), NutriDense (ND) and a conventional (C) hybrid were used. Twenty cows were assigned to each treatment at 7–12 d after calving and individually fed the treatment rations for 10 weeks. The same ration was fed to all cows with the only difference being the corn silage hybrid used. This ration contained 59% corn silage, 5.5% straw and 35.5% grain. Nutrient composition of this ration averaged 46.5% DM, 17.4% CP and 34.1% NDF. Nutrient composition of the BMR hybrid was 32.9% DM, 8.4% CP, 38.6% NDF and 36.5% starch. The ND hybrid was 32.9% DM, 8.36% CP, 41.3% NDF and 33.6% starch. The conventional hybrid was 36.3% DM, 7.8% CP, 38.3% NDF and 39% starch. NDF digestibility (30-h) values were 59.6, 46.8 and 49.4% for the BMR, ND and C hybrids. Data analysis was done using the GLM procedure in SAS with a covariate. Cows fed the BMR corn silage had greater DMI (26.1 kg/day; SEM = 0.32) than either the ND (23.5 kg/day) or the C (24.2 kg/day) hybrids ($P < 0.001$). Daily milk production was also greater (46.6 kg/day; SEM = 0.71)) for cows fed the BMR hybrid ($P < 0.0047$). Milk production was not different between the C (43.6 kg/day) and ND (43.5 kg/day) hybrids. Milk fat did not differ between the 3 hybrids. Milk true protein was lower in cows fed the ND ration (2.67%; SEM = 0.027) than cows fed either the BMR (2.77%) or C (2.78%) rations ($P < 0.007$). Feed efficiency (kg 3.5% FCM/kg DMI) was greater for cows fed the ND ration (1.87; SEM = 0.028) compared with either BMR (1.76) or C (1.74) rations ($P < 0.002$). Dairy cows fed BMR corn silage had higher milk production in this trial. However, cows fed the ration containing ND corn silage had significantly higher feed efficiency.

Key Words: corn silage, feed efficiency

814 Performance of dairy cows fed high water soluble carbohydrate sorghum silage. S. Amer* and A. F. Mustafa, *McGill University*.

Twelve lactating Holstein cows were used in a cross- over study (n = 2) to determine the performance of dairy cows fed high water soluble carbohydrate sorghum silage (SS, sweet sorghum, cultivar CSSH45) relative to alfalfa silage (AS). The sweet sorghum cultivar contained 8% water soluble carbohydrates while the regular counterpart (CFSH30) contained 3% water soluble carbohydrates. Sweet sorghum was harvested at early heading stage while alfalfa was a second cut crop. Experimental periods consisted of 14 d of diet adaptation and 8 d of data collection. Two isonitrogenous diets with 50:50 forage: concentrate ratio were formulated. Sweet sorghum silage and AS constituted 70% of the forage in each diet. Two lactating Holstein cows fitted with ruminal cannulas were used to determine the effects of dietary treatments on ruminal fermentation parameters. Relative to AS, SS contained 58% more NDF, 70% less CP but similar ADF concentration. Cows fed SS consumed ($P < 0.05$) less DM (23.3 vs. 26.1kg/d) and CP (4.1 vs. 4.7 kg/d) but more ($P < 0.05$) NDF (9.1 vs. 7.9 kg/d) than those fed AS. Milk yield (33.5 vs. 36.7 kg/d) was higher ($P < 0.05$) for cows fed AS than for those fed SS. However, energy-corrected milk was similar for both dietary treatments (average 37 kg/d). Cows consumed SS produced milk with greater ($P < 0.05$) concentrations of fat and total solids but lower ($P < 0.05$) concentrations of lactose and SNF. Ruminal pH was higher ($P < 0.05$) whereas ruminal NH3-N was lower ($P < 0.05$) for cows fed SS than those fed AS. Total VFA concentration and molar proportions of propionate and butyrate were greater ($P < 0.05$) whereas molar proportion of acetate was lower ($P < 0.05$) for cows fed SS than for those fed AS. It was concluded that SS when compared with AS, had a negative impact on feed intake and milk yield, whereas energy corrected milk and milk efficiency were similar.

Key Words: sweet sorghum silage, alfalfa silage, dairy cows

815 Effects of water soluble carbohydrate content of ensiling characteristics, chemical composition and in vitro digestibility of sorghum silage. S. Amer*[1], P. Seguin[1], F. Hassanat[2], R. Berthiaume[2], and A. Mustafa[1], [1]*McGill University*, *Ste-Anne-de-Bellevue, QC, Canada*, [2]*Dairy and Swine Research and Development Centre*, *Lennoxville, QC, Canada*.

A study was conducted to determine the effects of water soluble carbohydrate (WSC) concentration on ensiling characteristics, chemical composition and in vitro digestibility of forage sorghum in a completely randomized study. A low (2.5% of DM) and a high (8% of DM) WSC forage sorghum cultivars were field-grown (3 plots per cultivars) and harvested at early heading stage. Following harvest, forages were ensiled in mini-silos for 0, 2, 4, 8, 16, and 45 d. Results showed that both silages went through a rapid fermentation as indicated by the significant decline in pH between d 0 d 16 post-ensiling. However the decline in pH at all ensiling times was greater for high than low WSC sorghum silage. Lactic acid concentration followed a trend similar to that of pH. Chemical analysis of the 45-d silages showed that high WSC sorghum silage contained 11% less CP and 35% less acid detergent lignin than low WSC sorghum. However, NDF and ADF concentrations were similar for both silages. Asymptotic gas production and degradation rate were both higher for high than for low WSC sorghum silage. In vitro true DM digestibility was greater for high than for low WSC sorghum silage while in vitro NDF digestibility was unaffected by WSC concentration. In vitro protein synthesis as well as molar proportions of volatile fatty acids were similar for both types of sorghum silage. We concluded that increasing WSC concentration improved the fermentation and digestibility of forage sorghum silage.

Key Words: water soluble carbohydrate, sorghum silage, in vitro digestibility

816 A meta-analysis approach to model the effect of increased organic matter digestibility on milk solids production from dairy cows fed fresh ryegrass. D. Pacheco*[1], R. E. Vibart[1], and B. A. Barrett[2], [1]*Food, Metabolism & Microbiology*, *AgResearch Grasslands, Palmerston North, New Zealand*, [2]*Forage Improvement*, *AgResearch Grasslands, Palmerston North, New Zealand*.

Research efforts are underway to produce temperate forages with increased digestibility of NDF (NDFd) and organic matter (OMd) as a means for increasing the feeding value (FV: intake x nutritive value) of grazed forage. A database of feed composition and milk production comprising 132 treatment means from publications in which lactating dairy cows were fed at least 70% of the daily DMI as fresh perennial ryegrass (*L. perenne*) was collated. A 2 step approach using the MIXED procedure in SAS to account for random effects of study allowed quantifying the effect of OMd and other significant variables on the 2 elements of FV: prediction of DMI, and prediction of the feed conversion efficiency (FCE) expressed as milk solids yield (g of milk protein plus

milk fat) per kg of DMI. Initial bivariate data exploration determined that DMI had significant ($P < 0.01$) linear relationships with days in milk (DIM), body weight (BW) and OMd; and a quadratic effect of DIM was also apparent. The best model (RMSPE = 1.13; adjusted $r^2 = 0.62$) was DMI = 0.0188 (SE 0.0044) x BW (kg) + 0.0328 (0.015) x DIM - 0.0002 (0.00006) x DIM^2 + 0.0662 (0.0289) x OMd (g/100 g). Exploration of the relationships of FCE with variables in the database determined that FCE and DIM had a linear, negative relationship ($P < 0.01$). Feed conversion efficiency and OMd had a significant ($P < 0.05$) albeit weak relationship, with OMd values having little effect on FCE when DIM were greater than 200. The best model (RMSPE = 4.44; adjusted $r^2 = 0.94$) was FCE = 54.38 (SE 19.80) −0.254 (0.04) x DIM + 0.855 (0.24) x OMd. In seasonal, spring calving dairy systems such as the one predominating in New Zealand, the potential responses in milk production from ryegrass with greater OMd need to be assessed accounting for the timing of the expression of the improved forage trait. Improvements in OMd need to be achieved as early as possible during lactation to benefit both DMI and FCE. Responses in milk solids yield to greater OMd occurring after ryegrass transitions from vegetative to reproductive may be compromised by decreasing FCE in advanced lactation.

Key Words: ryegrass, digestibility, milk production

817 Effects of microbial corn silage inoculants on silage fermentation, microbial contents, aerobic stability, and milk production under field conditions. N. B. Kristensen*[1], K. H. Sloth[2], O. Højberg[1], N. H. Spliid[1], C. Jensen[3], and R. Thøgersen[3], [1]*Aarhus University*, *Tjele, Denmark*, [2]*Agro Tech A/S*, *Aarhus, Denmark*, [3]*Danish Agricultural Advisory Service*, *Aarhus, Denmark*.

The present study aimed to investigate the effects of 2 corn silage inoculation strategies (homofermentive vs. heterofermentive) under field conditions and to monitor responses in silage variables and milk production over the feeding season from January to August. Thirty 9 commercial dairy farms and 7 contractors participated in the study. Farms were randomly assigned to 1 of 3 treatments: Control (non active), Lactisil (inoculation with 1×10^5 *Lactobacillus pentosus*/g fresh crop and 2.5×10^4 *Pediococcus pentosaceus*/g fresh crop, Chr Hansen A/S; Hørsholm, Denmark), and Lalsil Fresh (inoculation with 3×10^5 *Lactobacillus buchneri* NCIMB 40788/g fresh crop (Lallemand Animal Nutrition, Blagnac, France). Data were analyzed by the MIXED procedure in SAS using a model containing the fixed effects of treatment, time, and their interaction. Contractor by treatment was designated as a random effect. Inoculation with Lactisil was without effect ($P > 0.10$) on any of the measured fermentation variables and aerobic stability except for a trend ($P < 0.10$) on ethanol. Inoculation with Lalsil Fresh doubled ($P < 0.01$) the aerobic stability (temperature increase 2.5°C above ambient 19.0 ± 0.5°C) being 37, 38, and 80 ± 8 h for control, Lactisil, and Lalsil Fresh, respectively. Lalsil Fresh increased ($P < 0.01$) silage pH and contents of acetic acid, propionic acid, propanol, propyl acetate, 2-butanol, propylene glycol, ammonia and free amino acids. Lalsil Fresh increased ($P < 0.01$) the counts of total lactic acid bacteria and reduced ($P < 0.01$) yeast counts. Inoculation treatment did not affect ($P = 0.49$) milk production at the farms when comparing actual test day results with predicted milk production based on the previous 2 yr test data. Under field conditions, the homofermentive inoculant was generally without effects on corn silage fermentation whereas heterofermentative inoculation increased aerobic stability and the silage contents of numerous fermentation variables.

Key Words: corn silage, fermentation, inoculation

818 Some factors with influence on the silage acidity and the aerobic stability. Y. Acosta Aragón*[1], K. Schoendorfer[2], S. Pasteiner[1], A. Schatzmayr[2], and G. Boeck[2], [1]*Biomin Holding GmbH*, *Herzogenburg, Lower Austria, Austria*, [2]*Biomin Research Center*, *Tulln, Lower Austria, Austria*.

The aim of this study was to quantify the influence of different silage quality parameters on the decrease of the pH value in the silage and the aerobic stability. Seven different trials with different substrates were ensiled under laboratory conditions in buckets (5 L). The products under study were the biological silage inoculants Biomin BioStabil Plus (grass, alfalfa) and Biomin BioStabil Mays (whole crop maize and wet corn grain silages), blends of homo- and heterofermentative lactic acid bacteria (L. plantarum, E. faecium and L. brevis), as well a product A (similar blend). The opening of the model silos occurred after 90 d. The changes in the pH values, the fermentation acid contents, ethanol, as well as the aerobic stability (AS) during 7 d (Honig, 1990), the dry matter (DM) losses and an organoleptic assessment using a negative point system according to the DLG- Schlüssel (2006) were measured. The database created with the results of the trials was analyzed using one way ANOVA and post hoc tests (Duncan, $P < 0.05$), as well as regressions to find out which fermentation parameters (DM; content of glucose and fructose, ethanol, propandiol, acetic, propionic, butyric acid and total acid; and the proportions between acetic acid and total acid, between lactic acid and total acid; thereafter named as variables entered) have an influence on the pH value content and the AS. According to the results exposed above, the acidification of the silages is determined by different parameters, in which the Lactic acid content plays an important role. The inclusion of the product tested bettered the acidification in the grass silages. The end pH- value was not affected by the use of additives in alfalfa and corn silages. Only the parameters acetic acid and ethanol played a negative role in the decreasing of the end pH-value. The AS is influenced negatively mainly by the DM, fructose, ethanol and the proportion of lactic acid to the total acid. The acetic and butyric acid content as well as the proportion between acetic and lactic acid and between acetic and the total amount of acid plays a positive role.

Key Words: silage, acidity, aerobic stability

819 Effect of herbage mass and pasture allowance on perennial ryegrass sward structure and milk yield during the grazing season. A. I. Roca-Fernández*[1], M. O'Donovan[2], J. Curran[2], and A. González-Rodríguez[1], [1]*Agrarian Research Centre of Mabegondo*, *La Coruña, Galicia, Spain*, [2]*Moorepark Dairy Production Research Centre*, *Fermoy, Co. Cork, Ireland*.

The effect of herbage mass (HM) and pasture allowance (PA) on dairy systems varies as the grazing season progresses due to changes in the sward structure. The longer term effects of HM and PA on milk output and grass production must be studied to identify the optimum level of HM and PA to graze. The aim of this study was to investigate the effect of 2 pre-grazing HM (Low, L-1600 and High, H-2400 kg DM ha^{-1}) and 2 PA (Low, L-15 and High, H-20 kg DM cow-1 d^{-1}) on the sward composition of perennial ryegrass in the upper and lower sward horizon (<and >4 cm) and its influence on milk yield. The study was conducted at Moorepark in rotationally grazed pastures, with each treatment assigned farmlets from April to October. Sixty-four spring calving Holstein-Friesian cows (primiparous and multiparous) were balanced on calving date and milk yield. Cows were randomized in a block design with a 2x2 factorial arrangement of treatments (LL, LH, HL and HH). Daily fresh herbage was allocated. Milk yield was recorded daily and milk composition twice weekly. Data was analyzed using PROC MIXED in SAS. The variables included in the model were HM,

PA and the interaction between HM and PA. The low HM treatments completed 9 grazing rotations compared with 7 rotations for the high HM treatments. Mean stocking rates achieved were of 4.0 (LL), 3.85 (LH), 4.01 (HL) and 3.93 cows ha^{-1} (HH). Sward utilization was greater ($P < 0.001$) when animals offered low PA (98.0%) compared with high PA (89.9%). Stem and dead DM yield were lower ($P < 0.001$) in the upper sward horizon for the low HM (221 and 170 kg ha^{-1}, respectively) compared with high HM (388 and 303 kg ha^{-1}, respectively). Grazing swards with low HM showed a tendency to increase ($P < 0.07$) milk yield and increased ($P < 0.05$) milk protein yield. The high PA had a positive effect ($P < 0.001$) on milk yield (19.5 vs. 18.1 kg day^{-1}, respectively) and milk solids (1.45 vs. 1.36 kg cow^{-1}, respectively) compared with low PA. The highest performance values were achieved by grazing swards at low HM and allocating cows at high PA which is linked to increased nutritive value in the swards.

Key Words: herbage mass, pasture allowance, sward structure

820 High reliance on grass for an improved milk fatty acids composition. A. I. Roca-Fernández*[1], A. González-Rodríguez[1], O. P. Vázquez-Yáñez[1], and J. A. Fernández-Casado[2], [1]*Agrarian Research Centre of Mabegondo*, *La Coruña, Galicia, Spain,* [2]*Agrarian and Fitopathologic Laboratory of Galicia*, *La Coruña, Galicia, Spain*.

Milk from grazing dairy cows had a higher content of polyunsaturated fatty acids (PUFA), especially more conjugated linoleic acid (CLA), and lower proportions of saturated fatty acids (SFA) than milk from silage-fed cows. Nevertheless, few researches are made trying to evaluate the influence of grazing time in milk fatty acids (FA) composition and its variation across the grazing season. The aim of this study was to investigate the effect on milk FA profile of different proportions of grazing in the ration of dairy cows and its variation across the season. Sixty-one autumn calving Holstein-Friesian dairy cows were balanced on calving date and milk yield and randomly assigned to one of 3 grazing treatments (G0: zero-grazing, G12: 12-h grazing and G24: 24-h grazing). Daily milk yields and weekly milk composition were registered from each cow. Sward characteristics and grass quality of each paddock was determined by NIRS System 5000 and milk FA composition was performed using gas chromatography. Daily herbage allowance was higher ($P < 0.05$) in G24 than in G12 (20.94 and 10.76 kg DM cow^{-1} day^{-1}, respectively). Grazing swards 24-h caused a decrease ($P < 0.05$) in short and medium chain fatty acids (SCFA, 8.34 and MCFA, 39.24 g 100 g^{-1} of FA in milk, respectively) and an increase ($P < 0.05$) in long chain fatty acids (LCFA, 42.29 g 100 g^{-1} of FA in milk). The highest ($P < 0.05$) content of monounsaturated and polyunsaturated fatty acids in milk (MUFA, 25.20 and PUFA, 4.24 g 100 g^{-1} of FA, respectively) were observed in G24. The CLA content showed an increase ($P < 0.05$) with grazing time, ranging from 0.72 to 1.23 g 100 g^{-1} of FA in milk for G12 and G24, respectively. The FA profile of milk showed some seasonality across the grazing season. In spring, the levels of CLA were 3 times higher in milk from cows grazing grass 24-h than in cows fed silage while at the end of the summer and in autumn these differences were reduced at half. High reliance on grass for sustainable dairy production systems might be a good tool to increase the added value of milk with an improved on milk FA composition.

Key Words: dairy cow, milk fatty acids composition, grazing time

821 Effect of stocking rate on sward characteristics and milk performance in sustainable dairy farms from humid areas. A. I. Roca-Fernández*, A. González-Rodríguez, and O. P. Vázquez-Yáñez, *Agrarian Research Centre of Mabegondo*, *La Coruña, Galicia, Spain*.

Stocking rate (SR) is one of the most important factors to control in sustainable dairy production systems from humid areas due to its influence on daily herbage allowance (DHA), herbage mass (HM), pasture dry matter intake (PDMI) and sward quality as well as its role on milk performance. The aim of this study was to investigate the effect of SR on PDMI, sward characteristics and milk yield of 44 spring (S, 15th February) and 28 autumn (A, 30th October) calving Holstein-Friesian cows grazing in rotationally grazed pastures of perennial ryegrass and white clover, stocked at medium (M, 3.9 cows ha^{-1}) and high SR (H, 5.2 cows ha^{-1}). Cows were balanced on calving date and milk yield and randomized in a block design with a 2x2 factorial arrangement of treatments (MS, MA, HS and HA). Milk yield and composition were determined. Pasture production, quality and sward utilization were measured during the grazing season. Cows grazed a total area of 19.2 ha, divided into 32 experimental paddocks. The medium SR completed 4 grazing rotations compared with 5 rotations for the high SR. The DHA and PDMI were lower ($P < 0.05$) in HA (14.9 and 10.3 kg DM d^{-1}, respectively) compared with MA (18.4 and 14.1 kg DM d^{-1}, respectively). The low herbage intake in HS was compensated with a higher ($P < 0.05$) sward quality (ADF, 291 g kg^{-1}; NDF, 518 g kg^{-1}; IVOMD, 781 g kg^{-1}) compared with MS (ADF, 310 g kg^{-1}; NDF, 529 g kg^{-1}; IVOMD, 756 g kg^{-1}). An improved on sward utilization was obtained in HS (83%) compared with MS (79%), enough to achieve a higher ($P < 0.05$) milk yield (HS, 25.3 vs. MS, 24.3 kg day^{-1}). The HA showed a detrimental effect on milk yield per cow (18.5 kg day^{-1}) but increased the amount of pasture harvested per hectare. There were differences ($P < 0.05$) for milk protein (HA, 32.0 and MA, 30.6 g kg^{-1}) and fat (HA, 39.9 and MA, 37.0 g kg^{-1}). This could be attributed to the higher pasture crude protein (HA, 153.8 and MA, 139.7 g kg^{-1}) to achieve a higher herbage quality. Increasing the SR is achieved higher sward utilization, grass quality, milk yield and milk quality in both, spring and autumn calving.

Key Words: dairy cow, stocking rate, sward characteristics

Growth and Development: Regulation of Adipogenesis and Adipose Tissue Development

822 Adipogenic differentiation state-specific gene expression as related to bovine carcass adiposity. C. L. Pickworth*[1], S. C. Loerch[1], F. L. Fluharty[1], D. H. Poole[2], S. G. Velleman[1], and J. L. Pate[2], [1]*The Ohio State University*, *Wooster,* [2]*The Pennsylvania State University*, *State College*.

The regulation of site and rate of fat deposition in cattle is not well defined. The study objective was to investigate adipogenic differentiation state-specific gene expression in feedlot cattle (>75% Angus; <25% Simmental parentage) of varying adipose accretion patterns. Four groups of 4 steers were selected from a group of 80 steers via ultrasound to have low backfat-low intramuscular fat (LBF-LIM), low backfat-high intramuscular fat (LBF-HIM), high backfat-low intramuscular fat (HBF-LIM), or high backfat-high intramuscular fat (HBF-HIM). Adipose tissue from the subcutaneous (SQ) and intramuscular (IM) depots were collected at harvest. The relative expression of adipogenic differentiation state-specific genes were evaluated using quantitative PCR. Data were analyzed using the mixed model of SAS and gene expression data were analyzed using covariate analysis with ribosomal protein L19 as the covariate. No interactions were observed ($P > 0.10$) between IM and SQ adipose accretion for any of the variables measured. Therefore, only the main effects of high and low accretion within a depot and the effects of depot are reported. No differences ($P > 0.10$) in mRNA between high and low adipose accretion within a depot were detected for any of the genes in spite of differences ($P < 0.001$) in cell density, diameter, and carcass measures. Preadipogenic delta like kinase 1 mRNA was higher ($P < 0.001$) in the IM than the SQ adipose tissue; conversely, differentiating and adipogenic genes (lipoprotein lipase, peroxisome proliferator activated receptorγ, fatty acid synthetase, and fatty acid binding protein 4) were higher ($P < 0.001$) in the SQ than the IM depot. Intramuscular adipocytes were smaller ($P < 0.001$) than SQ adipocytes and had greater ($P < 0.001$) expression of preadipogenic markers, indicating that more hyperplasia was occurring in the IM while the SQ was undergoing differentiation and hypertrophy. Adipogenic differentiation state-specific gene expression was not different in cattle with various phenotypes but adipogenesis in the SQ and IM adipose tissues appears to occur independently.

Key Words: gene expression, adipose, differentiation

823 Palmitoleic acid (C16:1) changes fatty acid profiles and alters gene expression in bovine adipocyte cultures. T. A. Burns*, S. K. Duckett, and S. L. Pratt, *Clemson University*, *Clemson, SC*.

Our objective was to determine if differences in fatty acid profiles or gene expression exist when adipocytes are exposed to increasing levels of C16:1. Three primary preadipocyte cell lines were isolated, propagated, and frozen for use in this study. Thawed cells were passaged 4 additional times and plated at a density of 1×10^5 cells/cm^2. Cells were allowed to reach confluence and held for 2 d. On D0, primary differentiation media [Dulbecco's modified eagles medium (DMEM) containing 10% fetal calf serum (FCS), and 2X antibiotic/antimycotic (AB/AM), insulin at 2.5 μg/mL, 0.25 μ*M* dexamethasone, 20 μ*M* troglitasone (TRO), 0.5 m*M* isobutylmethylxanthine, and 10 m*M* acetate] was applied for 2 d and replaced with secondary differentiation media [DMEM, 10% FCS, 2X AB/AM, insulin at 2.5 μg/mL, 5 μ*M* TRO, 10 m*M* acetate, containing 1 of 4 levels of C16:1(0, 50, 150, or 300 μ*M*)] from D2 to D12. Cells were harvested on D6 and D12 for fatty acid analysis using gas chromatography and gene expression by RT-qPCR. At 0 μ*M* C16:1, there was no effect of harvest day on levels of C16:1, C18:1c11, or total mg fatty acids. However, these fatty acids and total fatty acids increased ($P < 0.05$) linearly in response to increasing C16:1 supplement. Additionally, they were elevated ($P < 0.05$) in 50, 150, and 300 μ*M* C16:1-supplemented cells harvested on D12 compared with D6. In contrast, C16:0, C18:0, C18:1c9, decreased ($P < 0.05$) in response to increasing C16:1 in the media and were not affected by harvest day. The ratio of C18:1c9/C18:0 decreased ($P < 0.05$) in response to increasing C16:1 supplementation. Stearoyl-CoA desaturase (SCD) and fatty acid synthase mRNA expression was reduced ($P < 0.05$) on D6 in C16:1-supplemented groups for each cell line. Therefore, C16:1 may have a regulatory role in the transcription of SCD and fatty acid synthesis. In conclusion, supplementing cells with C16:1 produced changes in fatty acid composition of bovine adipocytes by D6 and influenced mRNA expression.

Key Words: adipocyte, palmitoleic acid, gene expression

824 Effect of fatty acids on adipocyte differentiation specific genes expression. P. Cheguru*, M. E. Doumit, G. Murdoch, and R. A. Hill, *University of Idaho*, *Moscow*.

Adipocyte differentiation has been extensively studied in vitro by using a standard hormonal cocktail induction treatment that includes dexamethasone, insulin and cAMP inducers like IBMX (isobutyl methyl xanthine). Pioneer work by Amri et al. (J. Lipid Res. 1991, 32; 1449–1456) provided evidence that fatty acids can also induce adipocyte-specific gene expression. We report here that long-chain fatty acids in the presence of insulin were able to induce lipid accumulation in mouse 3T3-L1 preadipocyte cell lines. 3T3-L1 cells were treated with either oleic acid (C18:1) or linoleic acid (C18:2) in the presence or absence of insulin. Confluent cells grown in complete growth medium were incubated with fatty acids in the presence or absence of insulin. Medium was changed every 2 d. Cells were stained with Oil Red O and RNA was collected on d 0, 2, 4, 6 and 8. Control cells were grown in complete growth medium only. Simultaneously, cells treated with hormonal cocktail containing dexamethasone, insulin and IBMX were observed at each time point. Oil Red O staining results showed that cells treated with fatty acids and insulin accumulated more lipid than cells treated with fatty acids alone or control cells. Cells treated with hormonal cocktail accumulated more lipid than other treatments. Adipocyte differentiation involves upregulation of PPARγ(peroxisome proliferator activated receptor γ), C/EBPα (CCAAT enhancer binding protein α), FABP4 (fatty acid binding protein 4) and SREBP-1c (sterol regulatory element binding protein-1c). Other genes like Pref-1 (preadipocyte factor-1) and GATA2 (GATA binding protein 2) will be downregulated. We hypothesize that long chain fatty acids can upregulate PPARγ, C/EBPα and FABP4 and downregulate Pref-1 gene expression. Lipid staining results confirm that cells treated with fatty acids and insulin had different metabolic changes than cells treated with fatty acids alone or control. We expect significant changes in adipocyte specific gene expression in cells treated with fatty acids and insulin at each time point.

Key Words: adipocyte differentiation, long-chain fatty acids, gene expression

825 Expression of genes associated with adipocyte differentiation differs with age and adipose tissue depot during growth. G. Go*, D.

T. Silvey, S. H. Choi, L. A. Gilmore, G. Ghahramany, and S. B. Smith, *Texas A&M University*, *College Station*.

We hypothesized that major subcutaneous (s.c.) adipose tissue depots would exhibit different developmental patterns of gene expression over time. Four Angus steers at each 9, 12, and 14 mo were harvested and s.c. adipose tissue samples were collected from over the chuck, rib, loin, sirloin, round, brisket, flank, and plate. AMPKα, CPT-Iβ, SCD, GPR43, PPARγ, and C/EBPβ were analyzed with qRT-PCR. Data were analyzed using the general linear model of SAS statistical analysis program. When significant, means were separated by Fishers protected least significant difference method. Over time, the major backfat depots, loin, rib, and sirloin s.c. adipose tissues, had the highest SCD (Δ9 desaturase) gene expression, whereas, anterior depots, brisket, plate, and flank s.c. adipose tissues, expressed less SCD RNA ($P < 0.001$). AMPKα gene expression was the greatest in round and the least in loin and rib s.c. adipose tissues. There were few significant differences in gene expression over time. However, across tissues, AMPKα and GPR43 (short chain fatty acid receptor) decreased over time, and CPT-Iβ, PPARγ, and SCD gene expression was greatest at 14 mo of age (all $P < 0.07$). We conclude that there were few differences across adipose depots in adipogenic expression, although age of steer had major effects on gene expression.

Key Words: adipogenic genes, subcutaneous adipose tissue

826 Hedgehog signaling mediates adipogenesis in C3H10T1/2 cells via down-regulation of COUP-TFII. W. F. Yue*, J. X. Zhao, M. J. Zhu, and M. Du, *Department of Animal Science, University of Wyoming*, *Laramie*.

Effective manipulation of depot specific adipose accumulation will dramatically enhance animal production efficiency. In human, adipogenesis plays a central role in the pathogenesis and pathophysiology of metabolic syndromes. Chicken Ovalbumin Upstream Promoter Transcription Factor II (COUP-TFII) is expressed during the early stages of adipocyte differentiation. Hedgehog signaling is known to inhibit adipogenesis. We hypothesized that hedgehog signaling inhibits adipogenesis through regulating COUP-TFII expression. C3H10T1/2 multipotent cells were used. Addition of cyclopamine (3.6 μ*M*), an inhibitor of the hedgehog signaling, promoted the mRNA expression of COUP-TFII, while addition of sonic hedgehog (20 n*M*) which stimulates hedgehog signaling decreased COUP-TFII expression by 38.1 ± 2.61% ($P < 0.05$). The mRNA expression of COUP-TFII was correlated with the expression of peroxisome proliferator-activated receptor (PPAR) γ, with cyclopamine treatment increasing PPARγ protein content by 73.4 ± 14.56% ($P < 0.05$). In addition, both CCAAT/enhancer binding protein (C/EBP) α and β, 2 transcription factors known to induce adipogenesis, were induced by 109.6 ± 18.20% and 137.0 ± 44.05% ($P < 0.05$) respectively when hedgehog signaling was inhibited by cyclopamine. In conclusion, hedgehog signaling decreases COUP-TFII expression and adipogenesis in C3H10T1/2 cells. COUP-TFII expression may stimulate early adipogenesis. Because hedgehog signaling is central to the morphogenesis and pattern formation during early animal development, hedgehog may regulate depot specific adipogenesis through COUP-TFII associated signaling pathways.

Key Words: COUP-TFII, adipogenesis, hedgehog

827 Characterization of fat mass and obesity associated gene (FTO) expression in the broiler chicken. A. Tiwari*, S. M. Krzysik-Walker, G. L. Hendricks III, and R. Ramachandran, *The Pennsylvania State University*, *University Park*.

Fat mass and obesity associated gene (FTO), also known as *Fatso* is a member of the Fe-II and 2-oxogluterate-dependent dioxygenase superfamily. The FTO gene product is highly conserved across vertebrate species and is ubiquitously expressed in multiple tissues. Studies in humans and rodents suggest that FTO is involved in regulation of food intake and lipolytic activity in adipose tissue. Mutations in a FTO intron have been associated with obesity and related metabolic disorders in humans. While the physiological role of FTO is beginning to be understood in mammals, the chicken homolog of FTO has not been described. Objectives of the present study were to clone full length chicken FTO cDNA and to quantify FTO expression in primary metabolic tissues, adipose, liver and skeletal muscle to determine if age or feeding status affect FTO expression in male broilers. Using rapid amplification of cDNA ends (RACE), we cloned the full length chicken FTO cDNA. Chicken FTO cDNA and its deduced protein sequences were found to be 68% and 69% homologous to that of human FTO, respectively. Using Western blotting, we detected FTO protein in hypothalamus, adipose tissue, liver, skeletal muscle, spleen, kidney, heart and testes of broiler chickens. Quantification of FTO protein by Western blotting revealed significantly greater expression in liver (ANOVA, $P < 0.05$; n = 5/treatment) of 8 week old broilers fasted for 48 h compared with *ad libitum* fed chickens maintained on standard commercial broiler feed. No significant difference in FTO protein expression, however, was found in 4-week-old versus 8-week-old broiler tissues (ANOVA, $P > 0.05$; n = 5/age group). We conclude that FTO is expressed in multiple chicken tissues and that FTO expression is influenced by feeding status in the broiler chicken. We are currently investigating the physiological role of FTO in broiler chicken metabolism.

Key Words: metabolism, liver, energy balance

828 Effect of nutrition and chronic infusion of leptin on intake and body composition of *Bos indicus* heifers at puberty. M. V. Carvalho, J. D. Magalhães, L. U. Gimenes, G. P. Rodrigues, and L. F. P. Silva*, *Universidade de São Paulo*, *Pirassununga, SP, Brazil*.

The amount of fat in the carcass has been proposed as a regulator of initiation of puberty in cattle. To test if changes in energy intake and in leptin concentration is capable of altering body composition at puberty, 36 prepubertal Nelore heifers, 18 to 20 mo-old, 275.8 ± 17.2kg BW and BCS of 5 ± 0.5 (1 to 9 scale) were randomly assigned to each of 3 treatments (n = 12): H (high energy diet), L (low energy diet), and LL (low energy diet + oLeptin). Diets were formulated to promote weight gain of 0.4kg/day (groups L and LL) or 1.2kg/day (H group). After 21 d of adjustment, heifers in LL group received subcutaneous injections of oLeptin at 4.8μg/kg BW twice a day, for 56 d. Groups H and L received similar injections of 2mL saline solution. Age at puberty was considered to be the age on first detection of a corpus luteum, confirmed by plasma concentrations of progesterone of >1ng/ml. Heifers were slaughtered during the luteal phase after the first estrus cycle. Individual intake was estimated using the markers chromic oxide and indigestible NDF for estimate total fecal excretion and digestibility, respectively. Leptin administration had no effect ($P > 0.05$) on dry matter intake, body weight gain, body composition and efficiency of energy use. High energy intake accelerated puberty and modified body composition at puberty. Heifers from the H group had heavier carcass weight (222 vs. 181.5 kg, $P < 0.01$), higher BCS (6 vs. 4.5, $P < 0.01$), larger longissimus muscle area (59 vs. 53 cm^2, $P < 0.01$), and greater subcutaneous fat thickness (5.4 vs. 3.4 mm, $P < 0.01$), than heifers from the L and LL groups together. Carcasses from the H group also had higher ether extract content (24.2 vs. 21.3, $P < 0.01$) than carcasses from the L and LL groups together. Animals receiving a high energy diet also had better efficiency of energy

use (0.25 vs. 0.16, $P < 0.01$). High energy intake during the prepubertal phase increased BW and carcass fat content at puberty, and improved the efficiency of dietary energy usage. These results do not support the hypothesis that puberty occurs at a constant percentage of body fat.

Key Words: carcass fat, cattle, maturity

829 Assessing heat load and dissipation using digital infrared thermography and serum cortisol profiles in horses during the summer months. Y. Dupre[1], A. Strohm[2], E. Keis[2], J. Harney[2], K. Moulton*[2], and P. L. Ryan[2], [1]*Tuskegee University*,[2]*Mississippi State University*.

During the summer months in southeastern United States environmental factors including high ambient temperature, high relative humidity and radiant energy contribute to heat stress in cattle, but little is known about this condition in horses. The objectives of this study were to evaluate heat load and dissipation in horses during the summer, determine whether coat color is a factor, and assess physiological responses by monitoring systemic cortisol. Fifteen mares (3–18 years) were assigned to one of 5 coat color categories (n = 3/group; bays, browns, gray, paint, palomino) and maintained on pastures with the same shade cover. Heat load was assessed using digital infrared thermal imaging (FLIR T400 camera) and rectal temperatures were recorded 4x/d (0600, 1200, 1600, 2000 h), 2 d/week for 6 weeks (June–July, 2009) along with ambient temperature, wind speed and humidity. Five regions of interest (ROI; flank, shoulder, eye, muzzle, perineum) were imaged at each time point. Minimum (MIN), maximum (MAX), average (AVE) and standard deviation (STDEV) thermal signatures were assessed for each ROI. Blood was collected at 0600, 1600 and 2000 h for serum cortisol. Data was analyzed using GLM procedures of SAS. LS means were calculated and separated using Fisher's LSD ($P < 0.05$). Bay and brown horses had the highest thermal signatures (AVE/MAX) at 1200 and 1600 h in all ROIs except the perineum and eye compared with all other groups ($P < 0.05$). Shoulder and flank regions had the highest AVE/MAX (~40°C) compared with other ROIs. For combined ROIs, bay/brown mares had the highest MAX value ($P < 0.01$). Grey mares had the greatest perineum MAX value (37.15–37.7°C) throughout the day ($P < 0.05$) compared with other groups (34.32–37.56°C) as well as the highest rectal temperature ($P < 0.05$). Serum cortisol was lower in paint horses ($P < 0.05$) compared with other coat colors at each time point, and declined from a high at 0600 to a low at 2000 h ($P < 0.05$) in all coat groups. In conclusion, coat color affects heat load and dissipation in horses, which is influenced by the darker color consistent with heat absorption. Lower serum cortisol was consistent with low thermal signatures in paint horses (pale skin pigment).

Key Words: heat stress, thermography, equine

830 Effects of selenium supplementation and prolonged exercise on antioxidant gene expression in equine skeletal muscle. S. White*, L. K. Warren, S. E. Johnson, and J. Bobel, *University of Florida*, *Gainesville*.

Twelve untrained Thoroughbred horses (mean ± SE; 11 ± 1 y; 565 ± 11 kg) were used to evaluate antioxidant gene expression in skeletal muscle in response to prolonged exercise after receiving 2 levels of dietary selenium (Se). Horses were randomly assigned to diets containing either 0.1 mg Se/kg DM (n = 6; CON) or 0.3 mg Se/kg DM (n = 6; SE) for 36 d. Horses were individually fed 1.6% BW/d of coastal bermudagrass hay (0.02 mg Se/kg DM), 0.4% BW/d of whole oats (0.24 mg Se/kg DM) and a mineral/vitamin premix containing no Se. Sodium selenite was added to achieve either 0.1 or 0.3 mg Se/kg DM in the total diet. On d 35, horses underwent 2 h submaximal exercise in a free-stall exerciser (total distance 26 km; heart rate 135 ± 39 bpm). Biopsies of the middle gluteal muscle were obtained before Se supplementation was initiated, before exercise, and at 6 and 24 h post-exercise. Gene expression in skeletal muscle was determined by quantitative RT-PCR using 18S as a reference gene. Differences in mRNA expression due to treatment and exercise were analyzed using the GLIMMIX procedure of SAS (v. 9.2). Muscle expression of *MT1B* ($P = 0.001$) and *MT3* ($P = 0.001$) both increased over 6-fold from pre- to 24 h post-exercise, indicating exercise was sufficient to elicit oxidative stress. Muscle expression of *TrxR1* was unchanged at 6 h but increased ($P = 0.02$) 2.5-fold at 24 h post-exercise, whereas *GPx1* and *GPx3* did not change through 24 h post-exercise. Expression of *SOD1* and *SOD2* were unchanged through 6 h post-exercise, but expression of both genes increased ($P = 0.001$ *SOD1*; $P = 0.0003$ *SOD2*) in CON horses and *SOD2* decreased ($P = 0.04$) in SE horses from 6 to 24 h post-exercise. Level of dietary Se had no overall effect on expression of *MT1B*, *MT3*, *TrxR1*, *GPx1*, *GPx3*, *SOD1*, or *SOD2* in muscle following exercise. Prolonged exercise in untrained horses appears to upregulate mRNA expression of some antioxidant enzymes in skeletal muscle. Short-term Se supplementation above the current NRC requirement did not alter selenoprotein expression in skeletal muscle, but may influence expression of other antioxidant enzymes following exercise.

Key Words: horse, selenoprotein, skeletal muscle oxidative damage

831 Fatty acid composition of synovial fluid in horses fed long chain polyunsaturated fatty acids: A pilot study. T. N. Ross*, T. M. Hess, J. D. Kisiday, C. W. McIlwraith, T. Engle, D. K. Hansen, J. Rexford, N. Schauermann, and C. Mulligan, *Colorado State University*, *Fort Collins*.

Studies utilizing oral α linolenic acid (ALA) and its metabolic derivatives, eicosapentaenoic acid (EPA) and docosahexaenoic acid (DHA), indicate a potential regulatory role in reducing joint inflammation by mediating cytokine production in arthritic human patients and plasma prostaglandin levels in arthritic horses. The primary study objective was to determine if dietary long chain fatty acids are incorporated into the synovial fluid of mature horses fed one of 3 dietary treatments. Twenty-one mature mixed breed mares, between 5 and 14 yr of age, with no history of joint disease and free of lameness were blocked by age, weight and body condition score and randomly assigned into one of 3 dietary treatment groups. Group 1 (FISH) received 69 mg/kg BW of n-3 EPA/DHA via a commercial fish oil supplement (Magnitude; JBS United, Sheridan, IN) daily; Group 2 (FLAX) received 68.6 mg/kg BW of n-3 ALA via a flaxseed supplement (Nutra-Flax) daily and Group 3 (CONT) did not receive n-3 supplementation. Total ration composition of n-3 fatty acids were approximately 143.5 mg/kg BW (FISH), 142.5 mg/kg BW (FLAX) and 78.7 mg/kg BW (CONT), respectively. On d 90, approximately 3 mL of synovial fluid was extracted from the right carpus of each horse and immediately placed into a 7 mL EDTA tube. Aliquots were assayed for fatty acid composition using gas chromatography. Data were analyzed using ANOVA, with significant differences ($P < 0.05$) further analyzed using Fisher's LSD test. Synovial fluid samples from the FISH group presented EPA and DHA in their synovial fluid, whereas the FLAX and CONT groups did not express detectable concentrations. The absence of EPA and DHA in the FLAX-fed group indicates inefficient conversion of these fatty acid metabolites from ALA. This is the first documented study evaluating synovial fluid fatty acid composition in horses receiving a dietary n-3 fatty acid supplement. Results indicate oral supplementation of EPA and DHA alters synovial fluid fatty acid composition. The presence of DHA and EPA in synovial fluid may potentially modify inflammatory processes in the joint.

Key Words: polyunsaturated fatty acids, horse, synovial fluid

832 Cushing's syndrome down-regulates glucose transporter mRNA abundance in the distal jejunum in the horse. A. Buckley, N. Taylor, R. Manjarin*, H. C. Schott, A. D. Woodward, and N. L. Trottier, *Michigan State University*, *East Lansing*.

Cushing's syndrome is commonly associated with the development of laminitis in the horse. High levels of glucocorticoids are known to induce insulin resistance and reduce cellular glucose uptake, however, the mechanisms are not known. Decreased capability for pre-cecal glucose absorption may increase carbohydrates flow to the large intestine in Cushing afflicted-horses, altering the hindgut microflora and increasing susceptibility to laminitis. The objective of this study was to test the hypothesis that horses affected by Cushing's Syndrome have lower mRNA abundance of genes encoding for glucose transporters and insulin receptor in the jejunum enterocytes, compared with healthy animals. Tissue from the distal jejunum was obtained from 8 adult horses (4 affected with Cushing's Syndrome and 4 healthy controls) shortly following euthanasia. The mucosa was gently separated from the sero-muscular layer, flash-frozen in liquid N, and stored at −80°C for RNA isolation. Gene expression of glucose transporters GLUT1 (SLC2A1), GLUT2 (SLC2A2), GLUT4 (SLC2A4), GLUT5 (SLC2A5), SGLT (SLC5A1) and insulin receptor (INSR) was assessed by measuring mRNA abundance using relative quantitative PCR. Succinate dehydrogenase complex subunit A (SDHA) and hypoxanthine phosphoribosyltransferase (HPRT) were used as reference genes in the study. Mixed model was used for data analysis. Compared with healthy control horses, mRNA abundance of insulin receptor and insulin-dependent glucose transporter GLUT4 decreased ($P < 0.01$) in distal jejunum of Cushing's horses. For GLUT1, GLUT2, GLUT5 and SGLT1, mRNA abundance did not differ between Cushing and control horses. Results indicate that Cushing's syndrome downregulates the gene expressions of insulin-dependent glucose transporter GLUT4 and insulin receptor in the distal jejunum of the horse. These results may offer a physiological mechanism for increased susceptibility to nutritionally induced laminitis in Cushing-afflicted horses.

Key Words: Cushing, horse, insulin

833 Proteomic analysis of synovial fluid and plasma from horses fed a high or low starch diet. E. A. Nowelsky*[1], J. K. Morrissey[1], D. S. Gibson[2], P. A. Harris[3], and W. B. Staniar[1], [1]*The Pennsylvania State University*, *University Park,* [2]*University of Colorado Denver*, *Aurora,* [3]*Equine Studies Group, Waltham Centre for Pet Nutrition*, *Melton Mowbray, UK*.

A tentative link has been suggested between osteochondrosis (OC) and feeding high starch diets in growing horses. The pathology of OC is multifactorial and it is therefore appropriate to explore using a technique that allows for characterization and quantification of the plasma (PL) and synovial fluid (SF) proteomes. The objective of this study was to determine if the concentration of dietary starch influences the proteomes of SF and PL and to isolate, identify and characterize proteins that are differentially present in relation to diet or sample type. Six yearlings, maintained on dry lot with ad libitum access to <5% starch hay, were used in this crossover study design conducted over 12 weeks with four 21-d periods. During periods 2 and 4, yearlings were split into 2 treatment groups, with one group receiving high starch feed (~40% starch on a DM basis)(HSF) and the other group receiving low starch feed (<10% starch on a DM basis)(LSF). All yearlings received LSF in periods 1 and 3. SF and PL samples were taken every 21 d and analyzed using 2D gel electrophoresis. Progenesis SameSpots software was used to analyze spot intensities using ANOVA and differences were considered significant at $P < 0.05$. Select spots were chosen for mass spectrometry. Changes in protein expression ranged from a 1.2 fold–2.5 fold change. Seven proteins were higher as a result of dietary treatment. Four of the 7 proteins, identified as isoforms of immunoglobulin gamma, were higher in SF from animals fed HSF. Two proteins, identified as isoforms of albumin, were higher in HSF samples. Fibrinogen, haptoglobin and clusterin were higher in PL. Alpha 1 antitrypsin was higher in SF. The grouping of isoforms and proteins with similar characteristics on the gel was useful in achieving the goals of this study. Proteins identified in this study initially do not have a clear mechanistic link with OC. This study demonstrates a novel approach to investigate protein expression changes in PL and SF that may affect joint health. The fluid specific proteomic profiles and individual proteins identified may be useful in future examination of equine biological fluids.

Key Words: equine, nutrition, proteomics

834 Effects of a 24-h feed withdrawal on SGLT1, GLUT5, and PepT1 gene expression in the small intestine and right ventral colon of the horse. B. E. Aldridge*, T. B. Lescun, and J. S. Radcliffe, *Purdue University*, *West Lafayette, IN*.

Fourteen horses were used to determine the effects of a 24 h feed withdrawal (FW) on gene expression in the small intestine and right ventral colon (RVC). Prior to FW, horses were fed hay ad libitum for 8 weeks. Following this adaptation period, horses were randomly allotted to either 24 or 0 h FW (7 horses/trt) with water provided ad libitum. Following 0 or 24 h of FW, horses were killed and segments of proximal jejunum (13.7 m proximal to the ileo-cecal junction), distal jejunum (9.1 m proximal to the ileo-cecal junction), ileum (5 cm proximal to the ileo-cecal junction) and right ventral colon (30 cm distal to the cecocolic junction) were removed for gene expression analysis of the sodium dependent glucose transporter (SGLT1), fructose transporter (GLUT5) and di- and tri-peptide transporter (PepT1) by using quantitative RT-PCR normalized to GAPDH. The GLM procedure in SAS was used to determine statistical differences between the intestinal sections of fed and non-fed horses, where horse served as the experimental unit. Horses maintained on a hay diet, had 82% more GLUT5 expression ($P < 0.05$) in the proximal jejunum (PJ), than horses subjected to a 24 h FW. However, in horses subjected to a 24 h FW, distal jejunal (DJ) SGLT1 expression increased ($P < 0.1$) 205% and PepT1 expression increased 288%, although this only approached a trend ($P = 0.13$). SGLT1, GLUT5 and PepT1 expression were not affected ($P > 0.1$) by FW in the ileum and right ventral colon. To compare gene expression across sections, the relative abundance was normalized to the distal jejunum. The PJ contained 13, 3.8 and 1.4- fold greater expression of SGLT1 ($P < 0.05$), GLUT5 ($P < 0.05$) and PepT1 ($P < 0.05$) compared with the DJ. Expression of SGLT1, GLUT5 and PepT1 were 34, 19 and 15% lower in the ileum than in the DJ, and 91, 63 and 84% lower in the RVC compared with the DJ. This data indicates that SGLT1, GLUT5 and PepT1 are expressed throughout the small intestine and in the RVC of the horse at varying concentrations, and that they are differentially regulated by a 24-h feed withdrawal.

Key Words: horse, gene expression, intestine

835 Effects of omega-3 fatty acid supplementation on plasma, red blood cell and muscle cell fatty acid compositions in horses. J. K. Rexford*, T. M. Hess, N. L. Schauermann, T. E. Engle, D. K. Hansen, K. D. Allen, and C. M. Mulligan, *Colorado State University*, *Fort Collins*.

The objective of this study was to examine the effects of dietary omega-3 fatty acid supplementation on plasma, red blood cell and muscle omega-3

fatty acid compositions in horses. Twenty-one mares were blocked by age, body weight and body condition score and randomly assigned to one of 3 dietary treatments. Treatments consisted of: 1) 142.5 mg/kg BW of n-3 fatty acids via a fish oil supplement and diet (FISH; Magnitude; JBS United, Sheridan, IN); 2) 142.5 mg/kg BW of n-3 fatty acids via a flaxseed meal from the supplement and diet (FLAX; Nutra-Flax^{TM}); and 3) control (CON) no supplemental fatty acid with 78.7 mg/kg BW of omega-3 fatty acids from the diet (mostly hay for all groups). Treatments were supplemented for 90 d. Blood samples and muscle middle gluteal biopsies were taken on d 0, 30, 60, and 90 of supplementation. Plasma and cell fatty acid profiles were analyzed via gas chromatography. Plasma linoleic acid (LA) and α linolenic acid (ALA) were 10 and 40% lower ($P < 0.008$) respectively in the FISH compared with FLAX and CON supplemented horses. Plasma eicosapentaenoic acid (EPA) and docosahexaenoic acid (DHA) were only detected in the FISH supplemented horses and increased 29% ($P < 0.001$) and 17% ($P < 0.005$) from d 30 to d 60. Red blood cell LA and ALA were not different between treatments. Red blood cell EPA and DHA were only detected in the FISH supplemented horses, where EPA increased 4% ($P < 0.005$) from d 30 to d 60. Red blood cell DHA increased 36% ($P < 0.004$) between d 30 and d 90. Muscle LA was 15% lower in the FISH supplemented horses compared with the other treatments. Muscle ALA was 42% lower ($P < 0.030$) in the FISH supplemented horses, compared with FLAX and CON groups. Muscle EPA was 32% higher ($P < 0.001$) in FISH supplemented horses compared with other treatments and increased by 40% from d 30 to d 60. Muscle DHA was 43% higher ($P < 0.001$) in the FISH supplemented horses compared with other treatments and increased by 38% between d 30 and 90. This is the first study to demonstrate that dietary fatty acid supplementation will affect muscle fatty acid composition in horses.

Key Words: equine, eicosapentaenoic acid, docosahexaenoic acid

836 Effects of an experimental feed additive on neutrophil-mediated killing of *Streptococcus equi* and on markers of innate immune function in horses. A. Rowson*[1], D. Sherwood[2], Y. Wang[1], S. Puntenney[1], and N. E. Forsberg[1], [1]*OmniGen Research LLC*, *Corvallis, OR,* [2]*Oregon State University*, *Corvallis*.

Effects of an experimental feed additive (OmniGen-EQ) on immune markers in horses was tested. Eighteen horses were assigned to 2 treatment groups which consisted of a control group and a treated group (9 animals/treatment). The control group consisted of 3 mares and 6 geldings which ranged in age from 2 to 17 years. The treatment group consisted of 3 mares and 6 geldings which ranged in age from 1 to 16 years. Animals on the control diet were allowed free-choice access to hay plus 1.8 kg/head/day of a supplement which contained approximately 18% crude protein, 2% crude fat and 6% crude fiber on an as-fed basis. Animals on the treated group received the same diet except for supplementation with the experimental product such that each horse received an intake of 108 g per day. Animals were individually fed supplement and maintained on treatment for 28 d. Blood samples were taken on d 0, 14 and 28 and neutrophils were isolated using Percoll gradient centrifugation. Ability of freshly isolated neutrophils to kill (phagocytose) an equine pathogen (*Streptococcus equi*) were assessed on d 28 using a pathogen killing assay. Killing assays were performed at ratios of 1 neutrophil:30 *S. equi* (1:30) and 1:60. Neutrophil RNA was isolated using Trizol and concentrations of L-selectin, interleukin-8 receptor (IL-8R) and RPL-19 mRNAs were assessed using quantitative (SYBR-green) reverse transcriptase PCR. RPL-19 mRNA was used as the background gene. Data were analyzed by ANOVA with effects consisting of Treatment, Day and Error. One horse on the control treatment died on d 25 due to colic. The additive improved neutrophil killing efficiency ($P < 0.05$) by 16 and 22% at dilutions of 1:30 and 1:60, respectively. Feeding OmniGen-EQ had no effect on neutrophil L-selectin and IL-8R mRNAs on d 14; however, concentrations of both mRNA species were increased several-fold ($P < 0.05$) after 28 d of feeding. These data demonstrate that feeding the experimental additive to horses improves markers of innate immune function.

Key Words: immunity, horse, neutrophil

837 Effects of OmniGen-AF on development of humoral immune responses in beef cattle and in rats following a vaccination program. S. B. Puntenney*, Y. Wang, A. Rowson, and N. E. Forsberg, *OmniGen Research LLC*, *Corvallis, OR*.

Two experiments were completed in which effects of OmniGen-AF on development of titer were examined. In the first study, male rats (8/trt) were assigned to a control diet (Teklad 8604) or to a diet containing OmniGen-AF (0.5% w/w) for 54 d after which all animals were given the control diet through d 87. Animals were vaccinated twice with an *E. coli* vaccine on d 10 and 24 of the study and blood was sampled from rats on d 0, 24, 37, 54, 73 and 87. *E. coli* titer within the IgG1 fraction was determined by ELISA. In the second study, Angus calves (ca. 250 kg) were assigned to one of 2 treatments (20 animals/trt): a control ration and to the same ration but supplemented with OmniGen-AF (56 g/hd/d) beginning at d 0. Animals were maintained on rations for 60 d and vaccinated with the Novartis Virashield vaccine on d 14 and again 1 mo later. A subset of animals (10/trt) was also vaccinated with the Epitopix SRP (*Salmonella*) vaccine following initial feeding with OmniGen-AF. Serum neutralization assays against the BVDV-1, BVDV-2 and IBR were completed by the Oregon State University College of Veterinary Medicine Diagnostic Laboratory. Titer directed against the SRP vaccine was assessed by Epitopix. IgG1 *E. coli* titer in rats was significantly ($P < 0.05$) elevated on d 24, 37 and 54 of the study. No differences between treatments ($P > 0.05$) were noted following withdrawal of the additive on d 54 of the study. OmniGen-AF increased development of BVDV-1 and *Salmonella* titer by almost 2-fold; however, these effects were not significant ($P = 0.112$ and 0.118, resp). BVDV-2 titer was not detectable in either treatment group. OmniGen-AF increased IBR titer significantly ($P < 0.05$). In previous studies, we reported that OmniGen-AF increased ($P < 0.05$) development of *E. coli* titer in calves vaccinated with the Pfizer J5 *E. coli* vaccine. These studies extend those observations and indicate that pre-feeding OmniGen-AF may increase humoral immune responses to vaccines. Further work is needed to determine conditions under which one might reliably derive benefit to humoral immunity.

Key Words: immunity, OmniGen-AF, vaccination

838 Passive immunity to a commercial *E. coli*-SRP vaccine in beef cattle colostrum from cows grazing native range. B. W. Wileman*[1], D. U. Thomson[1], K. C. Olson[2], and L. A. Pacheco[2], [1]*College of Veterinary Medicine, Kansas State University*, *Manhattan,* [2]*College of Animal Sciences and Industry, Kansas State University*, *Manhattan*.

E. coli O157:H7 is a contaminant of beef and associated with food-borne illnesses in humans. Initial colonization of the calf with the organism is believed to occur shortly after birth. Recently an *E. coli* SRP vaccine received conditional licensure in the United States for the control of *E. coli* O157 in cattle. The objective of this study was to determine if *E. coli* O157:H7SRP specific antibodies from vaccinated cows can be passively transferred to beef calves in native range conditions. Cows (n = 20) were randomly assigned to treatments: SRP vaccine or placebo control. Vaccines were administered 60 and 30 d before projected calving date. Samples were collected at the time of calving from cows (fecal, blood and colostrum) and calves (pre-suckle blood sample). Blood samples were obtained from calves at 6, 12, and 24 h and at 7, 14 and 21 d postpartum. Serum total protein (STP) and *E. coli* O157:H7 SRP antibody levels were measured. Dam vaccine history had no effect on the calf STP level ($P > 0.05$). However, length of time postpartum had a significant effect on the calf STP levels ($P < 0.001$). A vaccine treatment by time postpartum interaction was observed for the calf serum *E. coli* O157:H7 SRP antibody levels ($P < 0.01$). This interaction was explained by no vaccine treatment difference in calf serum *E. coli* O157:H7 SRP antibody levels pre-suckle, but a significant increase in calf *E. coli* O157:H7 SRP post-suckle titers in the calves born to SRP vaccinated cows compared with calves born to placebo cows. The results from this study show successful *E. coli* O157:H7 SRP antibody passive transfer in beef calves under natural conditions and indicates that early immunization against *E. coli* O157:H7 could play a role in preventing animals from shedding the organism at harvest. Further research is needed to study possible cross protection of this vaccine in other cattle diseases.

Key Words: immunity, colostrum, vaccine

839 Effect of colostrum supplementation on health and performance of pre-weaned and post-weaned dairy calves. B. Ozer*[1], M. Chahine[1], C. M. Matuk[1], M. E. de Haro Martí[2], and M. Nelson[1], [1]*University of Idaho*, *Twin Falls*, [2]*University of Idaho*, *Gooding*.

The objective of this study was to determine the effect of a commercially available colostrum supplement on health parameters in Holstein dairy heifers. Fifty 7 Holstein female calves raised on a commercial facility in southern Idaho were randomly assigned to one of 2 treatments which consisted of maternal colostrum (MC, n = 27) or maternal colostrum supplemented with bovine-serum based colostrum supplement (MCS, n = 30). All colostrum treatments (3.8 L) were administered using an esophageal tube within 1 h of birth. A second feeding of colostrum (2 L) was administered 8 h following first feeding. Blood samples were collected at 24 ± 3 h of age and tested for total serum protein (TSP). Pre-weaned period rectal body temperature was measured every other day. Health evaluations were conducted daily by study personnel until calves were 3 mo of age. Pre-weaned fecal (FC), dehydration (DH) and respiratory (RS) scores were recorded. TSP concentrations were significantly greater ($P < 0.01$) in calves fed MC (TSP = 6.17 ± 0.09 g/dL) compared with calves fed MCS (TSP = 5.84 ± 0.09 g/dL). Rectal body temperature did not differ between MC and MCS and averaged 39.0°C ± 0.03. No differences were detected in pneumonia, diarrhea, or mycoplasma incidence which averaged 61.7%, 10.5%, and 38.3% respectively. MCS calves had a greater ($P < 0.006$) incidence of abnormal RS score (58.5%) compared with MC (27.3%). FC and DH scores did not differ between treatments and averaged 27.6% and 12.7% respectively. Thus in this study, adding a supplement to maternal colostrum did not achieve any positive effect on performance and health parameters of dairy calves.

Key Words: colostrum, colostrum supplement, total serum protein

840 Evaluation of immunological status of newborn dairy calves when respective dams were fed a stepwise moderate energy diet or a controlled energy diet during the dry period. J. S. Osorio*[1], P. Ji[1], G. Invernizzi1,2, J. K. Drackley[1], and J. J. Loor[1], [1]*University of Illinois*, *Urbana,* [2]*University of Milan*, *Milan, Italy*.

Decreases in dry matter intake and increases in concentrations of non-esterified fatty acids and cortisol during the periparturient period have been associated with an impaired immunological status in dairy cows. Controlling energy intake during the dry period has been proposed to diminish these conditions during early lactation. The extent of these effects on the immunological status of newborn calves is unknown. Holstein cows (n = 12) were randomly assigned to a stepwise moderate energy (ME) diet (1.49 Mcal/kg) or a controlled energy (CE) diet (1.30 Mcal/kg) during the close-up period (−21 to 0 d relative to calving). All cows were fed CE during the far-off period (−50 to −21 d relative to calving). At birth, calves were separated from dams and during the first 24 h received at least 3.8 L of dam's colostrum with minimum 60 mg/dL of solids density. Blood samples were taken at birth (Pre-colostral) and 48 h (Post-colostral) using vacutainer tubes with ACD, EDTA, or serum. RNA was extracted from isolated blood peripheral neutrophils, and whole blood phagocytosis was assessed through flow cytometry (BD Biosciences LSR II). Body weight, withers height, and hip height were recorded at birth. Data were analyzed using the MIXED procedure of SAS (v. 9.2). Results indicated that dams that were fed a CE diet during the complete dry period gave birth to heavier ($P = 0.01$) calves than ME cows. Preliminary analysis of whole blood phagocytosis showed no difference in percentage of phagocytozing cells from either pre ($P = 0.88$) or post ($P = 0.72$) colostral blood samples from calves born from dams on either diet. However, the phagocytosing population of cells behaved differently between CE and ME treatments when observed from pre- to post-colostral blood samples. All phagocytosing cells were clumped in pre-colostral samples regardless of dam's diet, but only cells from calves born to dams fed CE divided into 2 populations from the post-colostral blood samples. Further analyses are being conducted to fully discern the biological meaning and significance of these results.

Key Words: calves, phagocytosis, immunology

841 Characterization of immune and metabolic responses in the blood of dry cows induced with sub-acute ruminal acidosis (SARA). A. D. Kroeker*[1], S. Li[1], S. Shekhar[1], A. Ceballos[2], E. Khafipour[1], D. O. Krause[1], J. C. Plaizier[1], and J. C. Rodriguez-Lecompte[1], [1]*University of Manitoba*, *Winnipeg, Manitoba, Canada*, [2]*Cornell University*, *Geneseo, NY*.

Subacute ruminal acidosis (SARA) increases lipopolysaccaharide endotoxin (LPS) in the rumen, due to lysis of gram-negative bacteria. This LPS can translocate into the blood during SARA, which causes inflammation. The objective of this study was to determine the systemic immune and metabolic responses in the blood of cows with 2 forms of SARA. Six dry, non-pregnant, dairy cows were used in a Latin Square with 3 periods of 4 wk. During wk 1–3 of all periods cows received the control diet containing 70% forage and 30% mixed concentrates (DM basis). During wk 4, cows either received the control diet(T1) control diet), treatment 2 (T2, alfalfa pellet-induced SARA (API_SARA), 45% mixed concentrate, 32% alfalfa pellets, and 23% other forages), or treatment 3 (T3) (GPI_SARA, 38% wheat-barley pellets, 32% other mixed concentrate, and 30% forages). Blood cell, serum chemistry, acute-phase proteins (fibrinogen, serum amyloid A (SAA), haptoglobin (Hp, and LPS binding protein (LBP), and peripheral blood leukocyte cell surface marker (CD14) parameters were evaluated. The durations of the rumen pH below 5.6 were 56.4, 225.2 and 298.7 min/d for control, API_SARA, and GPI_SARA, respectively. This shows that both forms of SARA resulted in similar depressions of rumen pH, and that SARA was induced. Treatments did not affect leukocyte and differential count, red blood cells, hemoglobin, mean corpuscular volume (PCV), mean corpuscular hemoglobin, mean corpuscular hemoglobin concentration, and clinical chemistry parameters. However, PCV decreased in T2 and T3 cows. Also, urea was lower in T2 cows 9 d after the beginning of treatment. There were increases in SAA and LBP in T3. There were no changes in the total protein to fibrinogen ratio, suggesting no inflammatory activity; however, the albumin to globulin ratio increased in T3 cows during the second period of the study. No differences were found the proportion of peripheral blood neutrophils and monocytes expressing CD14. In conclusion, our results suggest that immunological and metabolic parameters were not affected by SARA

Key Words: SARA, LPS, CD14

842 Comparison of long-term progestin-based protocols to synchronize estrus in postpartum beef cows. J. M. Nash*, D. A. Mallory, C. C. Selby, K. G. Pohler, M. R. Ellersieck, M. F. Smith, and D. J. Patterson, *University of Missouri*, *Columbia*.

The objective of the experiment was to compare follicular dynamics, ovulatory response to GnRH, steroid hormone concentration patterns, and synchrony of estrus and ovulation among estrous-cycling and anestrous postpartum beef cows following treatment with long-term progestin-based protocols. Beef cows (n = 40) were assigned to treatments based on age, days postpartum, BCS and estrous cyclicity status. Blood samples were taken 10 and 1 d before treatment to determine estrous cyclicity status (progesterone ≥0.5 ng/mL estrous cycling). CIDR Select (T1, n = 20) treated cows received a controlled internal drug-release insert (CIDR;1.38 g progesterone) from d 0 to 14 followed by GnRH (100 μg, i.m.) on d 23, and PG (25 mg, i.m.) on d 30. Cows assigned to the 14-d CIDR-PG (Show-Me-Synch T2, n = 20) treatment received a CIDR insert from d 0 to 14 and PG on d 30. Ultrasound was used to determine response to GnRH for T1 treated cows or follicle turnover for T2 treated cows coincident with timing of GnRH for T1; follicle size at AI; and pregnancy diagnoses. T1 treated cows had a higher ovulatory response to GnRH than cows in T2 ($P < 0.001$; T1 = 17/20, 85% ovulatory response; T2 = 1/20, 5% follicle turnover); however, progesterone at PG did not differ between treatments ($P = 0.17$). Mean diameter of the dominant follicle at GnRH, PG and AI did not differ between treatments ($P > 0.05$). Estrous response, determined from Heatwatch, during the 2 synchronized periods, following CIDR removal and after PG, did not differ ($P = 1.0$) between treatments. Variances for interval to estrus after CIDR removal and PG were similar for both treatment groups ($P > 0.05$). Synchronized AI conception rates did not differ between T1 and T2 treated cows ($P > 0.05$; 72% vs. 58%, respectively); and there was no difference in synchronized AI pregnancy rates between treatments ($P > 0.05$; T1 = 68%; T2 = 55%). In summary, CIDR Select and Show-Me-Synch protocols were equally effective at synchronizing estrus in postpartum beef cows.

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Key Words: AI, beef cow, CIDR insert

843 Comparison of long-term progestin-based protocols to synchronize estrus prior to fixed-time AI in beef heifers. D. A. Mallory*, J. M. Nash, M. R. Ellersieck, M. F. Smith, and D. J. Patterson, *University of Missouri*, *Columbia*.

This experiment was conducted to compare pregnancy rates resulting from fixed-time AI (FTAI) after administration of either one of 2 long-term controlled internal drug release (CIDR)-based protocols. Heifers from a single location were assigned to treatments by age, BW, and reproductive tract score (RTS; 1 = immature to 5 = estrous cycling). Heifers assigned to the CIDR Select treatment protocol (n = 192) received a CIDR insert (1.38 g progesterone) from d 0 to 14, followed by GnRH (100 μg, i.m.; Cystorelin) 9 d after CIDR removal (d 23) and prostaglandin $F_{2\alpha}$ (PG; 25 mg, i.m.; Lutalyse) 7 d after GnRH (d 30). Heifers assigned to the 14-d CIDR-PG treatment protocol (Show-Me-Synch; n = 200) received a CIDR insert from d 0 to 14 followed by PG 16 d later (d 30). Artificial insemination was performed at predetermined fixed times for heifers in both treatments at 72 or 66 h after PG for the CIDR Select and Show-Me-Synch groups, respectively. All heifers were administered GnRH (100 μg, i.m.) at the time of AI. Heifers were exposed for a 42 d natural service clean-up period beginning 10 d after FTAI. There were no differences between treatments for age ($P = 0.74$), BW ($P = 0.92$), or RTS ($P = 0.67$). FTAI pregnancy rates tended ($P = 0.07$) to be greater among Show-Me-Synch (124/200; 62%) compared with CIDR Select (98/192; 51%) treated heifers. Final pregnancy rates did not differ ($P = 0.72$; CIDR Select, 85%; Show-Me-Synch, 83%) between treatments. Based on the odds ratio, Show-Me-Synch treated heifers were 1.62 times more likely to conceive to FTAI than heifers synchronized with CIDR Select. Pretreatment estrous cyclicity status did not affect ($P = 0.32$) FTAI pregnancy rate; however, estrous cycling heifers assigned to Show-Me-Synch had a tendency to have higher FTAI pregnancy rates (63%) than those assigned to CIDR Select (53%; $P = 0.06$). In summary, both long-term progestin based protocols were effective in synchronizing estrus before fixed-time AI in beef heifers.

This project was supported by National Research Initiative Competitive Grant no. 2005-55203-15750 from the USDA Cooperative State Research, Education, and Extension Service.

Key Words: AI, beef heifer, CIDR

844 Comparison of long- versus short-term progestin-based protocols to synchronize estrus and ovulation prior to fixed-time AI in postpartum beef cows. D. A. Mallory*, J. M. Nash, M. R. Ellersieck, M. F. Smith, and D. J. Patterson, *University of Missouri*, *Columbia*.

This experiment was designed to compare pregnancy rates in postpartum beef cows resulting from fixed-time AI (FTAI) after treatment with long- versus short-term controlled internal drug release (CIDR)-based protocols to synchronize estrus and ovulation. Angus cows were assigned to treatments by age, BCS, and days postpartum (DPP). Cows assigned to the long-term 14-d CIDR-PG (Show-Me-Synch; n = 99) treatment protocol were administered CIDR inserts (1.38 g of progesterone) from d 0 through 14. Prostaglandin $F_{2\alpha}$ (PG, 25 mg, i.m.) was administered 16 d after CIDR removal, on d 30 of treatment. Cows assigned to the short-term treatment protocol (7-d CO-Synch + CIDR; n = 104), received GnRH (100 μg, i.m.) and CIDR inserts on d 0. CIDR inserts were removed 7 d later at the time PG was administered (d 7). Blood samples were collected on d −9 and immediately before treatment initiation to determine pretreatment estrous cyclicity status of cows (progesterone ≥0.5 ng/mL; Show-Me-Synch, 54/99 = 55%; 7-d CO-Synch + CIDR 51/104 = 49%; $P = 0.52$). Continuous estrus detection was performed using HeatWatch; transmitters were fitted at PG and removed at AI. AI was performed at predetermined fixed times (72 h, Show-Me-Synch; 66 h, 7-d CO-Synch + CIDR) and all cows were administered GnRH (100 μg, i.m.) at AI. There were no differences ($P > 0.10$) between treatments for age, BCS, or DPP. Pregnancy rates were greater ($P < 0.01$) among cows that exhibited estrus before FTAI than for those that did not (52/73 = 71% and 55/130 = 42%, respectively). Pregnancy rates resulting from FTAI did not differ between treatments ($P > 0.10$); technicians ($P > 0.10$); AI sires ($P > 0.10$); or on the basis of pretreatment estrous cyclicity status ($P > 0.10$). Final pregnancy rates did not differ between treatments ($P = 0.53$). In summary, pregnancy rates resulting from FTAI following treatment with Show-Me-Synch and 7-d CO-Synch + CIDR were similar among postpartum beef cows.

This project was supported by National Research Initiative Competitive Grant no. 2005-55203-15750 from the USDA Cooperative State Research, Education, and Extension Service.

Key Words: AI, beef cow, CIDR

845 Effect of $PGF_{2\alpha}$ administration at CIDR insertion on AI pregnancy rates in beef heifers. B. L. Sparks*[1], S. L. Lake[2], J. Berry[2], K. Heaton[3], R. P. Lemenager[1], L. A. Horstman[1], K. S. Fisher[1], P. J. Gunn[1], and G. A. Bridges[1], [1]*Purdue University*, *West Lafayette, IN,* [2]*University of Wyoming*, *Laramie,* [3]*Utah State University*, *Logan*.

The objective of this study was to compare 3 estrous synchronization protocols in beef heifers. Heifers managed at 5 locations were assigned to the 7 d Select Synch + CIDR & timed-AI (TAI; 7dSS; n = 298), 5 d Select Synch + CIDR & TAI (5dSS; n = 366), or an experimental 7 d protocol where $PGF_{2\alpha}$ (PGF) was given at CIDR insertion (7dMOD; n = 373). On d −7, the 7dSS treatment received a CIDR and GnRH (100 μg), while the 7dMOD treatment received a CIDR and PGF (25 mg). On d −5, the 7dMOD treatment received GnRH and the 5dSS treatment received a CIDR and GnRH. On d 0, CIDR were removed and all heifers received 2 25 mg doses of PGF given 8 h apart. Estrus was detected twice daily for 60 h after CIDR removal and heifers detected in estrus were AI by the AM/PM rule. At 72 h after CIDR removal heifers not detected in estrus were TAI and received GnRH. Bulls were placed with the heifers 7 d after TAI for the remainder of the breeding season. Pregnancy was diagnosed approximately 35 d after TAI and bull removal, respectively. The effect of treatment, location, and the interaction on estrous response, interval to estrus, conception rate, TAI conception rate, overall AI and breeding season pregnancy rate were analyzed using SAS. The treatment by location interaction was not significant for any variable, thus data were pooled. Estrus response was greater ($P < 0.05$) in the 7dSS (67.1%) and 7dMOD (69.4%) treatments than the 5dSS (56.0%) treatment. Interval to estrus was shorter ($P < 0.01$) in the 7dSS (46.7 ± 0.5 h) and 7dMOD (47.7 ± 0.7 h) treatments compared with the 5dSS (51.9 ± 0.5 h) treatment. Conception rate of heifers in estrus was greater ($P < 0.05$) in the 5dSS (61.9%) and 7dMOD (66.4%) treatments than the 7dSS (50.0%) treatment. Conception rate to TAI did not differ between treatments (45.8%). More ($P < 0.05$) heifers became pregnant to AI in the 5dSS (57.1%) and 7dMOD (58.7%) treatments than the 7dSS (47.3%) treatment. Breeding season pregnancy rates were similar between treatments (86.4%). In conclusion, the 5dSS and 7dMod protocols yielded greater AI pregnancy rates in beef heifers than the 7dSS protocol.

Key Words: beef, estrous synchronization, heifer

846 Influence of inducing luteal regression prior to a fixed-time AI CIDR protocol in postpartum beef cows on pregnancy success. G. A. Perry*, B. L. Perry, and J. H. Krantz, *Department of Animal & Range Sciences*, *Brookings, SD*.

Most fixed-time insemination protocols utilize an injection of GnRH at the beginning of the protocol to initiate a new follicular wave. However, the ability of GnRH to initiate a new follicular wave is dependent on the stage of the estrous cycle. We hypothesized that administering $PGF_{2\alpha}$ 3 d before initiating a fixed-time AI protocol would improve synchrony of follicular waves and result in greater pregnancy success. Therefore, our objective was to determine whether inducing luteal regression 3 d before a fixed-time AI protocol would improve pregnancy rates. Multiparous crossbred cows at 2 farms (n = 296 and n = 97) were randomly assigned to one of 2 treatments: 1) $PGF_{2\alpha}$ (25mg; i.m.) on d −9, GnRH (100μg; i.m.) and insertion of a CIDR on d −6, $PGF_{2\alpha}$ (25mg; i.m.) and CIDR removal on d 0 (PG-CIDR) or 2) GnRH (100μg; i.m.) and insertion of a CIDR on d −5 and CIDR removal with $PGF_{2\alpha}$ (25mg; i.m.) at CIDR removal and 4 to 6 h after CIDR removal (5d CIDR). Cows were time-inseminated between 66 and 72 h (PG-CIDR) or 70 to 74 h (5d CIDR) after CIDR removal. Pregnancy rates to fixed-time AI were determined by ultrasonography 76 to 82 d after AI in herd 1 and 35 d after AI in herd 2. In herd 1, PG-CIDR cows were longer postpartum ($P < 0.01$; 71 ± 1.2 d) than 5d CIDR cows (65 ± 1.1 d). In herd 2, there was no difference ($P = 0.58$; 79 ± 2.0 and 81 ± 2.0 d for PG-CIDR and 5d CIDR, respectively). There were no differences between treatments ($P = 0.07$), locations ($P = 0.35$), or treatment by location ($P = 0.19$) on BCS. Pregnancy rates were 59% (89/149) and 46% (68/147) for PG-CIDR and 5d CIDR in herd 1, respectively ($P = 0.02$); and 77% (37/48) and 67% (33/49) for PG-CIDR and 5d CIDR in herd 2, respectively ($P = 0.28$). When data from both herds were combined pregnancy rates remained different between protocols [$P = 0.01$; PG-CIDR = 126/197 (64%); 5d CIDR = 101/196 (52%)]. In summary, pregnancy rates resulting from fixed-time AI were improved by inducing luteal regression 3 d before initiation of a fixed-time AI protocol.

Key Words: estrous synchronization, fixed-time AI, beef cows

847 Influence of luteal regression prior to GnRH on LH pulse frequency and synchrony of follicular growth. J. K. Grant*[1], F. M. Abreu[2], and G. A. Perry[1], [1]*Department of Animal & Range Sciences*, *Brookings, SD,* [2]*USDA-ARS Ft. Keogh*, *Miles City, MT*.

Research has reported that luteal regression before a GnRH injection decreased progesterone concentrations and increased synchrony of follicular growth and estrus. The objective of this study was to determine the effects of luteal regression before a GnRH injection on LH pulse frequency and synchrony of follicular growth. Angus-cross beef heifers (n = 15) were assigned to one of 3 treatments: 1) $PGF_{2\alpha}$ on d −9, GnRH and insertion of a CIDR on d −6, and $PGF_{2\alpha}$ and CIDR removal on d 0 (PG-CIDR), 2) $PGF_{2\alpha}$ on d −9, GnRH on d −6, and $PGF_{2\alpha}$ on d 0 (PG-No CIDR), or 3) GnRH and insertion of a CIDR on d −7 and $PGF_{2\alpha}$ and CIDR removal on d 0 (7d CIDR). Follicular growth was determined daily by transrectal ultrasonography. Blood samples were collected daily for determination of progesterone concentrations. On d 4 after CIDR insertion (d −3 for 7d CIDR and d −2 for PG-CIDR and PG-No CIDR), blood samples were collected every 15 min for 8 h to determine LH pulse frequency. There was a treatment ($P = 0.04$), time ($P < 0.01$), and treatment x time ($P < 0.01$) interaction on progesterone concentrations. PG-No CIDR had decreased concentrations compared with PG-CIDR and 7d CIDR, which were similar. There was a tendency ($P = 0.09$) for LH pulse frequency to be greater among PG-CIDR (3.4 ± 0.24) and PG-No CIDR (3.4 ± 0.24) compared with the 7d CIDR (2.6 ± 0.40), but area under the curve ($P > 0.76$) and mean LH concentrations ($P > 0.76$) did not differ. Follicular growth rates did not differ between treatments ($P > 0.14$), but there was a tendency for decreased variance in growth rate among PG-CIDR (0.03) compared with PG-No CIDR ($P = 0.1$; 0.10) and 7d CIDR ($P = 0.06$; 0.20). In addition, variance in dominant follicle size on d 0 was decreased in PG-CIDR (0.2) compared with PG-No CIDR ($P < 0.01$; 7.8) and 7d CIDR ($P = 0.01$; 5.1). In summary, luteal regression before a GnRH injection tended to increase LH pulse frequency and decrease variation in follicle growth and decreased variation in follicle size on d 0.

Key Words: LH, estrous synchronization, follicular growth

848 The influence of two doses of PGF2α given at 2 or 12 hour intervals on luteolysis and pregnancy rate to timed AI with the 5-d CO-Synch + CIDR program. L. H. Cruppe*[1], M. Maquivar[1], E. M. Jinks[1], G. E. Fogle[1], M. L. Mussard[1], A. V. Pires[2], and M. L. Day[1], [1]*The Ohio State University*, *Columbus*, [2]*University of São Paulo*, *Piracicaba, SP, Brazil*.

The objectives of these experiments were to assess the impact of the interval between 2 PGF2α doses in the 5-d CO-Synch + CIDR on

reproductive performance (Expt 1) and luteal regression (Expt 2) in beef cows. Cows were assigned, within parity, by days postpartum to treatments. Blood samples for progesterone (P4) analysis were collected on d −15 and −5 to classify cows as cyclic or anestrus. All cows received 100 µg of GnRH (Cystorelin) at the time of CIDR insertion on d −5. In Expt 1, all cows (n = 254) received their first 25 mg dose of PGF i.m. (Lutalyse) on d 0 (h 0) and at the time of CIDR withdrawal and tail paint application. A second dose of PGF was given at either h 2 (2hPGF) or h 12 (12hPGF). At h 72, cows received 100 µg GnRH and timed-AI (TAI). Blood samples were collected on d 3 (h 72), 10 and 15 and analyzed for P4, and h 72 samples from cows that were not detected in estrus were analyzed for estradiol (E2) concentration. In Expt 2, cows (n = 31) received the 2hPGF and 8hPGF treatments as described, with the exceptions that the CIDR was withdrawn at h −2 and the second GnRH/TAI was not performed. Rather, estrous detection was performed from d 0 to d 7 and blood samples for P4 collected at h 0, 2, 4, 12, 14, 24, 48, 72 and 96. Ultrasonography performed on d −5, −1, 3 and 10 was used to detect existing CL, induction of ovulation with the initial GnRH, regression of CL with PGF and formation of a new CL, respectively. In Expt 1, TAI pregnancy rate did not differ between 2h- and 12hPGF treatments (60.8% vs. 58%). Concentrations of P4 on d 3, 10 and 15 did not differ between treatments or pregnancy status. Concentration of E2 at h 72 did not differ with pregnancy status. In Expt 2, P4 concentrations, incidence and timing of estrus, luteal regression and other ovarian characteristics determined by ultrasonography did not differ between treatments. In conclusion, reduction of the interval to the second PGF dose from 12 to 2 h in the 5-d CO-Synch + CIDR treatment did not influence TAI pregnancy rate or the occurrence of luteal regression.

Key Words: cattle, PGF2α, timed-AI

849 Use of two coincident doses of PGF2α with the 5-d CO-Synch + CIDR estrous synchronization program. L. H. Cruppe*[1], L. A. Souto[1], M. Maquivar[1], P. Gunn[3], M. L. Mussard[1], D. Wolfenson[4], A. V. Pires[2], G. A. Bridges[3], and M. L. Day[1], [1]*The Ohio State University*, *Columbus*, [2]*University of São Paulo*, *Piracicaba, SP, Brazil*, [3]*Purdue University*, *West Lafayette, IN*, [4]*The Hebrew University*, *Rehovot, Israel*.

The aim of this study was to determine the effect of timing of the second dose of PGF2α (PGF) in the 5-d CO-Synch + CIDR program on timed-AI (TAI) pregnancy rate. Spring-calving crossbred beef cows (n = 662) at 5 locations were assigned, within parity (primi- or multiparous), by days postpartum to treatments. At 4 locations, blood samples for progesterone analysis were collected on d −15 and −5 of the experiment to determine if cows were cyclic or anestrus. All cows received 100 µg of GnRH (Cystorelin) at the time of CIDR insertion on d −5. On d 0 (h 0), the CIDR was withdrawn, tail paint applied, and all cows received their first 25 mg dose of PGF i.m. (Lutalyse). A second dose of PGF was administered either immediately following the first injection, coincident with CIDR withdrawal (CoPGF; n = 218), h 2 (2hPGF; n = 226) or h 8 (8hPGF; n = 218). At h 72, all cows received 100 µg GnRH, TAI and a tail paint score (TPS; 1 = paint absent; 2 = partial disappearance; 3 = paint undisturbed). Estrus detection and AI were performed from d 16 to 24 after TAI in 4 of 5 herds and then cows were exposed to intact bulls for the remainder of the breeding season. Pregnancy rate to TAI was determined via ultrasonography between d 28 to 43 of the breeding season and final pregnancy rate was determined after the breeding season. Data were analyzed using Glimmix procedure of SAS. Pregnancy rates to TAI did not differ and were 69.7% in the CoPGF, 65.5% in the 2hPGF and 66.1% in the 8hPGF treatments. Irrespective of treatment, TAI pregnancy rate was greater ($P = 0.05$) in multiparous (68.6%) than primiparous (59.8%) cows. There were no interactions of treatment with reproductive status, location, AI technician and sire for TAI pregnancy rate. The proportion of animals with TPS 1 (57.1%), 2 (19%) or 3 (23.9%) did not differ among treatments; however, TAI pregnancy rates were greater ($P < 0.01$) in animals with TPS 1 (73.3%) and 2 (72.2%) than with TPS 3 (48.1%). In conclusion, 2 coincident doses of PGF at CIDR withdrawal in the 5-d program results in similar TAI pregnancy rates as when given either 2 or 8 h apart.

Key Words: cattle, PGF2α, timed-AI

850 Evaluation of beef cow and calf separation systems to improve reproductive performance of first-calf cows. P. G. M. A. Martins*, D. B. Araujo, and J. D. Arthington, *University of Florida, Range Cattle Research and Education Center*, *Ona*.

Our objectives were to compare the effects of a traditional 48-h calf withdrawal to early-weaning and repeated 48-h calf withdrawals on time to first postpartum ovulation and measures of cow and calf performance. Sixty-four primiparous, Brahman x British crossbred cow-calf pairs were randomly allotted to 3 treatments: EW (early weaned; cows and calves permanently separated); IW (interval weaned; cows and calves separated for 48 h on 4 occasions at 20 d intervals); and CON (control; cows and calves separated a single time for 48 h). Treatments were initiated at the start of a 90-d breeding season (average days postpartum = 97 ± 19 d). Blood samples were collected on 10 d intervals over 100 d for determination of progesterone concentrations. Resumption of cyclicity was defined as 2 consecutive samples with concentrations of progesterone ≥1.5 ng/mL. Cow and calf BW was determined at the start (d 0), middle (d 50), and end (d 100) of the study. Pregnancy was diagnosed by transrectal ultrasonography at 44 d after the end of the breeding season. By d 30 of the breeding season, there were more EW cows cycling than IW and CON cows ($P = 0.03$; 90.9, 61.9, and 66.7% cycling for EW, IW, and CON cows, respectively). Calf BW did not differ at the beginning of the breeding season (average BW = 96 ± 4.1 kg) but was greater ($P < 0.001$) for EW vs. IW and CON calves at the end of the study (d 100; 142, 143, and 142 kg for EW, IW, and CON calves, respectively; SEM = 5.3). In the first year of this experiment, early calf weaning improved cow and calf BW gain and hastened the time to first postpartum ovulation compared with cows subjected to single or repeated 48-h calf withdrawals.

Key Words: cow, calf, weaning

851 Comparison of RFI evaluated as heifers with RFI reevaluated again as mature cows. S. L. Morgan*[1,2], D. A. Neuendorff[1], A. W. Lewis[1], J. P. Banta[1], T. D. A. Forbes[3], A. L. Loyd[2], and R. D. Randel[1], [1]*Texas AgriLife Research*, *Overton,* [2]*Texas AgriLife Research*, *College Station,* [3]*Texas AgriLife Research*, *Uvalde.*

Although the idea of residual feed intake (RFI) was introduced over 45 yrs ago, it is only recently that this topic has acquired great interest. Many studies have investigated the creditability of RFI evaluated in weaned cattle and their subsequent performance in the areas of reproduction, meat science and genetics. However, relatively few studies have evaluated the repeatability of this post–weaning RFI in mature cattle. This study was designed to examine the correlation between post–weaning and mature RFI in *Bos indicus* cows. After the breeding season, 37 multiparous Brahman cows (3–7 yrs of age) with previous RFI data and palpated to be in the first trimester of gestation, were retrained to eat from a Calan gate system. Cows were fed twice daily (0800 and 1600) a 2.5% BW/d diet for 70d with body weight and body condition scores recorded weekly and feed adjusted accordingly. Using the past and present data, RFIs for the initial (RFI1) and repeat (RFI2) trials were calculated. Females were classified according to their RFI values, with a negative RFI = efficient and positive RFI = inefficient. Chi-squared test revealed that 62.2% remained in the same classification, while 37.8% changed, $P = 0.04$. To further investigate repeatability, cows were sorted into High (>0.5 SD), Intermediate (<0.5 SD >) and Low (<0.5 SD) RFI groups. The change in classification groups were determined to be (±0) 51.35%, (±1) 43.24% and (±2) 5.41%, $P < 0.001$. A positive Pearson correlation ($r = 0.51$, $P < 0.001$) was also observed between RFI1 and RFI2 value rankings within yr cohorts, concluding that post-weaning RFI may be a moderately accurate predictor of mature feed efficiency.

Key Words: RFI, repeatability, cow

852 Level of maternal winter supplement and feed restriction during postweaning development influences circulating concentrations of IGF-I in heifers during the peripartum and rebreeding period. A. J. Roberts*, R. C. Waterman, T. W. Geary, L. J. Alexander, and M. D. MacNeil, *USDA-ARS, Fort Keogh Livestock and Range Research Laboratory, Miles City, MT*.

Objective of this research was to evaluate effects of 2 levels of supplemental feed provided to cows during late gestation and 2 levels of feed provided to their daughters during postweaning development on circulating concentrations of IGF-I in the daughters before calving, after calving and before breeding. Heifers were produced over a 3-yr period from dams that were fed levels of harvested feed from mid and late gestation (Dec to March) that were expected to provide marginal (MARG) or adequate (ADEQ) nutrition while grazing dormant winter forage through this period. After weaning, heifers were fed to appetite (CON) or restricted (REST) to 80% of that consumed by CON on common BW basis during a 140-d period ending 1-mo before breeding. Heifers were managed together through breeding to Dec when they were separated so CON could be fed like ADEQ cows and REST could be fed like MARG cows up to 2 to 3-wk before start of calving in March. Concentrations of IGF-I (determined by RIA) in serum samples (n = 828) obtained 8 to 12-d before start of calving, 2 to 4-wk after calving and 0 to 18-d before start of breeding were analyzed by the MIXED procedure of SAS using a model for repeated measures. Concentrations of IGF-I were influenced by interaction of dam and heifer treatments, being greater ($P < 0.05$) in CON heifers from ADEQ or MARG fed dams and REST heifers from MARG dams than in REST heifers from ADEQ dams. Concentrations of IGF-I were greater ($P = 0.05$) in heifers that gestated male than female calves, and in heifers that subsequently became pregnant than those that did not ($P < 0.001$). Results provide support that the dietary treatments imposed on cows resulted in a uterine programming effect in their heifers, as was evident by differences in circulating concentrations of IGF-I in heifers that were restricted fed during postweaning development.

Key Words: heifer development, IGF-I, uterine programming

853 Winter grazing system and supplementation of beef cows during late gestation influence heifer progeny. R. N. Funston*, D. M. Larson, A. F. Summers, J. L. Martin, and D. C. Adams, *University of Nebraska West Central Research and Extension Center*, *North Platte*.

A 2 × 2 factorial study evaluated effects of cow winter grazing system and last trimester supplementation on heifer progeny. Composite cows (yr 1 n = 109; yr 2 n = 114; yr 3 n = 116) grazed either range (WR) or corn residue (CR) during winter and within grazing treatment received 0.45 kg/d (DM) 28% CP cubes (PS) or no supplement (NS). Heifer calves (yr 1 n = 56; yr 2 n = 56; yr 3 n = 54) grazed dormant pasture for 114 d post-weaning and were individually fed for 87 d before natural service breeding (45 d). Dam PS reduced ($P = 0.04$) heifer birth date and CR increased ($P = 0.07$) heifer birth BW. Both PS and CR increased ($P \leq 0.05$) heifer weaning BW, however, adjusted weaning BW was only lower ($P = 0.03$) if the dam grazed WR with NS. Heifer ADG during

the individual feeding period was greater ($P = 0.03$) in heifers from CR NS dams. Heifers from PS dams were younger ($P = 0.09$) at puberty and more tended ($P = 0.11$) to be pubertal by breeding if the dam grazed WR with PS. Heifers from WR NS dams weighed less ($P \leq 0.09$) at breeding and pregnancy diagnosis than WR PS. Pregnancy rate tended ($P = 0.13$) to be greater for heifers born to PS dams. Individually fed heifer DMI was not affected ($P = 0.17$) by treatment, however, heifers from dams that grazed CR with PS gained the least ($P = 0.03$) during individual feeding and had the lowest ($P = 0.04$) G:F. In contrast, there were no differences ($P > 0.10$) in efficiency when expressed as RFI. The heifer's first calf production was unaffected ($P > 0.10$) by dam treatment. Heifers from dams that grazed WR with NS had lower ($P = 0.01$) BW before the second breeding season but similar ($P = 0.97$) pregnancy rates. Cows grazing CR with NS produced the most valuable heifer calf at weaning, however, heifers from cows that grazed WR with NS cost the least to develop per pregnant heifer. Winter grazing system and late gestation supplementation impacted heifer progeny BW, feed efficiency, and reproduction.

Key Words: fetal programming, maternal nutrition, supplementation

854 Gastrointestinal nematode egg shedding rates in temperate adapted Angus and tropically adapted Brahman and Romosinuano calves at weaning. C. C. Chase, Jr.*[1], L. C. Gasbarre[2], S. W. Coleman[1], D. G. Riley[1], and E. E. Connor[2], [1]*USDA-ARS-STARS*, *Brooksville, FL,* [2]*USDA-ARS-BFGL*, *Beltsville, MD*.

Gastrointestinal nematode egg shedding rates were determined at weaning for 3 years in temperate adapted *Bos taurus* (Angus, n = 107), tropically-adapted *Bos taurus* (Romosinuano, n = 126), and tropically-adapted *Bos indicus* (Brahman, n = 87) calves in the subtropics (Florida). Each year, fecal samples were obtained from purebred calves on the day of weaning and the next day. Purebred calves were born and raised at 2 locations (i.e., 2 farms) until after weaning. Eggs per gram of feces were determined for each calf each day and the average of the 2 d was analyzed. The Proc Mixed procedure of SAS was used for statistical analyses and the model included the effects of location, year, breed, sex, and interactions. Location ($P < 0.10$), year ($P < 0.05$), breed ($P < 0.003$), and sex ($P < 0.10$) affected average eggs per gram of feces. Angus had the highest average eggs per gram of feces (179 ± 22.6); Brahman had the lowest average eggs per gram of feces (88 ± 24.0); and Romosinuano had intermediate eggs per gram of feces (compared with Angus and Brahman; 149 ± 21.6). There was however, a 3 way interaction among year by breed by sex ($P < 0.02$). Analysis by year indicated that although average eggs per gram of feces was consistently ranked from Angus > Romosinuano > Brahman over the 3 years, that only in year 2 was breed and breed by sex significant. Breed by sex ($P < 0.01$) in year 2 was due to extremely low average eggs per gram of feces in both male and female Brahman (25 ± 45.4 and 58 ± 48.4) compared with both Angus (183 ± 45.4 and 195 ± 48.4) and Romosinuano (245 ± 36.0 and 39 ± 37.4). In the subtropics, tropically-adapted *Bos taurus* (Romosinuano) and tropically-adapted *Bos indicus* (Brahman) in particular appear to offer some resistance to gastrointestinal nematodes compared with temperate adapted *Bos taurus* (Angus).

Key Words: *Bos indicus*, tropical, GI nematodes

855 Effect of calving season on net returns and risk of cow-calf production in western Canada. T. K. Sirski[1], D. G. Brewin[1], S. L. Scott*[2], A. D. Iwaasa[3], H. A. Lardner[4], and H. C. Block[2], [1]*University of Manitoba, Winnipeg, Canada*, [2]*Agriculture and Agri-Food Canada, Brandon Research Centre, Brandon, Canada*, [3]*Agriculture and Agri-Food Canada, Semiarid Prairie Agricultural Research Centre, Swift Current, Canada*, [4]*Western Beef Development Centre, Lanigan, Canada*.

Data from a 3-site study on the effects of calving season (CS) on cow-calf production in western Canada were used in a Monte Carlo simulation to evaluate net returns and risk. At each of the 3 locations (Brandon, MB (BR), Lanigan, SK (LA), and Swift Current, SK (SC)), production data were collected from crossbred cows (n = 120, BR; n = 100, LA; n = 50, SC) for 2 production cycles running from the start of one CS through to the beginning of the next CS. Cows were allocated to early calving (EC; March) or late calving (LC; June), with 2 replicates per CS per location. Each production cycle was divided into 4 feeding phases: drylot, bale grazing, swath grazing and pasture. Costs were compiled for each CS for feed and straw use, veterinary services, drugs and vaccines, equipment use, labor, land rental and fencing. Costs for mineral, salt, breeding, taxes, water, trucking, marketing and facilities were based on provincial publications for cow-calf costs of production. Revenues for each calving system were calculated using the study′s production data and prices provided by CanFax Research Services (Calgary, AB) for 2000–2009. To simulate the stochastic nature of key input variables, including weaning weight, steer and heifer price, cull cow price and days in each feeding system, 5000 iterations of the @Risk add-in (Palisade Co., Ithaca, NY) for MS Excel were used. Simulated net returns were higher ($P < 0.05$) for LC than those for EC at all 3 locations. In SC, the variance for LC was greater ($P < 0.05$) than that for EC, indicating greater risk within the system. At BR and LA, the variances were not affected ($P > 0.05$) by CS. Results indicate that CS impacts net returns at each location and the risk posed by each CS differs with location.

Key Words: calving season, risk, stochastic simulation

856 Estrous response and pregnancy rates of beef heifers exposed to bulls during an estrus synchronization protocol that included a 14-d CIDR, PGF2α, and, timed AI and GnRH. J. G. Berardinelli*[1], S. Tauck[1], J. Wilkinson[1], J. Olsen[1], T. Gibbs[1], K. C. Davis[1], J. Dafoe[2], and D. Boss[2], [1]*Montana State University*, *Bozeman,* [2]*Northern Agricultural Research Center*, *Havre, MT*.

The objective was to evaluate estrus synchronization responses and AI pregnancy rates (PR) of beef heifers exposed to bulls during a protocol that included a controlled internal drug release device (CIDR) for 14 d, PGF2α (PG), and, timed AI (TAI) and GnRH. Three trials were conducted in 2 consecutive yr (Yr 1 and 2) at 2 locations (L1 and 2). In each trial, heifers were stratified by birth date, BW, BCS, and presence of a corpus luteum and assigned randomly to be exposed (BE; n = 110) or not exposed (NE; n = 110) to bulls. Heifers were exposed to bulls on the day of CIDR insertion (D −32) and remained with bulls until PG injection (D 0). CIDRs were removed 14 d (D −18) after insertion. On D 0 heifers received PG and bulls were removed from BE heifers. Heifers were observed for estrus during the next 60 h from 0600 to 2400 h daily in 2 trials (Yr 1 and 2, L1) and am:pm in the other trial (Yr 2, L2). Heifers that showed estrus by 60 h after PG were bred by AI 12 h later. Heifers that did not show estrus by 60 h were TAI at 66 to 72 h after PG and given GnRH. Proportionate data were analyzed by chi-squared analyses and intervals to estrus after PG were analyzed by ANOVA using PROC GLM of SAS. Model included treatment, YR, location and their interactions. Fewer ($P < 0.05$) BE heifer showed estrus and had longer ($P < 0.05$) intervals to estrus in Yr 1 at L1 and than NE heifers (Yr 1, L1) or BE and NE heifers in Yr 2 at L1 and 2). Thus, more ($P < 0.05$) NE heifers in YR at L1 were bred by AI 12 h after PG than BE heifers in Yr1 at L1 and BE and NE heifers in Yr2 at L1 and 2. Overall AI pregnancy (PR) tended ($P = 0.06$) to be greater for BE (66%)

than NE (54.5%) heifers. Pregnancy rate for BE heifers was greater ($P = 0.055$) than that for NE heifers bred 12 h after estrus; whereas, PR to TAI did not differ between BE and NE heifers. These results indicate that AI PR for heifers inseminated 12 h after estrus may be improved by exposing heifers to bulls during an estrus synchronization protocol that included CIDR for 14 d, followed 18 d later with PGF2α (PG), and, TAI and GnRH.

Key Words: biostimulation, CIDR, estrus synchronization

857 The relationship of cow size to calf weaning weight in a commercial cow/calf operation in the southern Great Plains. G. L. Mourer*, C. P. McMurphy, E. Devuyst, and D. L. Lalman, *Oklahoma State University*, *Stillwater*.

Recent increases in cow/calf enterprise production costs have resulted in renewed interest in identifying critical factors that influence efficiency of production. A better understanding of the relationship of cow size and weaning weight is necessary before informed culling or selection decisions based on cow size can be made. A total of 737 individual cow and calf weaning records collected over 6 yr from a commercial Angus and Angus x Hereford commercial cowherd were evaluated. Cows calved in spring or fall seasons and grazed native tallgrass prairie or bermudagrass pasture year around with supplemental protein during winter and supplemental grass hay when ice or snow covered standing forage. Calves were weaned at 212 ± 20 d regardless of calving season. Means ± SD for cow age, cow BW at weaning, cow BCS at weaning, calf birth weight, calf BW at weaning, calf weight as a percentage of cow BW at weaning (BWW) were 4.96 ± 1.75, 581 kg ± 83, 4.71 ± 0.67, 35.61 kg ± 5.53, 211 kg ± 38.35, 0.42 ± 0.07, respectively. The mixed procedure of SAS was used with cow sire breed, calf sire breed, sex of calf and calving season declared as fixed effects and year of birth used as a random effect. Cow BW at weaning was adjusted to a constant BCS (5.0) and age (5.0 yr) before analysis. Weaning weight was influenced by direct sire, but not maternal sire. SimAngus sired calves were 29.5 kg and 21.8 kg heavier than Charolais and Angus sired calves, respectively ($P < 0.05$). For every 0.45 kg increase in birth weight, weaning weight was increased by 0.86 kg ($P < 0.05$). Spring calving cows weaned 17.7 kg heavier calves than fall calving cows ($P < 0.05$). An increase in cow BW of 45.6 kg resulted in an increase in calf weaning weight of 4.56 kg ($P < 0.05$). Further research is needed to determine if this marginal increase in calf weaning weight per 45.6 kg of increased cow weight is economical.

Key Words: cow size, weaning wt, southern Great Plains

858 Infrared thermography for detection of hoof lesions in dairy cattle. A. Orman[1] and M. I. Endres*[2], [1]*University of Uludag*, *Bursa, Turkey*, [2]*University of Minnesota*, *St. Paul*

Lameness is one of the most important health, economic, and welfare problems in dairy farms today. The objective of this study was to investigate the use of infrared thermography (IRT) for detection of different types of hoof lesions. Early detection of lesions could result in a reduction of severe cases of lameness. A total of 139 lactating dairy cows housed either in a tie-stall or a free stall barn were used. Thermal images of the rear feet were taken with a HSI3000AS (Palmer Wahl) camera and evaluated using Wahl HSI 3000 Imager software. Hoof lesions identified in the study included white line disease (WLD), sole ulcer (SU) and digital dermatitis (DD). Hoof temperatures at the coronary band (CB) and the skin (S) were recorded. Cows were scored for locomotion on a scale of 1 to 5, with 1 = normal and 5 = severely lame. Results for temperature (°C) and locomotion scores (mean (SD)) are reported on Table 1. CB temperatures were higher for all types of hoof lesion ($P < 0.05$) than for healthy hooves. S temperature was higher for WLD ($P < 0.01$) compared with healthy hooves. ΔT (temperature difference between coronary band and skin) was higher ($P < 0.01$) in SU hooves than healthy hooves. Locomotion scores (LS) were similar to healthy cows for all groups except for WLD cows ($P < 0.01$). These results indicate that IRT has potential as a method for detection of hoof lesions, but further research is needed.

Table 1.

Lesion	CB Temp	Skin Temp	ΔT	LS
WLD	34.1(2.3)*	33.2(2.0)**	0.9(0.9)	3.0(0.8)**
SU	33.8(1.6)*	31.6(2.3)	2.1(0.8)**	3.0(0.9)
DD	33.1(1.6)*	31.9(1.5)	1.2(0.7)	2.4(0.7)
Healthy	32.6(1.9)	31.5(1.7)	1.1(0.9)	2.2(0.7)

*$P < 0.05$; **$P < 0.01$ (within column).

Key Words: lameness, thermography, hoof lesions

859 Relationship between udder and leg hygiene score and somatic cell count. M. Q. Shahid*, E. M. Shane, and M. I. Endres, *University of Minnesota*, *St. Paul*.

The objective of this prospective observational study was to evaluate the relationship between cow hygiene and somatic cell count. In addition, the association between milk production and somatic cell count was investigated. Five commercial dairy herds with sand bedded freestalls were used. Herd size ranged from approximately 450 to 1500 lactating cows. Cows were enrolled in the study during January and February 2008. Composite lower rear leg and udder hygiene scores (scale of 1 to 5, with 1 = clean and 5 = very dirty) were collected from approximately 4100 cows during 4 visits spaced 3 mo apart. Scores were recorded and determined by one individual throughout the entire study. Monthly somatic cell count (SCC) values were collected during each visit. Data were analyzed in a model that included effects of animal, sampling period, somatic cell scores (SCS), parity and DIM. The relationship between SCS and hygiene scores was analyzed using PROC MIXED analysis. Hygiene scores (LSMean (SE)) were 2.78 (0.58). Mean SCC and SCS were 294,000 (828,000) cells/ml and 2.76 (1.98), respectively. The analysis indicated that an increase in hygiene scores was associated ($P < 0.0001$) with an increase in SCS. The regression coefficient for SCS and hygiene score was 0.17. A unit increase in hygiene score was associated with a 59,000 cells/ml increase in somatic cell count. The other variables which were significantly associated with SCS were parity, DIM and total milk yield ($P < 0.0001$). Daily milk yield was 39.0 (11.6) kg/cow. The regression coefficient of SCS with parity, DIM and milk yield were 0.35, 0.002 and −0.019, respectively. Every 9,700 cells/ml increase in somatic cell count was associated with a 1 kg reduction in milk yield. Results of this study indicate that striving to maintain cows cleaner can contribute to improved milk quality and milk yield in freestall housed dairy herds.

Key Words: milk quality, SCC, hygiene

861 Association between stall surface and various welfare measurements on dairy herds utilizing recycled manure solids for bedding freestalls. A. W. Husfeldt* and M. I. Endres, *University of Minnesota*, *St. Paul*.

The objective of this observational study was to investigate the association between stall surface and various animal welfare measurements on dairy operations that utilize recycled manure solids as bedding material. The study included 34 dairy operations with herd sizes ranging from 100 to 3800 lactating cows. Forty 5 percent of the herds had mattresses and 55% percent had deep bedded stalls. Farms were visited once between July and October 2009. Approximately 50% of the lactating herd was scored for hygiene (scale of 1 to 5 with 1 = clean, 5 = very dirty), hock lesion prevalence (scale of 1 to 3, with 1 = no lesion, 2 = hair loss, 3 = swollen hock) and lameness prevalence. Lameness prevalence was evaluated by locomotion scoring (1 = normal locomotion, 5 = severely lame; ≥ 3 = lame). Hygiene scores (mean(SD)) were 2.6(0.3), hock lesion prevalence was 60.1(20.8) percent, and severe hock lesion (score 3) was 10.5(8.8). Lameness prevalence was 16.1(9.9) percent and severe lameness prevalence (score 4 and 5) was 5.2(5.0) percent. Hygiene scores (LSmean(SE)) for mattress and deep bedded herds were 2.6(0.05) and 2.5(0.04), respectively. There was an association ($P = 0.05$) with stall surface. Hock lesion prevalences (score 2 and 3) for mattress and deep bedded herds were 63.8(2.5) and 46.7(1.9) percent, respectively. There was an association ($P < 0.001$) between stall surface and hock lesion prevalence. Severe hock lesion prevalences (score 3) were 14.0(1.0) and 6.6(0.7) percent for mattress and deep bedded freestalls, respectively. Stall surface was associated ($P < 0.001$) with severe hock lesion prevalence. Lameness prevalences were 20.6(1.1) and 16.7(0.8) percent for mattress and deep beds, respectively. Stall surface was associated with lameness prevalence ($P < 0.001$). Severe lameness prevalences (scores 4 and 5) for mattress and deep bedded stalls were 6.5(0.5) and 5.1(0.4) percent, respectively and they were also associated with stall surface ($P = 0.04$). Based on these results it appears that deep bedded freestalls with recycled manure solids provide better animal welfare than recycled solids on top of mattresses.

Key Words: welfare, lameness, stall surface

862 Shade utilization and distribution of dairy cows in response to environmental conditions. A. L. Adams*, T. H. Friend, G. A. Holub, S. M. Garey, and C. L. Terrill, *Texas A&M University*, *College Station*.

The means by which dairy cows respond to heat stress is important to cow comfort. The objective of this study was to determine the effects of environmental conditions on shade utilization and pen distribution of cows. Three pens of dairy cows, averaging 186 cows per pen, were

observed for 72 consecutive hours during one trial in June and one trial in August in the Texas panhandle. The number of cows standing or lying in the shade, open lot, and at the bunk was recorded at 1 h intervals. Environmental conditions were also recorded. Soil temperatures at 5.1 cm below the surface were recorded every hour in transects starting under the shade structure and continuing 3.0 m, 6.1 m, 9.1 m, and 12.2 m from the eastern and western sides of the shade structure. Cow locations and shade use were analyzed in a mixed model. A significant increase in shade utilization occurred at 1200 – 1400 h ($P < 0.0001$). Shade utilization increased as cloud cover decreased ($P = 0.011$), wind speed decreased ($P = 0.0034$), and black globe temperatures increased ($P = 0.025$). Temperature-humidity index (THI) did not have a significant effect on shade use ($P = 0.19$). When black globe temperatures were high and the proportion of cows in the shade increased, cows spent more time standing ($P = 0.054$; $P = 0.015$, respectively). Cloud cover ($P = 0.45$), THI ($P = 0.74$), and wind speed ($P = 0.96$) did not affect the proportion of cows standing. Cows spent the most time at the feed bunk at 1900 – 2000 h ($P = 0.0004$). When cloud cover and wind speed were high, cows spent more time at the feed bunk ($P < 0.0001$; $P = 0.005$, respectively). Cows tended to spend more time at the feed bunk when THI was low ($P = 0.076$), but black globe temperatures did not have an effect ($P = 0.97$). Soil temperatures under the shade structures were consistently cooler than soil temperatures in the lots and were negatively related to the proportion of cows lying in the shade. These results suggest that multiple environmental parameters need to be considered when determining the comfort and well-being of dairy cows.

Key Words: dairy, behavior, heat stress

863 Associations between housing systems and animal welfare measurements assessed by survival analysis. K. M. Lobeck*, M. I. Endres, S. M. Godden, and J. Fetrow, *University of Minnesota*, *St. Paul*.

The objective of this study was to determine when dairy cattle become lame in cross-ventilated (CV) freestall barns compared with naturally ventilated (NV) freestall barns. Data were collected from October 2007 to August 2009 on 4 commercial herds. Twenty-five cows were enrolled per season at calving time starting from fall 2007 until summer 2008 for a total of 100 cows per farm. Cows were enrolled in the study for an entire lactation or up to 1 year. Cows were scored every 2 mo for BCS (scale of 1 to 5 with 1 = thin, 5 = obese), hock lesion (scale of 1 to 3, with 1 = no lesion, 2 = hair loss, 3 = swollen hock) and lameness. Lameness was evaluated by locomotion scoring (1 = normal locomotion, 5 = severely lame; ≥ 3 = lame). CV animals reached median cumulative lameness incidence at 360 DIM, whereas NV animals reached median cumulative lameness incidence at 328 DIM ($P < 0.001$). Cows housed in NV barns were 2.9 times more likely to become lame than those housed in CV barns ($P < 0.001$). Each additional parity was associated with a 32% increase in the hazard of becoming lame ($P = 0.002$). Each additional 0.25 increase in body condition score resulted in a 7% decrease in hazard of becoming lame ($P = 0.03$). Cows that calved summer 2008, winter 2008, and spring 2008 were 7.3 times, 5.5 times, and 4.7 times ($P < 0.001$) more likely to become lame than fall 2007 cows, respectively. Cows that calved summer 2008 were 1.6 times more likely to become lame than those that calved spring 2008 ($P = 0.006$). For severe lameness (score 4 and 5), cows housed in NV barns were 2.2 times more likely to become lame than NV barns ($P = 0.03$). There was a trend for parity to increase the hazard of becoming lame by 27% ($P = 0.06$). There was also a trend for cows with hock lesions to be 1.9 times more likely to be lame than those without any hock lesion ($P = 0.09$). There was no difference between NV and CV barns for hock lesion incidence. Parity was associated with a 14% increase in hazard of having a hock lesion ($P = 0.001$). These results indicate that animals housed in CV barns were less likely to become lame than those housed in NV barns, however, there were no differences in hock lesion incidence.

Key Words: lameness, welfare, hock lesion

864 Feed management practices on California dairies. N. Silva-del-Río*[1], J. M. Heguy[2], and A. Lago[3], [1]*University of California Cooperative Extension*, *Tulare County,* [2]*University of California Cooperative Extension*, *Stanislaus and San Joaquin Counties,* [3]*APC, Inc*, *Ankeny, IA*.

The aim of this study was to obtain information on current feed management practices for the high milk yield pens on California′s Central Valley dairies. In summer 2009, a feed management survey was mailed to dairy producers in Tulare, Stanislaus, and San Joaquin counties; the first, third, and seventh largest producing dairy counties in California, respectively. Producers received an envelope containing an invitation letter, a one-page survey, and a pre-paid return envelope. Response rate was 16.9% (120/710). Herd size ranged from 160 to 6,600 cows (median = 950). Dairies fed total mixed rations (TMR) once (28.8%), twice (64.0%), or 3 or more times daily (7.2%). Two dairies reported that TMR was fed 6 times per day. Feed was pushed daily between 1 and 4 times (47.7%), 5 and 8 times (42.4%), and 9 or more times (9.9%). Overall, 44.5% of the producers fed for refusals. Targeted refusals were: 2% or less (50.0%), 2 to 5% (34.0%), or more than 5% (16.0%). Refusals were fed to heifers on 79.6% of dairies. TMR particle length was evaluated in 57.2% of the dairies: weekly (19.2%), monthly (21.7%), and occasionally throughout the year (13.3%). In 2008, dairies reformulated the ration fed to high producing cows 1 to 3 times (30.1%), 4 to 6 times (28.8%), 7 to 9 times (6.8%), and 10 or more times (34.3%). Four dairies reported reformulating the ration at least 20 times. Thirty-nine dairies cited a single reason for ration reformulation: new forage analysis (n = 21), new feedstuff (n = 11), new DM results (n = 3), and price (n = 4). Most dairies (62.9%) indicated 2 or more reasons for reformulating diets. Feed management software is used in 39.3% of the dairies to track dry matter intake (n = 42), cost of errors by feeders (n = 36), cost of feed and ingredient order in the mixer (n = 33), feed delivery time (n = 24), and inventory (n = 23). Some dairies routinely evaluated feed efficiency (n = 53) and milk urea nitrogen (n = 31). Only 24 dairies reported having written feed management protocols. Although dairy owner and manager responses are subjective, survey results help us to identify areas where feed management can be improved, such as feed bunk management and record keeping.

Key Words: feeding management, survey, dairies

860 Relationship between environmental climate and physiologic response under stress conditions of dairy cows measured using thermal imaging in southeastern Sicily. G. Azzaro[1], R. Petriglieri[1], R. Ben Younes[2], M. Caccamo*[1], S. Carpino[1], G. Cascone[3], A. D'Emilio[3], R. Mazzarella[3], and G. Licitra[1,4], [1]*CoRFiLaC, Regione Siciliana*, *Ragusa, Italy*, [2]*Production Animale, Institut National Agronomique de Tunisie*, *Tunisia*, [3]*DIA, Catania University*, *Catania, Italy*, [4]*DACPA, Catania University*, *Catania, Italy*.

The influence of heat stress and physiologic response of dairy cows on performance have been reported in several studies. This study was part of a wider experiment aiming to assess the influence of the combination of environmental climate and floor material on physiological and productive performance of dairy cows. Thirty lactating dairy cows (137 ± 60 DIM; 38.26 ± 6.8 Kg/d milk yield) in a Sicilian herd were grouped

based on milk yield level and lactation stage. Cows in each group were randomly assigned to 2-level treatment of floor (concrete vs rubber) in the alleys in the barn and observed from June through September 2009 under heat stress condition. During this period, temperature humidity index (THI) was measured every 30 min using a thermologger. The physiological response to heat stress was measured every 2 weeks at 3 p.m. in terms of rectal temperature (RT) and respiratory rate (RR). At the same time, temperature of the entire body surface (BS), muzzle (MS), eyes (ES), and rump (RS) were measured using digital infrared thermal imaging. To capture thermal images of the entire body surface, cows were constrained ahead a panel cooled with water. The entire body surface was automatically selected through binarization using ImageJ software, whereas rump, eyes, and muzzle areas were manually selected from pictures. Daily average THI was highly correlated with RT and RR (0.57 and 0.48, respectively), whereas the highest correlation was with BS and RS (0.79 and 0.71, respectively). Both MS and ES were not correlated. Moderate correlations were found between RT and RR with BS (0.47 and 0.45, respectively). Same results were found for RS. No correlation was found between RT and RR with MS, whereas ES had a low ($P < 0.05$) correlation. The high correlation found in this study between BS with environmental temperature and physiologic response of cows makes the thermal imaging method on the entire body surface a promising non-invasive technique to assess heat stress effect.

Key Words: heat stress, body temperature, thermal imaging

Production, Management and the Environment: Environment 2

865 Effects of heating broiler hatching eggs during 6 or 11 days of storage on hatchability. J. T. Brake*[1], M. Güçbilmez[2], S. Özlü[2], R. Shiranjang[2], and O. Elibol[2], [1]*North Carolina State University, Department of Poultry Science, Scott Hall, Raleigh,* [2]*Department of Animal Science, Faculty of Agriculture, University of Ankara, Ankara, Turkey*.

The effects of heating hatching eggs during pre-incubation storage was studied. Freshly collected hatching eggs from 2 young broiler breeder flocks were stored for 1 d in a hatchery egg storage room at 18C and 75% RH in paper egg flats. The eggs were then transferred to plastic setter trays and either remained in the storage room (Control) or were subjected to a heat treatment regimen of 26C for 2 h, 37.8C for 3 h, and 26C for 2 h in a Petersime setter at either 1 or 6 d of storage before being returned to the storage room. A portion of the eggs were heated when transferred to setter trays (Heat 1-6 d) and stored for 5 d more while a portion of the eggs were heated at transfer to setter trays and then stored for 10 d more (Heat 1-11 d). Another group of eggs was heated after 6 d of storage (Heat 6-11d) and then stored 5 d more before incubation. Control eggs stored for 6 d or 11 d were o-incubated in each experiment. The same process was repeated for Experiments 1 and 2 (29 and 28-wk-old breeders, respectively). All eggs were set in a single incubator. A tray of 150 eggs constituted a replicate and 6 or 12 replicate trays (900 or 1800 eggs in total) were set per heating treatment in Experiments 1 and 2, respectively. Data for 6 d and 11 d of storage were subjected to a one-way ANOVA separately where storage treatments were compared to heating treatments. The hatchability of fertile eggs decreased ($P < 0.05$) with length of egg storage in both experiments due to increased ($P < 0.05$) early deads (Exp. 1 and 2) and late deads (Exp. 2). There was no benefit of heating eggs during 6 d of storage (Heat 1-6d) but hatchability of fertile eggs stored for 11 d was increased ($P < 0.05$) by heating at either 1 (Heat 1-11d; 89.2%) or 6 d (Heat 6-11d; 92.4%) of storage as compared to control (83.8%). The heating at 6d of the 11 d storage period produced the numerically best results in both experiments. These data demonstrated that heating eggs before and/or during storage for 11 d reduced early embryonic mortality and increased fertile hatchability of eggs from younger broiler breeder flocks.

Key Words: egg storage incubation, egg storage, egg storage time

866 Assessment of microbial communities involved in decomposition of specified risk material using a passively aerated laboratory-scale composter. S. Xu*[1,2], T. A. McAllister[2], J. J. Leonard[1], and O. G. Clark[3], [1]*University of Alberta, Edmonton, AB, Canada*, [2]*Agriculture and Agri-Food Canada, Lethbridge Research Centre, Lethbridge, AB, Canada*, [3]*McGill University, Ste-Anne-de-Bellevue, QC, Canada*.

The occurrence of bovine spongiform encephalopathy (BSE) in Canada has resulted in the implementation of regulations to remove specified risk material (SRM) from the food chain. Composting may be a viable alternative to rendering for SRM disposal. A study was conducted to assess SRM decomposition during composting, as well as the microbial communities involved. Two matrices (beef manure + barley straw or beef manure + wood shavings) were composted in 6 passively aerated, laboratory-scale composters (n = 3 per matrix) with SRM samples and thermocouples implanted at 3 depths. Data were analyzed using the Mixed procedure of SAS, with time and compost depth treated as repeated measures. Both compost types heated rapidly, exceeding 55°C after 3 d, with oxygen concentration remaining over 16% on 12 out of 15 d. At completion, wood shavings compost had higher water ($P < 0.001$) and total carbon ($P = 0.005$) contents and lower electrical conductivity ($P < 0.001$) as compared with straw compost. Approximately 50% of SRM was decomposed after 15 d of composting, with 30% of this occurring within the first 5 d. Phospholipid fatty acid (PLFA) analysis revealed that gram-positive bacteria were predominant in compost at d 5. Gram-negative bacteria had declined by d 5 but recovered by d 15. Fungi appeared to be suppressed at temperatures above 55°C and did not appear to recover in wood shavings compost. At d 5, Actinomycetes had increased in straw compost, but declined in wood shavings compost. By d 15, they had increased in both compost types. Although temporal changes were evident, compost matrices or depth within the composter did not obviously influence microbial communities or SRM decomposition. These results suggest that SRM decompose rapidly during composting and that both mesophilic and thermophilic microbial communities play a role in this decomposition.

Key Words: bovine spongiform encephalopathy, composting, phospholipid fatty acid analysis

867 Effect of improved production efficiency on pork's carbon footprint: Derived environmental benefits of ractopamine in the US swine herd. G. Boyd*[1], D. Anderson[2], A. Sutton[3], C. Hogan[1], and A. Marks-Callahan[4], [1]*Camco, Broomfield, CO,* [2]*Colorado State University, Fort Collins,* [3]*Purdue University, West Lafayette, IN,* [4]*Elanco Animal Health, Greenfield, IN*.

Increasing production efficiency in swine can improve environmental stewardship. Ractopamine (RAC; Paylean) is an approved feed ingredient that enhances feed efficiency, increases growth rate and increases leanness in finishing swine. Assumptions driving derived environmental benefits are that (1) increased leanness of RAC-fed pigs results in fewer animals needed to produce the same amount of pork protein, and (2) improved feed conversion leads to lower land requirement for feed production thereby decreasing resource, energy, and fuel demands. These changes, in addition to a reduction in manure output, lower greenhouse gas (GHG) emissions. The objective was to quantify these annual savings in metric tons of CO_2-equivalents (tCO_2e). The derived environmental benefits associated with RAC were quantified using a published meta-analysis of RAC growth performance response and 2008 US swine production data, assuming that all finishing pig diets in the US included either 5 or 10 mg RAC/kg feed for the last 28 d. Total GHG emission savings were quantified using emission factors for energy and fossil fuel demands associated with the cradle-to-gate portion of the pork production chain. Results of the calculations are as follows: The number of finisher pigs and sows required to produce the same amount of pork protein was reduced by 5.3% and 6.3% with the inclusion of 5 or 10 mg RAC/kg feed, respectively. Days-to-market were reduced by 3.0 and 2.8, respectively. Derived GHG emissions savings were 1.87 million or 2.23 million tCO_2e/yr, respectively with approximately 63% from reduced manure, 32% from reduced feed production, and 4% from pig housing. The GHG emissions due to RAC manufacture and distribution accounted for less than 0.01% of the calculated savings. Use of 5 or 10 mg RAC/kg feed in finisher pig diets for the last 28 d of feeding significantly aids in mitigating GHG emissions from pork operations.

Key Words: production, environment, swine

868 Analysis of the association of number of piglets born alive with sow level and management factors. S. S. Anil*[1], L. Anil[2], J. Deen[1], S. K. Baidoo[2], M. E. Wilson[3], and T. L. Ward[3], [1]*Veterinary Population*

Medicine, University of Minnesota, *St Paul,* [2]*Southern Research and Outreach Center, University of Minnesota*, *Waseca,* [3]*Zinpro Corporation*, *Eden Prairie, MN*.

Genetics, management and nutritional factors influence the production performance of breeding female pigs. Trace minerals are important to maintain high production performance and claw integrity. The bioavailability of trace minerals depends on both the quantity and form (organic or inorganic). This study analyzed the association of small litter size at birth (≤10 vs. > 10 piglets born alive) with factors of parity, mummies, stillborn, housing system, form of trace mineral supplementation and claw lesions (white line and side wall defects), using multivariate logistic regression model (Proc logistic, SAS v 9.1), using 1010 parity records. These records pertained to 1, 2 or 3 parities of 518 sows of mixed parity, housed in group pens with electronic sow feeders (n = 296) and conventional gestation stalls (n = 222). The sows were randomly allocated to 2 groups and fed either a control diet (ITM, inorganic sulfate minerals, n = 257; Zn −125 ppm, Mn - 40 ppm and Cu - 15 ppm) or a treatment diet containing complex trace minerals as a partial substitution of inorganic minerals (CTM, n = 261; Zn - 50 ppm, Mn −20 ppm and Cu - 10 ppm), fed at isolevels of total trace mineral supplementation. Information on farrowing performance was collected from the PigCHAMP database of the research unit. Claw lesions of these sows were assessed at mid-gestation by the same person in 1, 2 or 3 parities. Results indicated that the likelihood of <10 live born piglets was lower ($P < 0.05$) in sows of parities 1 and 2 (OR 0.39) and in sows of parities 3–5 (OR 0.29) compared with sows of parity > 5. Mummies and preweaning mortality were positively and total sidewall lesion was negatively associated with the likelihood of having <10 live born piglets ($P < 0.05$ for all). Sows receiving the diet containing ITM were 40% more ($P < 0.05$) likely to have < 10 live born piglets compared with sows fed CTM. These results are indicative of the relationship between sow level and nutritional factors with litter size at birth.

Key Words: trace mineral supplementation, production, sow

869 Nutritional evaluation of kernel meal from non-toxic genotype and of detoxified kernel meal from toxic genotype of *Jatropha curcas* in rat. Y. Chen[1], J. X. Liu[1], H. Y. Liu*[1], H. P. S. Makkar[2], and K. Becker[2], [1]*Institute of Dairy Science, Zhejiang University*, *Hangzhou 310029, P.R. China*, [2]*Institute for Animal Production in the Tropics and Subtropics (480b), University of Hohenheim*, *Stuttgart 70593, Germany*.

Two genotypes of *Jatropha curcas* are known, toxic and non-toxic. Phorbol esters are main toxic substances in the seeds of the toxic genotype. *Jatropha* kernel meal after oil extraction is rich in protein (50–62%), and contents of essential amino acids except lysine are comparable to that of soybean meal. After removing phorbol esters and heat-labile antinutrients such as lectins, the meal could be used as a source of protein for animal feeding. Twenty-four male Sprague-Dawley (SD) rats, at an age of 21 d and weighting on average 70 g, were used to evaluate the nutritional value of the kernel meals from the non-toxic genotype and the toxic genotype after detoxification. Four dietary treatments were designed for growth and nitrogen balance trials. Protein-free basal diet consisted of following ingredients (%): cornstarch 80, oil 10, cellulose 5, salt 4 and multivitamin complex 1. In the other 3 diets, part of cornstarch was replaced by casein (CAS), heated meal from the non-toxic genotype (NTM), and detoxified *Jatropha* meal (DTM) at 10% crude protein in diets. Amino acid composition was similar among diets CAS, NTM and DTM. All data were analyzed using the GLM procedure of SAS software system with rat as the repeated subject. No significant difference was observed ($P > 0.05$) in feed intake of rats fed DTM and NTM (300 vs. 343 g) diets, but both intakes were significantly lower than that of rats on diet CAS (406 g). Weight gains of rats fed diets DTM (43 g) and NTM (62 g) were also significantly lower than that of rats on CAS (133 g). Protein efficiency ratio was 3.08, 1.35 and 1.78; and protein retention efficiency was 74.0, 37.8 and 45.1% for diets CAS, DTM and NTM, respectively. True digestibility and biological value of diet NTM were 84.5 and 65.6%, respectively, slightly higher ($P > 0.05$) than those of DTM (81.9 and 61.6%). In summary, the inferior growth rate in both diets containing NTM and DTM is attributed to low intake, while their digestibility and biological value are comparable to those of most of the seed meals.

Key Words: *Jatropha* kernel meal, toxicity, biological assay

Ruminant Nutrition: Dairy: Fats and Carbohydrates

870 Insulin signal transduction in adipose tissue of peripartal dairy cows fed two levels of dietary energy prepartum. P. Ji*, J. S. Osorio, J. K. Drackley, and J. J. Loor, *University of Illinois*, *Urbana*.

Homeorhesis plays a major role in controlling nutrient partitioning from late prepartum through early lactation during which the fetus or mammary gland are the main targets of energy flow. Coincidently, the responsiveness of peripheral tissues such as adipose to insulin is diminished during early lactation. However, it remains unclear if prepartal dietary energy level affects adipose tissue responsiveness and what molecular mechanisms might be involved. To test the adipose responsiveness to insulin in late gestation, subcutaneous adipose tissue was biopsied at −10 and 7 d relative to parturition from dairy cows fed controlled energy (high straw, CE; NEL = 1.30 Mcal/kg) or moderate-energy (ME; NEL = 1.49 Mcal/kg) diets during the close-up period. Adipose tissue explants were initially incubated in DMEM medium at 37°C with 5% CO2 for 30 min as an adaptation period. Explants serving as negative controls were removed after adaptation. Remaining explants were transferred to wells containing fresh DMEM medium for a time-course (15, 30, or 60 min) insulin challenge (1 μg/L). Total cellular protein was isolated from duplicate explant cultures (both control and challenged) for quantification of tyrosine phosphorylation of IRS1 (IRS1-pY) and Thr308-phosphorylation of Akt (Akt-pThr308). IRS1-pY residue serves as the docking site for the SH2 domain of the protein, which mediates signal transduction of insulin; Akt is phosphorylated and activated in the Thr308 motif and plays a pivotal role in the PI3K pathway that is activated upon insulin stimulation. Total IRS1 phosphorylation was used to normalize the IRS1-pY data. Preliminary results revealed significant main effects of dietary energy level ($P < 0.01$) and incubation time ($P < 0.01$). IRS1-pY phosphorylation was higher in tissue from cows fed ME vs. CE after 15 min and 60 min, leading to a diet × time effect ($P < 0.05$). In tissue from cows fed CE, the response to insulin peaked at 30 min after challenge. Overall, results indicated that level of dietary energy affected the sensitivity of adipose tissue to exogenous insulin in vitro.

Key Words: Insulin response, IRS1, peripartal dairy cow

871 Duodenal infusion of α-linolenic acid affect fatty acids metabolism in mammary gland of lactating dairy cows. G. Yang, J. Q. Wang*, D. P. Bu, Khas-Erdene, Q. S. Liu, L. Y. Zhou, P. Sun, and K. L. Liu, *State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences*, *Beijing, P. R. China*.

Increasing the α-linolenic acid (LNA; 18:3 *cis*-9, *cis*-12, *cis*-15) plasma concentration might affect fatty acids (FA) metabolism in the mammary gland. Objective was to determine the effects different arterial concentration of 18:3 *cis*-9, *cis*-12, *cis*-15 (18:3n-3) would have on mammary uptake and synthesis of FA in lactating dairy cows duodenally infused with LNA, via arterial-rectificative venous concentration (AC-RVC) differences and mammary gland balance. Four primiparous lactating Chinese Holstein cows fitted with duodenal cannula were administered 2 treatments in a crossover design: rich-LNA fatty acid infusion at varying concentrations (0, 100, 200, 300, and 400 g/d) vs. basal infusate control. Arterial concentration of 18:3n-3 quadratically increased (29.24, 134.1, 218.3, 219.3, and 216.4 mg/L plasma) as LNA infusion levels increased from 0 to 400 g/d. The mammary extraction rate and uptake of 18:3n-3 was linearly increased as LNA infusion increased. The AC-RVC differences of 18:3n-3 and total FA increased more rapidly than arterial concentrations with all treatments. Increasing LNA infusion linearly increased the balances of 10:0 and 12:0, while linearly decreased the 14:1 and 15:0 balances, which suggested an inhibitory effect on termination process with 12 carbon during FA synthesis in mammary gland. Increasing arterial concentration of 18:3n-3 affects uptake and synthesis of FA in the mammary gland of lactating dairy cows. It is also suggested that the use of arterial-rectificative venous concentration differences maybe an acceptable way to investigate mammary gland metabolism of FA.

Key Words: α-linolenic acid, mammary gland metabolism, dairy cows

872 Effects of different rumen inert fatty acids on fermentation, anti-oxidative status, and microbiota in the rumen, in the absence or presence of dietary antioxidant. Y. M. Wang[1], J. H. Wang[1], C. Wang*[1], J. X. Liu[1], H. Cao[2], F. C. Guo[2], and M. Vázquez-Añón[3], [1]*Institute of Dairy Science, Zhejiang University*, *Hangzhou 310029, P.R China*, [2]*Novus International Research Center*, *Beijing 100085, P. R. China*, [3]*Novus International, Inc.*, *St. Louis, MO 63147, USA*.

In vitro gas test was employed to evaluate the effect of fatty acids of different degrees of saturation on rumen fermentation of sheep in vitro, in the absence or presence of dietary antioxidant (AOX; Agrado plus, Novus International). The experiment was carried out in a 2 × 2 factorial design, with fatty acid type (at 0 and 50% saturation) as one factor and AOX (0 or 500 mg/kg) as another one. Calcium salt of long-chain fatty acids (50% unsaturated fatty acids, UFA) was supplemented as a source of UFA, and palm acid was supplemented as the source of saturated fatty acid (SFA). Substrate consisted of 100 mg corn powder and 100 mg Chinese wild ryegrass hay. Fermentation patterns and anti-oxidative status were not affected by fatty acid type. Inclusion of UFA significantly increased the populations of protozoa relative to total bacterial 16S rDNA, but showed negative effect on *Fibrobacter succinogenes*. Addition of AOX significantly increased gas production and organic matter digestion at 24h incubation. Molar proportion of propionate tended to increase at the expense of acetate due to AOX addition. Addition of AOX tended to decrease malondialdehyde value and increase superoxide dismutase activity. An interaction between AOX and fatty acid type was observed on *Ruminococcus flavefaciens* and *R. albus*. Addition of AOX to UFA-treated substrate significantly increased these 2 bacteria, but not in SFA treatment. In summary, supplementation of UFA results in inferior effect on fiber-digesting bacteria, while this negative effect can be alleviated by AOX addition, but not in SFA treatment. Rumen fermentation and anti-oxidative status tended to be improved by AOX addition, regardless of the fatty acid type.

Key Words: fatty acid type, antioxidant, rumen fermentation

873 Incorporation of essential and non-essential fatty acid into distinct lipid classes in cultured bovine and porcine liver slices. C. Caldari-Torres*, A. J. Lengi, M. L. McGilliard, D. M. Shepherd, J. A. Stamey, and B. A. Corl, *Virginia Polytechnic Institute and State University*, *Blacksburg*.

Ruminants, compared with non-ruminants, segregate fatty acids into specific lipid classes, allowing for essential fatty acid (EFA) conservation. The mechanisms involved in this selective esterification of fatty acids (FA) remain undefined. The aim of this study was to examine FA esterification patterns in ruminant and non-ruminant liver slices. We performed in vitro culture of bovine and porcine liver slices with radiolabeled FA to track esterification of EFA and non-EFA into lipid

classes. Liver slices were incubated in media containing radiolabeled non-EFA ([1-^{14}C]16:0 or [1-^{14}C]C18:1), or EFA ([1-^{14}C]C18:2 or [1-^{14}C] C18:3). In a preliminary study C18:1 incorporation by bovine liver slices increased linearly with time ($R^2 = 0.95$, $P < 0.001$) and tissue weight ($R^2 = 0.96$, $P < 0.001$). Mean FA incorporation was higher for porcine than for bovine liver slices (23.9 versus 15.9 ± 1.8 nmol•2 h^{-1}•150 mg $tissue^{-1}$, $P = 0.03$). Liver cultures of both pig and cattle incorporated non-EFA more readily than EFA (22.9 vs 16.9 ± 1.6 nmol•2 h^{-1}•150 mg $tissue^{-1}$, $P < 0.001$). Pigs esterified a higher proportion of FA into triglycerides (TG) than phospholipids (PL) (3.7 vs. 2.2 ± 0.3 nmol•2 h^{-1}•150 mg $tissue^{-1}$, $P < 0.001$). Cattle did not exhibit preferential esterification of FA into either lipid class, but esterified more non-EFA into TG compared with PL (1.3 vs. 0.9 ± 0.3 nmol•2 h^{-1}•150 mg $tissue^{-1}$, $P = 0.002$). A higher proportion of EFA than non-EFA was incorporated into PL by cultured bovine liver slices (1.4 vs. 0.9 ± 0.3 nmol•2 h^{-1}•150 mg $tissue^{-1}$, $P = 0.02$). There were no differences in esterification patterns of EFA and non-EFA into the TG lipid class of cattle, or the PL or TG lipid classes of pigs. An increase in PL/TG ratio was observed when bovine liver slices were cultured with EFA, compared with non-EFA (1.09 vs. 0.69 ± 0.1 nmol•2 h^{-1}•150 mg $tissue^{-1}$, $P = 0.001$). There was no difference in PL/TG ratio in porcine liver slices cultured with EFA or non-EFA. Results suggest that liver esterification patterns of cattle and pigs differ, with esterification patterns of ruminants possibly facilitating greater EFA esterification into PL.

Key Words: fatty acid, liver, cattle

874 Effects of feeding increasing levels of concentrate on milk fatty acid composition in grazing dairy cows. L. Antonacci[1], G. A. Gagliostro*[1], V. I. Cejas[2], and M. A. Rodriguez[2], [1]*Instituto Nacional de Tecnología Agropecuaria (INTA)*, *Balcarce, Provincia de Buenos Aires, Argentina*, [2]*Instituto Nacional de Tecnología Industrial (INTI)*, *San Martín, Buenos Aires, Argentina*.

Increased intake of concentrate may shift rumen biohydrogenation of C18:3 and C18:2 fatty acids (FA) toward 10t C18:1 reducing the t11 C18:1 (VA) and 9c, 11t C18:2 (CLA) contents in milk. Twelve Holstein cows grazing spring pastures (alfalfa 70%, orchardgrass 30%) were blocked by days in milk (DIM) and randomly assigned to 3 treatments in a replicated Latin square. At the start of the experiment the 6 cows from square 1 (514 kg LW) were producing 28.2 kg milk/d and averaged 35 DIM. In Square 2, LW, milk yield and DIM were 554 kg, 31.3 kg/d and 197 d respectively. Periods lasted 19 d., the first 14 d as adaptation and the last 5 d for sampling period. Treatments (C3, C6, and C9) were 3 levels (3, 6, and 9 kg/d) of concentrate (90.4% DM) containing (g/kg DM) CP (160), starch (351), soluble carbohydrates (149), ether extract (39.7) and NDF (248). Supplements were thoroughly consumed by cows. Data were analyzed with effect of square, period, cow within square; treatment, interaction between period and treatment (NS) and residual error. Cows from C9 produced more milk (27.5 vs. 23.6 kg/d) and protein (885 vs. 735 g/d) compared with C3 ($P < 0.05$) without depressing milk fat content (29.9 g/kg) or pasture intake (11.94 kg DM/cow/d) ($P < 0.69$). Concentration (g/100g FA) of de novo (C4:0-C15:1, 21.78), preformed (>17:0, 48.2), saturated (59,41) or unsaturated (40.34) FAs were not affected whereas that of t10 C18:1 resulted lower ($P < 0.03$) in C9 (0.52) compared with C6 (0.59) and C3 (0.58). Milk fat content (g/100g FA) of VA (3.23; 3.76 and 3.72) and CLA (1.93; 2.01 and 1.92) resulted high in all treatments (C3, C6 and C9) and not affected by concentrate intake ($P > 0.24$). The atherogenicity index of milk fat averaged 1.84 (±0.12) across treatments ($P > 0.77$). When pasture represented from 82 to 58% of total DM intake of cows increasing concentrate intake from 3 to 9 kg/cow/d had only minor effects on t10 C18:1 concentration in milk without depressing VA and CLA contents.

Key Words: grazing dairy cows, concentrate levels, milk fatty acid

875 Effects of dietary fat supplements and forage:concentrate on feed intake, feeding and chewing behavior of Holstein dairy cows. S. Kargar, M. Khorvash, M. Alikhani, and G. R. Ghorbani*, *Isfahan University of Technology*, *Isfahan, Iran*.

Hydrogenated palm oil and yellow grease as saturated and unsaturated fat supplements, respectively, were investigated for effects on feed intake, diurnal fluctuation of eating and ruminating, meal patterns, and chewing behavior. Eight multiparous Holstein dairy cows were used in a replicated 4 × 4 Latin square experiment with 21 d periods. Treatments were 1) no supplemental fat and 34:66 forage:concentrate (F:C) ratio (Control), 2) 2% hydrogenated palm oil and 34:66 F:C ratio (HPO), 3) 2% yellow grease and 34:66 F:C ratio (YG), and 4) 2% yellow grease and 45:55 F:C ratio (YGHF). All data were analyzed using the MIXED procedure of SAS (SAS, 2003). Preplanned statistical contrasts were used to test the effect of fat supplementation (Control vs. HPO + YG); the effect of source of fat supplement (HPO vs. YG); and the effect of forage to concentrate ratio within diets supplemented with yellow grease (YG vs. YGHF). Dry matter intake (DMI) was not affected by fat supplementation regardless of type of fat (27.0 ± 1.11; $P = 0.81$), but cows fed diets with larger F:C ratio ate 7.5% less (25.3 vs. 27.2 ± 1.11; $P \leq 0.002$) . There were no treatment effects on meal patterns by fat supplementation (15.0 ± 0.9; $P = 0.76$), source of fat (15.0 ± 0.9; $P = 0.26$), and F:C ratio (16.0 ± 0.9; $P = 0.41$) but intermeal interval (69.0 ± 4.8; $P \leq 0.04$), eating rate (0.074 ± 0.004; $P \leq 0.03$), and meal size (1.76 ± 0.12; $P \leq 0.001$) were lower in cows fed yellow grease and eating rate was less for the diet with greater NDF content (0.064 ± 0.004; $P \leq 0.001$). Total chewing time (minutes per kilogram of DMI) was not affected by fat feeding (29.9 ± 1.6; $P = 0.85$) nor type of fat supplementation (29.9 vs. 29.8 ± 1.6; $P = 0.93$) but was more for the diet with greater F:C ratio and NDF content (34 ± 1.6; $P \leq 0.01$). In the current study, DMI was not decreased while meal size decreased. Our findings agree with the conclusion that chewing activity might be determined largely by dietary forage NDF content.

Key Words: chewing behavior, forage to concentrate ratio, fat

876 Effects of rapidly rumen fermentable source of starch in prepartum diet on metabolism and performance of multiparous Holstein cows during the periparturient period. H. R. M. Alamouti*[1], H. Amanlou[1], and K. Rezayazdi[2], [1]*University of Zanjan*, *Zanjan, Iran*, [2]*University of Tehran*, *Karaj, Tehran, Iran*.

Thirty-four multiparous Holstein cows were used in a completely randomized design and assigned to 1 of 2 treatments to evaluate the effects of 2 diets varying in ruminal fermentable source of starch, namely ground corn (GC) and rolled wheat (RW), on metabolism and performance of multiparous cows in the periparturient period. The cows were fed diets as a total mixed ration (TMR) with similar energy and crude protein content including 1) 185.7g/kg GC, or 2) 185.7g/kg RW from −22.10 ± 7.1 d relative to expected calving until calving. After calving, all cows received the same lactation diet until 28 d. Cows were group fed from the beginning of the study to −7 d relative to expected calving, fed individually from d −7 to 7 d in milk (DIM), and again group fed to 28 DIM. Dry matter intake (DMI), energy intake, energy balance (EB) and body condition score (BCS) were not different between treatments. The pre-partum diets affected ($P < 0.05$) urinary pH during the last week pre-partum. The RW diet increased ruminal propionate concentration

compared with the GC diet in periparturient period. There was no effect of pre-partum starch source on overall plasma concentration of glucose, nonesterified fatty acid (NEFA), β-hydroxybutyrate (BHBA), albumin, triglyceride (TG), cholesterol, aspartate aminotransferase (AST), insulin, and cortisol during the periparturient period. Cows fed the RW diet during the pre-partum period had greater calcium during 28 d ($P = 0.09$) of lactation compared with cows fed the GC diet. Multiparous cows fed the RW diet produced greater milk protein content ($P = 0.08$). Multiparous cows fed the RW diet had lower milk urea nitrogen (MUN) than cows fed the GC diet ($P < 0.05$). The results of this study show that a rapidly fermentable source of starch (wheat grain) can be included in pre-partum diets without compromising dairy cow metabolism and performance and can smooth the transition of multiparous Holstein cows from gestation to lactation.

Key Words: periparturient period, rapidly fermentable carbohydrates, Holstein cows

877 Effects of cereal grain level in early lactating diets on metabolism and performance of Holstein cows. H. amanlou[1], N. Fazli[1], S. S. Mosavi[1], H. R. Mirzaei Alamouti*[1], and M. Moeini[2], [1]*University of Zanjan*, *Zanjan, Iran*, [2]*Abhar Islamic Azad University*, *Zanjan, Abhar, Iran*.

Acidosis is a major constraint in consumption of cereal grains (CG) in early lactating Holstein dairy cows diet. The objective of this study was to determine effects of CG (corn + barley mix) levels in early lactating cows diet on dry matter intake (DMI), milk yield and contents, chewing activity, apparent dry matter digestibility and plasma metabolites concentration. Sixteen multiparous Holstein cow, body weight (BW), 605 ± 25.82 kg and body condition score (BCS), 3.09 ± 0.06, were used in a completely randomized design and assigned to 3 diets; 1) 31% CG and 38% nonfiber carbohydrate (NFC), 2) 25.5% CG and 35.5% NFC and 3) 20% CG and 33% NFC. Cows were individually fed the total mixed ration with similar net energy for lactation (1.7 Mcal/kg) and crude protein (19.2%) from 20 ± 2.2 d in milk during 6 week. Milk yield and content were determined 3 times per day. Daily DMI and weekly nutrient intake were determined. Blood was sampled into heparinized tubes from the coccygeal vein at the beginning and final day of the study and plasma metabolites were measured. Data were analyzed using MIXED Procedure from SAS and cows nested in the diets were as random effects. Different variance-covariance error structures were tested. No significant differences observed between the diets in DMI, BCS, BW and apparent dry matter digestibility. Cows fed the diet 3 had lower ($P < 0.01$) chewing activity than the others diets. Milk yield; 31.4, 36.2 and 39.4, milk fat percentage; 3.7, 3.09 and 3.46, for the diets 1, 2 and 3, respectively, and milk fat and lactose yield were significantly ($P < 0.05$) different between the diets. Plasma glucose concentration was lower ($P < 0.05$) in cows fed the diet 3 than the diets 1 and 2 (58.34 vs. 66.6 and 65.8 mg/dL). Plasma concentration of calcium, phosphorous, total protein, albumin and nonesterified fatty acids were not different. In summery, this study showed that cereal grains can be replaced with byproduct feeds high in digestible fiber in early lactating dairy cow diets without compromising lactation performance and metabolism.

Key Words: early lactation, cereal grain, Holstein cow

878 Effects of dietary chromium propionate on glucose metabolism and insulin sensitivity in growing cattle. J. W. Spears*[1], C. S. Whisnant[1], G. B. Huntington[1], K. E. Lloyd[1], K. Krafka[2], and A. Lamptey[2], [1]*North Carolina State University*, *Raleigh,* [2]*Kemin AgriFoods North America, Inc.*, *Des Moines, IA*.

Thirty-six Angus and Angus × Simmental heifers, averaging 291 kg, were used to determine the effects of dietary Cr (as Cr propionate) on glucose metabolism and serum insulin concentrations following glucose administration. Heifers were stratified by weight within a breed and randomly assigned to treatments. Treatments consisted of 0, 3, 6, or 9 mg supplemental Cr/d from Cr propionate. Based on DMI the daily doses of Cr were equivalent to 0.47, 0.94, and 1.42 mg supplemental Cr/kg DM. Heifers were individually fed a corn-silage based diet at a level of 2% of BW. Each heifer was also fed 0.45 kg of a ground corn supplement daily that served as a carrier for supplemental Cr. Glucose tolerance tests were performed on d 44 of the study. Glucose was infused via jugular catheters at a level of 0.45 g/kg $BW^{0.75}$ over a course of 1 to 2 min. Blood samples were collected at −10, 0, 5, 10, 15, 30, 45, 60, 90, 120, 150, and 180 min relative to glucose dosing for glucose and insulin determination. Area under the glucose response curve was lower (1603 vs. 1964 mg.dL/min; $P = 0.03$) in heifers supplemented with Cr from 0 to 45 min following glucose challenge. Serum insulin concentrations were lower ($P < 0.01$) in Cr-supplemented heifers than in controls following glucose infusion. The molar ratio of insulin to glucose was affected by treatment ($P = 0.02$), being higher in controls, and time ($P = 0.01$). Serum insulin and serum insulin to glucose ratios did not differ among heifers supplemented with 3, 6, or 9 mg Cr/d. Results indicate that Cr propionate supplementation increased tissue sensitivity to insulin in growing heifers. Based on insulin sensitivity, Cr requirements of growing heifers do not exceed 3 mg Cr/d or 0.47 mg Cr/kg DM.

Key Words: chromium, cattle, insulin

879 The effect of rumen-protected choline on milk yield and composition of Holstein dairy cows. M. Ardalan*, M. Dehghan-Banadaky, and K. Rezayazdi, *Department of Animal Science, University College of Agriculture and Natural Resources, University of Tehran*, *Karaj, Iran*.

Forty Holstein dairy cows in their first and second lactation were used in a lactation study from 4-week prepartum through 10-week postpartum to investigate the effect of feeding ruminally protected source of choline on productive performance of Holstein dairy cows. Cows (20 cows per treatment = 12 cows in 1st lactation and 8 cows in 2nd lactation) were housed in individual tie stalls. Animals were randomly assigned to receive one of the following treatments, using block randomization based on parity: 60 g/d of rumen-protected choline product (RPC) or without supplement (control). The repeated measurements of milk yield and composition were analyzed as a linear mixed model (Proc Mixed) with the best fitted covariance structure of SAS. The statistical model included the fixed effects of treatment, parity, time (week of lactation), treatment × time, and the random effect of cow within treatment and parity. The error covariance structure used for the repeated measures was the first-order heterogeneous autoregressive structure. The treatments significantly affected actual milk yield, 4% fat-corrected milk (FCM), and energy-corrected milk (ECM) across lactation weeks ($P < 0.05$). The actual milk yield, FCM, and ECM were greater for RPC-fed cows than control group ($P < 0.05$). The treatments had significant effect on protein percentage of milk and RPC-fed cows had greater percentage of milk protein than controls ($P < 0.05$). Treatments significantly affected lactose percentage of milk across lactation weeks and RPC-fed cows had greater amount than control cows ($P < 0.05$). The treatments did not significantly affect milk percentages of total solids (TS) and solids-not-fat (SNF). The supplementation of RPC resulted in an increase in milk urea nitrogen ($P < 0.05$). Results indicated that the supplementation of RPC can improve the lactation performance of dairy cows.

Key Words: rumen-protected choline, lactation performance, milk yield

880 Impact of biotin on production performance of lactating dairy cows: A meta-analysis. B. Chen* and J. X. Liu, *Institute of Dairy Science, Zhejiang University*, *Hangzhou 310029, P. R. China*.

A meta-analysis of the impact of biotin on production outcomes of dairy cattle was conducted following a search of the literature. Studies included in the data file met all the following criteria to improve the accuracy of the analysis: (1) publications were in English and Chinese; (2) the populations studied were lactating dairy cows; (3) the details on production outcomes were provided enough for analysis of biotin effect; and (4) addition level of biotin was at 0.96 mg/kg DM or 20 mg/d. Since the strict criteria of literature selection, only 11 studies were identified with 7 containing production data. Data for each trial were extracted and analyzed using meta-analysis software in Stata. Subsequently, meta-regression was used to investigate sources of heterogeneity of response, and Sub-group meta-analysis to get the conclusion. Estimated effect sizes of biotin were calculated on DMI, milk production, milk fat percent, and milk protein percent. Biotin had positive effect on the DMI, but the effect was influenced by DMI per body weight (BW). When the DMI was higher than 3.3% of BW, the biotin significantly improved DMI; however, the experiments with the DMI lower than 3.3% of BW was so few that they could not be used to draw a conclusion. Biotin had the effect on milk production, but the heterogeneity test I^2 was equal to 89.7%, indicating that this effect was not consistent. The meta-regression revealed that the effect of biotin on the milk production was significantly associated with the productive capacity of animals ($P = 0.013$). The sub-group analysis of dairy cattle with milk yield higher than 35kg/d indicated that biotin could improve milk performance of high-yielding animals, but the heterogeneity was also high ($I^2 = 78.3\%$). The effect size test of the dairy cattle with low yield ($P = 0.28$) did not exhibit the statistical significance. There is no effect of biotin on the milk fat percent ($P = 0.27$) and milk protein percent ($P = 0.80$).

Key Words: biotin, milk production, lactating dairy cow

881 Effects of acidified by-products and pre-partum DCAD on serum calcium, post-partum health and performance when fed to prepartum transition dairy cows. D. J. Rezac*[1], E. Block[2], D. Weber[2], M. J. Brouk[1], and B. J. Bradford[1], [1]*Kansas State University*, *Manhattan,* [2]*Arm & Hammer Animal Nutrition*, *Princeton, NJ*.

Two products designed to deliver supplemental anions were evaluated for their effects on total serum calcium, postpartum health events, DMI, and performance of transition dairy cows relative to a control diet that did not contain supplemental anions. Diets differed in dietary cation-anion difference (DCAD) and anion source. Treatments were diets including BIO-CHLOR (BC, DCAD +2.5 mEq/100g DM; n = 14), SoyChlor (SC, DCAD −0.2 mEq/100g DM; n = 15), and control (CON, +18.8 mEq/100g DM; n = 13). Treatments began 21 d before expected calving

and continued through parturition; upon calving, all animals received the same diet. Milk yield was measured through 21 d in milk and milk samples were collected daily between 5 and 21 d in milk. Data were analyzed using mixed models with repeated measures. Prepartum DMI was 9.0, 8.5, and 7.5 kg/d for CON, BC, and SC treatments, respectively. Prepartum intake tended to be lower for SC than CON ($P = 0.09$), but postpartum intake and milk yield were similar among treatments. Milk protein, lactose, and urea nitrogen concentrations were highest for SC and lowest for BC with CON being intermediate ($P < 0.05$). Postpartum plasma glucose tended to be greater for cows fed CON vs. the anion supplemented diets ($P = 0.08$; 67, 57, and 64 mg/dL for CON, BC and SC, respectively). Serum calcium concentrations did not differ between dietary treatments and only tended to be different ($P = 0.07$) over time; values were not indicative of hypocalcemia. With limited sample size, no significant effects of treatment were detected for incidence of postpartum health disorders or plasma BHBA concentration. Although DMI tended to be depressed in the prepartum period by SC, this intake depression was not accompanied by negative effects on performance or health in the postpartum period. Results suggest that cows were not adequately stressed to cause hypocalcemia and/or DCAD values near 0 were insufficient to improve postpartum health and performance.

Key Words: dietary cation-anion difference, peripartum, hypocalcemia

883 Effect of feeding potassium carbonate on milk fatty acids in early lactation cows. J. H. Harrison*[1], R. L. Kincaid[1], E. Block[3], and T. Jenkins[2], [1]*Washington State University*, *Puyallup,* [2]*Clemson University*, *Clemson, SC,* [3]*Arm & Hammer Animal Nutrition*, *Princeton, NJ*.

Thirty Holstein cows (15 per treatment) were used in a continuous design lactation study to evaluate the effectiveness of potassium carbonate as a cation source to increase dietary DCAD from ~25 to 42 units, mEq/100g. The study was conducted from mid August to mid December 2007. Cows were fed individually via Calan feeding gates one of 2 treatment diets formulated to be equal in all nutrients except potassium. The formulated potassium level of the control diet was 1.2% of DM and increased to 2.0% of DM using potassium carbonate (DCAD Plus, Church & Dwight, Princeton, NJ) for the DCAD + treatment. Diets consisted of (% DM): alfalfa hay (13.4), corn silage (12.1), blue grass straw (8.6), corn distillers grains with solubles (10.3), whole cottonseed (6.2), and concentrate (49.4). Cows were assigned at random to one of the 2 dietary treatments at ~15 DIM and continued through ~105 DIM. Milk samples from 8 cows per treatment during wk 2, 5, and 9 of lactation were analyzed for individual fatty acids. Milk composition data were analyzed as a mixed model with the fixed effects of treatment, week, and their interactions, and the random effect of cows within treatment, using an AR(1) correlation structure for the errors.. Milk fat % and yield were significantly different ($P < 0.01$) between treatments (4.31% and 1.75 kg/d for DCAD+ and 3.96% and 1.55 kg/d for control). The added dietary potassium carbonate decreased unsaturated and trans fatty acids, and increased C18:0 in milk. The following milk fatty acids were significantly lower (% of total fat) in milk of cows receiving potassium carbonate: C16:1, t6, t8 C18:1, t10 C18:1, c9, t11 CLA. The concentration of C18:0 in milk fat was significantly greater at 14.2% for DCAD+ fed cows compared with 12.6% for control cows. The results indicate that added dietary potassium carbonate affects milk fat % and milk fatty acid profile in early lactation cows, and suggests a role of potassium at the rumen level in the process of bio-hydrogenation.

Key Words: milk fatty acids, milk fat, potassium carbonate

884 Effects of rumen-protected choline on performance and hepatic fat metabolism in periparturient dairy cattle. R. Zom[1], J. van Baal[1], M. J. de Veth[2], R. M. A. Goselink[1], H. C. A. Widjaja-Greefkes[1], J. A. Bakker[1], and A. M. van Vuuren*[1], [1]*Wageningen UR Livestock Research*, *Lelystad, the Netherlands*, [2]*Balchem Corporation*, *New Hampton, NY*.

The effects of rumen-protected choline (RPC) on feed intake, milk yield, milk composition and hepatic fat metabolism were evaluated in periparturient dairy cows. Multiparous cows (38) were blocked in pairs. Cows within each block were assigned at random to either RPC (60 g RPC/day; Reashure, Balchem Corp.) or control group (no RPC). Treatments were applied from 3 weeks antepartum until 6 weeks postpartum. Cows received ad libitum forage mixtures of corn silage, grass silage and straw (ante- and postpartum ration containing 12% and 15% CP and 5.5 and 6.5 MJ/kg DM NEL, respectively). Concentrates fed through concentrate feeders, were gradually increased from 0.6 kg/day (3 weeks antepartum) up to 2 kg at calving and up to 9.6 kg at 18 d postpartum. Feed intake and milk yield were recorded daily, and milk composition (fat, protein) was determined weekly. Liver biopsies were taken from 8 pairs of cows at 3 weeks ante- and 1, 3 and 6 week postpartum to measure hepatic TAG and mRNA expression levels of relevant genes by quantitative PCR, using β-Actin as housekeeping gene. Gene expression (relative to antepartum level) and TAG were tested by ANOVA; all other treatment effects were tested by mixed model analysis using the REML procedure. Feed intake and milk protein yield were significantly higher at the start of lactation for cows receiving RPC (P=0.03). No significant effect on milk production (average 40.8 kg/d) or milk composition (average 45 g fat and 33 g protein per kg milk) in the first 6 weeks of lactation were observed. RPC reduced hepatic TAG concentrations in week 1 (P=0.04) and week 3 (P=0.12) postpartum. RPC supplementation upregulated mRNA levels of transcription factor PPARδ (mediator of lipogenic genes) and counteracted the downregulation of organic cation/carnitine transporter SLC22A5/OCTN2 expression in liver. In addition, RPC decreased the expression of carnitine palmitoyltransferase 1A (involved in mitochondrial fatty acid uptake). These data suggest that the reduction in hepatic TAG concentrations when supplementing RPC coincides with an altered hepatic fatty acid metabolism.

Key Words: dairy cattle, choline, fatty liver

885 Dietary cation-anion difference for lactating dairy ewes. A. Schlageter, G. Caja*, M. Ben Khedim, A. A. K. Salama, S. Carné, and E. Albanell, *Universitat Autònoma de Barcelona*, *Bellaterra, Barcelona, Spain*.

A total of 40 ewes of 2 dairy breeds (Manchega, n = 20, Lacaune, n = 20) at mid lactation (84 ± 27 DIM) were used to determine the effects of diets differing in dietary cation-anion difference (DCAD) on their lactational and acid-base performances. DCAD (mEq/100 g DM) values were calculated as $(Na^+ + K^+) - (Cl^- + S^{2-})$. Ewes were allocated to 8 groups of 5 animals and blocked by breed, BW and milk yield (Manchega, 71.0 ± 7.7 kg BW and 0.59 ± 0.15 L/d; Lacaune, 69.2 ± 8.0 kg BW and 0.97 ± 0.17 L/d). Dietary treatments were applied for 10 wk and consisted of total mixed rations in which the DCAD value was modified from anionic to cationic values being: 7, 26, 45 or 64 mEq/100 g DM. Individual dry matter intake (DMI) was measured at wk 5 and 10 using polyethylene glycol (PEG 6000) as indigestible external marker. Milk yield and milk composition were recorded weekly and biweekly, respectively. Jugular blood samples for acid-base balance were taken and analyzed at wk 4, 8 and 10. The DMI and DMI/kg $BW^{0.75}$ showed linear ($P < 0.005$) and quadratic ($R^2 = 0.96$ to 0.99, $P < 0.01$) responses by effect of DCAD. Maximum intake was calculated between 40 and

45 mEq/100 g DM. Milk yield showed a positive linear response (R^2 = 0.78 to 0.80, $P < 0.05$) to DCAD but ECM did not vary. There were no significant effects of treatment in milk composition. Moreover, we observed differences in acid-base blood indicators according to diet and breed. Manchega ewes showed a neutral stage, while Lacaune ewes passed from metabolic acidosis (anionic treatments) to a neutral stage (cationic treatments). Urine pH showed a linear response ($P < 0.001$) by effect of DCAD and was a representative indicator of the DCAD values in the ration. Blood Cl^- and K^+ showed linear ($P < 0.001$) and quadratic ($P < 0.05$) responses by effect of DCAD in Lacaune ewes, increasing both ions in the anionic treatments. According to the obtained results, diets containing DCAD values in the range of 40 to 50 mEq/100 g DM are recommended for lactating dairy ewes. High yielding dairy ewes were more sensitive to DCAD than low yielding ewes as result of their greater feed intake.

Key Words: cation-anion balance, dairy ewes, nutrition

886 Effects of feeding organic minerals (Availa-4 and 4-Plex) on milk production and reproductive performance in lactating dairy cows: A meta-analysis. A. R. Rabiee[1], I. J. Lean*[1], M. A. Stevenon[2], and M. T. Socha[3], [1]*SBSibus*, *Camden, NSW, Australia*, [2]*EpiCentre, Massey University*, *Palmerston North, New Zealand*, [3]*Zinpro Performance Minerals*, *Eden Prairie, MN*.

We evaluated the effectiveness of supplementation with the organic minerals (OMs) Availa-4 and 4-Plex (Zinpro Corporation) on milk production and milk components, and reproductive performance in lactating dairy cows using effect size meta-analytical methods that weight responses by size of study and precision of response. Twenty papers and reports on the effects of OMs were considered. In some, but not all studies, equal amounts of inorganic minerals were fed to controls. Criteria for inclusion in the study were data on the form of OMs, number of cattle, an adequate description of randomization, production and reproduction, and associated measures of variance (SE or SD), and/or P values. The OMs significantly increased milk production by 0.93 kg (95% CI = 0.61 to 1.25, $P < 0.001$), milk fat by 0.04 kg (95% CI = 0.02 to 0.05, $P < 0.001$) and milk protein by 0.03 kg (95% CI = 0.02 to 0.04, $P < 0.001$) per day. There was a small, non-significant reduction in milk SCC in cows supplemented with OMs. All production outcomes, except milksolids (yield) and milk SCC, were heterogeneous. Meta-regression analysis showed that feeding before calving, feeding for a full lactation after calving and the use of other supplements (yeast, monensin, rBST) increased the responses over feeding after calving only, feeding for part of lactation or not using other supplements, respectively. Supplementation of cows with OMs significantly reduced days open (WMD = 13.5 d; $P = 0.006$) and number of services per conception (WMD = 0.27; $P = 0.02$) in lactating dairy cows. The risk of pregnancy on d 150 of lactation was greater in cows fed OMs (RR = 1.07, $P = 0.07$), but OMs had no significant effect on the interval from calving to first service and 21 d pregnancy rate. There was no evidence of heterogeneity for each of the reproductive outcomes evaluated.

Key Words: meta-analysis, dairy cows, organic minerals

Sexed Semen Symposium: Applying Sexed Semen in Cattle

887 Current status of sexed semen technology. G. Seidel*, *Colorado State University*, *Fort Collins*.

For practical purposes, sexed semen first became commercially available in North America in 2006, using the Beltsville method of flow cytometry/cell sorting. No other method has proven effective for sexing semen. Several million doses of sexed semen have been produced to date at the industry standard of ~90% purity. Purity can be adjusted to exceed 95%, but sort rates decrease greatly at >90% purity, and thus achieving such purity becomes very expensive. Sort rates increase at 75–80% purity compared with 90% and decrease costs accordingly. Sort rates at 90% purity can exceed 5,000 live sperm/sec of each sex per sorter nozzle. When considering processing losses and other logistical issues, about 7–8 insemination doses of 2,000,000 sperm of each sex can be produced per sorter nozzle/h under ideal conditions. This sperm dose became the industry standard as the optimal compromise between cost and fertility. Doubling the number of sexed sperm/insemination dose only increases pregnancy rates 2–4% for most bulls. Under good management, proper semen handling, etc., for most bulls in properly controlled experiments, pregnancy rates with sexed semen at 2,000,000 sperm/dose generally fall between 70 and 90% of those of unsexed semen at conventional doses of ≥10,000,000 sperm. Numbers of good embryos recovered when superovulated donors are inseminated with sexed semen of most bulls are approximately half of numbers recovered after using conventional semen AI. ET pregnancy rates per embryo produced with sexed semen are normal. Calves produced via AI of sexed semen do not differ ($P > 0.1$) in any respect from those produced via conventional semen, although there is less dystocia with female than male calves. Procedures for sexing bovine sperm have improved in several small but important ways over the past decade. Further improvements in efficiency resulting in decreased costs are likely. The biggest challenge will be to improve fertility of sexed semen.

Key Words: sexed semen, bovine, fertility

888 The evolution of sex-sorted semen in the US dairy industry. J. M. DeJarnette*, *Select Sires, Inc.*, *Plain City, OH*.

The introduction of sex-sorted semen in the US was accompanied by a deliberate effort not to oversell expectations. Results of early adopters typically met or exceeded expectations and spurred increased demand. High sperm loss limited the genetic caliber of sires offered, however high milk and heifers prices minimized concern for this limited supply product. As market acceptance and sorting experience grew, the genetic quality of sires offered also increased. Notable improvements in sorting efficiency has further facilitated the ability to offer higher levels of sire genetics but remains a limitation to use of the most elite sires. Market dynamics abruptly changed in 2009 when rapidly growing production capacity was met with a ~50% reduction in milk prices. Demand for sexed-semen immediately responded in kind. As the market begins to recover, producer philosophies for application of sexed semen appear to have experienced a more permanent evolution. Greater consideration is now given to semen price and to the genetic potential of both male and female. The economic value, real or perceived, of female calves from genetically superior lactating cows has stimulated greater interest in this application. Use of conventional beef semen in lower genetic value dairy cows has gained in popularity but use of sexed beef semen is unlikely until conception rate issues are resolved. Numerous research efforts have attempted to improve the conception rates of sex sorted semen with only modest evidence of success and little evidence that equality to conventional semen is achievable. Appropriate selection of sires submitted for sorting remains the most reliable method of influencing the fertility potential of sex sorted semen, which in most non-biased trials remains at 70 to 80% of conventional. Reduced purity products increase sorting efficiency and allow for more economical pricing of sexed semen, but with no improvement in conception rates, the economic implications of fewer females must be closely scrutinized. Sex sorting technology appears to have achieved a permanent place in the dairy industry, though efficiencies and applications are likely to continue to evolve.

Key Words: sexed semen, flow cytometry, economics

889 Implications of sex-sorted dairy semen for genetic change. B. G. Cassell*, *Virginia Polytechnic Institute and State University, Blacksburg*.

Sex-sorted semen can increase selection intensity of dams of replacements, but many dairy herds have no genetic evaluations for female selection. Genomic predictions from low density SNP chips may overcome this limitation in the future. Dairy herds that routinely use recently proven bulls in AI sampling programs increase genetic merit of service sires by about $25 Net Merit $;per year through genetic trend. Younger animals in such herds are genetically superior to older animals, and increased use of young animals as dams of replacements would improve genetic progress in the absence of genetic evaluations. First parity dams produce about 33% of calves born in typical herds, while second and third or later parity dams produce about 26% and 41% of calves born. With 26, 40, and 67 mo of age at calving and slightly higher frequencies of single female births to first parity dams through fewer twins, average age of dam of single birth heifers is about 45.7 mo with conventional semen. Use of sexed semen for first service only in heifers reduces average age of dam to 44 mo, while single heifer births/100 deliveries increases from 47.1 to 52.2. Genetic merit of dams increases a negligible $4 in Net Merit $ over conventional semen. If all heifer matings use sexed semen, age of dam drops to 41.9 mo, but genetic merit only increases by $8. Significantly more heifer calves result, as single heifer birth rates increase to 60.2/100 deliveries. Herds could eliminate 70% of third and greater parity cows as dams of replacements while maintaining heifer birth rates equal to conventional semen use. A variety of uses of these cows could diversify and improve dairy farm income. Elimination of older cows as dams of replacements reduces age of dam of replacements to 34.9 mo and increases genetic merit of dams by about $23. This change more than doubles genetic change per year in the dam-daughter path compared with conventional semen, primarily because of shorter generation intervals. However, improvement in this path could be offset by relative small reductions in genetic merit of service sires.

Key Words: sex-sorted, genetic change

890 Economic aspects of the use of sexed semen in dairy heifers and cows considering herd constraints. A. De Vries*, *University of Florida*, *Gainesville*.

Selective use of sexed semen in heifers and cows may increase genetic progress from the daughter-dam path and allows all calves from low producing cows to be sold because they are not needed to replace culled cows. Economic aspects of the insemination mix in dairy heifers and cows was evaluated with a linear programming model. The model considered 3 semen types (sexed dairy, conventional dairy, conventional

beef), 5 levels of milk production, and 10 parities including heifers. Each parity had 20 voluntary culling opportunities for non-pregnant animals. Heifers were allowed 5 insemination opportunities and cows 10. The model contained 2,425 decision variables. Genetic value of heifer calves was a function of service sire net merit, age of the dam, and level of milk yield of the dam. Heifers were assumed to be genetically equal. Inputs were lactation curves, milk price, feed costs, insemination costs, service rates, conception rates, dystocia costs, involuntary culling risks, and other costs. All bull calves and crossbred calves were sold, as well as excess heifer calves. The optimal decisions resulted in $335 profit/cow per yr when only conventional semen was allowed without a constraint on the number of heifer calves. Additional choice of sexed semen increased profit/cow per yr to $339 with sexed semen being used in the first inseminations in heifers and higher producing first parity cows. Profit/cow per yr increased to $368 when beef semen was offered as a third choice but fewer dairy heifer calves were born than were needed to replace culled cows. Setting the number of born heifer calves equal to the number needed to replace culled cows, profit/cow per yr was $321 considering only conventional dairy semen. Sexed semen was not used when offered. When beef semen was also offered, profit/cow per yr increased to $353 with beef semen used in lower producing cows and conventional semen and some sexed semen in higher producing cows and heifers. The optimal insemination mix often included sexed semen but depended greatly on the relative value of dairy bull calves, dairy heifer calves and crossbred calves.

Key Words: sexed semen, economics

891 Use of n-alkanes to estimate intake and digestibility of vegetative crops by young sheep. H. Dove* and W. M. Kelman, *CSIRO Plant Industry*, *Canberra, ACT, Australia*.

The development of longer-season wheat cultivars in Australia has allowed increasing use of wheat as a grazing resource in winter, replacing either pasture or forage oats. There are few data for diet composition, intake or forage digestibility in young sheep grazing wheat forage, especially in comparison with oats or pasture. Over 2 years, we used the n-alkane method to estimate diet composition (year 2), OM intake, fecal output and diet digestibility in 30 kg Merino sheep. In July of year 1, sheep grazed wheat, oats or a phalaris-based pasture for 22d at 33 animals/ha. In year 2, they grazed wheat for 34d at 33 animals/ha, within a larger fertilizer-response study. In each year, data were analyzed as replicated randomized blocks using plot mean data. There were no fertilizer effects on intake variables in year 2, so overall means are reported. In year 1, OM intakes did not differ significantly between sheep grazing oats (1162 g/d), wheat (1403 g/d) or pasture (1510 g/d). However, fecal OM excretion was significantly greater ($P = 0.01$) in animals grazing pasture (362.1 g OM/d) than crop (mean 146.2 g OM/d). OM digestibility of the pasture was thus significantly less (0.758; $P < 0.05$) than for either oats (0.861) or wheat (0.901), which did not differ. Digestible OM intakes (mean 1140 g OM/d), liveweight gains (mean 254 g/d) and liveweight gains/kg OM intake (mean 189 g/kg OMI) did not differ between treatments. Crop growth in year 2 was reduced by drought and by the end of the grazing period, crop biomass was < 400 kg DM/ha and constrained intake. The crop also contained more weeds. Nevertheless, alkane-based estimates of diet composition showed that 89% of forage intake was from wheat. Herbage intake (862 g OM/d), whole-diet digestibility (0.762) and liveweight gain (162 g/d) were all less than in year 1. Liveweight gains/kg of OM intake were very similar (190 g/kg OMI) to year 1, suggesting that reduced liveweight gains were due to lower intakes. The results also indicate that in year 1, the digestibility of crop forage was greater than pasture, but OM and DOM intakes by young sheep were similar across forages.

Key Words: alkanes, intake, wheat forage

892 Effect of level of intake on digestibility of NDF of soybean hull diets in sheep. D. C. Hein, M. L. Thonney*, D. A. Ross, and D. E. Hogue, *Cornell University*, *Ithaca, NY*.

Including soybean hulls in ruminant diets increases feed intake and production. This is likely due to the high fraction of digestible NDF (dNDF) in soybean hulls, which may optimize VFA production for rumen health. High feed intakes, however, decrease digestibility. Therefore, the objective of this project was to quantify the effect of level of feed intake on digestibility of NDF in soybean hull diets. Diets were fed at intake levels of 2, 3, or 4% of BW (%BW). Each intake level was fed to 8 pens of 2 weaned, 17-kg ram lambs (24 pens) and to 8 pens of 1 mature, 66-kg, non-lactating ewe (24 pens). On an as-fed basis, the lamb diet included 71.7% soybean hulls, 21.5% soybean meal, 4.5% molasses, 1% vitamin-mineral premix, 0.5% calcium carbonate, 0.5% chromic oxide, 0.25% vitamin E premix, and 0.025% Deccox, while the ewe diet contained 72% soybean hulls, 20% corn, 2% soybean meal, 4.5% molasses, 1% mineral-vitamin premix, and 0.5% chromic oxide. After a 10-d adaptation period, feces were collected for 2 d. Uneaten feed was recorded to determine actual feed intake. The fecal samples and 2 feed samples from each experiment were dried and ground for determination of NDF, dry matter, and chromic oxide concentrations. Apparent dry matter digestibility (DMD) and dNDF were quantified using chromic oxide as a marker. In ram lambs, with actual intakes ranging from 1.7 to 4.1%BW, regression analyses showed a linear effect with apparent DMD decreasing ($P < 0.001$) by 8.1 ± 1.16 percentage units and dNDF decreasing ($P < 0.001$) by 12.1 ± 1.57 percentage units for each percentage unit increase in DMI as %BW. In mature ewes, with actual intakes ranging from 1.6 to 3.9%BW, digestibility values at low intakes were not as high as in lambs and the depression in digestibility was less pronounced, with DMD decreasing ($P = 0.034$) by 2.9 ± 1.28 percentage units and dNDF decreasing ($P = 0.009$) by 4.5 ± 2.00 percentage units for each percentage unit increase in DMI as %BW. These experiments demonstrated a linear decrease in digestibility of NDF with increasing intake that accounted for 75 to 85% of the associated depression in apparent DM digestibility.

Key Words: digestion, NDF, sheep

893 Evaluation of feeding value of corn distillers dried grains with solubles for sheep. G. Abdelrahim*[1], J. Khatiwada[1], N. Gurung[1], J. Vizcarra[1], and C. Kerth[1], [1]*Alabama A & M University*, *Normal, AL,* [2]*Tuskegee University*, *Tuskegee, AL*, [3]*Auburn University*, *Auburn, AL*.

Corn distillers dried grains with solubles (DDGS) which have become very popular over the past 15 yr due to their energy value in relation to corn, price, flexibility in feeding, and reduction in incidence and duration in acidosis, are a by-product of the fuel ethanol industry. The objectives of this study were to evaluate the effects of varying levels of dietary DDGS inclusion on: dry matter intake, average daily gains, and carcass composition of sheep. Twenty-four lambs (40.1 ± 48.6 kg initial BW, and 8 to 9 mo of age) were obtained and used in a randomized complete-block design (n = 2 replications per treatment). Diets, on a dry matter basis, were: control, 10% DDGS, and 20% DDGS. All diets contained 50% fescue/bermudagrass mix hay, and 50% of the respective concentrate mixes. The concentrate mixes containing DDGS were formulated to be isonitrogenous at 16% crude protein. The DDGS replaced corn and soybean meal in the concentrate mixes so that diets contained desired amounts of DDGS. Lambs were allowed 7-d adjustment period, followed by 7-d transition period to the DDGS diets. After 135-d feeding period final weight was determined, lambs were slaughtered, and carcass characteristics were measured. Both growth and carcass quality data were analyzed as a completely randomized design. Final body wt (62.5, 61.3, and 63.0) was not different between treatments ($P > 0.05$). Also, no differences were observed ($P > 0.05$) in hot carcass wt (30.7, 30.1, and 30.3), cold carcass wt (30.8, 30.0, and 30.2), body wall fat (2.0, 2.2, and 2.0), ribeye area (6.55, 7.0, 7.0), 12th rib fat (0.9, 1.1, and 0.85), and kidney and pelvic fat (2.3, 1.89, 2.13) between treatments. Based upon the findings of this research, DDGS can replace a portion of the ground corn and soybean meal commonly fed to lambs, and maintains or enhances performance.

Key Words: distillers dried grains with solubles, sheep, performance

894 The effect of processing type of feedstuff on the fattening performance of Awassi ram lambs. H. Ustuner*, S. Dikmen, and I. I. Turkmen, *University of Uludag*, *Bursa, Turkey*.

The objective of this study was to investigate the effect of processing type of feed on the fattening performance of Awassi ram lambs. A total of 26, 3-mo-old Awassi ram lambs were used and randomly allocated into 3 groups (group 1, fed with mash feed, n = 8; group 2, fed with

pellet feed, n = 9; group 3, fed with extruded pellet feed, n = 9). Lambs were individually fed with the same ingredient of concentrate feed (2.5 Mcal/kg) and had free access to water until 43 kg of slaughter weight. The initial live weight of lambs were similar ($P > 0.05$) 29.56 ± 1.27, 29.89 ± 1.07 and 28.89 ± 0.83 for group 1, 2 and 3, respectively ($P > 0.05$). At the end of fattening period the final live weights of lambs were also similar ($P > 0.05$). The results showed that total weight gain and average daily gain (ADG) of ram lambs during the study were 12.75 ± 1.05 kg and 180.90 ± 17.70 g for group 1, 12.78 ± 0.90 kg and 25.10 ± 21.50g for group 2, and 14.56 ± 0.55 kg and 287.80 ± 23.40 g for group 3, respectively. The difference of ADG among groups were significant ($P < 0.01$). The best feed conversion rate (FCR) was estimated for the lambs in group 3 (6.50 ± 0.30) while the other FCR results were greater than group 3 (8.20 ± 0.50 and 6.90 ± 0.40 for group 1 and group 2, respectively) ($P < 0.05$). Lambs fed with extruded pellet feed (group 3) tend to have lower fattening period (19 d less) than group 1 ($P = 0.07$). The results of the current study shows that feeding of Awassi ram lambs with extruded feed had positive effects on fattening performance, feed conversion rate and fattening period, which are economically important for sheep farms.

Key Words: Awassi lambs, extruded feed, fattening performance

895 Effect of anaerobic enzyme matrix on fiber digestibility. H. M. Gado*[1] and B. E. Borhami[2], [1]*Ain Shams University*, *Department of Animal Production, Faculty of Agriculture, Cairo, Egypt*, [2]*Alexandria University*, *Department of Animal Production, Faculty of Agriculture (El-Shatby), Alexandria, Egypt*.

The intend of this study was to verify the effect of nutritive value aerobic constancy of rice straw. Also, if it could be enhanced by addition of exogenous cellulases, hemicellulase, protease and α amylase enzymes (ZAD) preparations at ensiling. Rice straw was chopped to 5 cm without treatment (control) or after treatment with ZAD (1 or 3 L/ 1 ton of DM of rice straw) including 30 kg of sugar cane molasses and 20 kg of DDGS. The enzymes were sprayed on the rice straw at ensiling (50% of water was added). Ten 500-kg replicates of chopped (5 cm) rice straw were ensiled for 30 d in plastic bales. Five plastic bales per treatment were used for chemical analysis and 5 for aerobic constancy monitoring. The silage juice was analyzed for organic acids, pH, water-soluble carbohydrates (WSC), ammonia-N, and soluble N. Samples were analyzed for crude protein (CP), neutral detergent fiber (NDF), and acid detergent fiber (ADF). In vitro digestibility of DM (IVDMD), NDF (IVNDFD), and ADF (IVADFD) were determined. Materials treated with ZAD had lower ($P < 0.05$) DM losses, and lower ($P < 0.05$) pH and ammonia-N concentration than control silages. Residual WSC concentration was greater ($P < 0.01$) in ZAD treated silages either 1 or 3 L than in control silages. Compared with control silages, NDF concentration was lower ($P < 0.01$) in silages treated with 3 L followed 1 L of ZAD. Aerobic constancy was increased ($P < 0.05$) by ZAD. ZAD at 3L increased the IVDMD and IVNDFD at 6 and 48 h. The 48-h IVADFD was also increased ($P < 0.01$) by treatment with 3L ZAD. These results show that 3L ZAD applied at ensiling can improve the digestibility, fermentation, and aerobic constancy of rice straw silage.

Key Words: nutritive value, rice straw, ZAD

Teaching/Undergraduate and Graduate Education Symposium: Beyond PowerPoint: Use of Technology in the Classroom

896 AG*IDEA: A national consortium of universities for offering distance education program in agriculture. K. L. Esbenshade*[1] and D. L. Boggs[2], [1]*North Carolina State University*, *Raleigh*, [2]*Kansas State University*, *Manhattan*.

AG*IDEA (Agriculture Interactive Distance Education Alliance) is a national consortium of universities offering programs and courses in agriculture and related disciplines. Chartered in 2008, AG*IDEA consists of 15 member universities, with 15 additional universities intending to join. AG*IDEA is an affiliate of Great Plains IDEA operating under their policies and guiding principles, and has a Board of Directors, an Executive Committee, and annual meetings. Institutional membership requires approval of the administrative head for agriculture, and the institution's chief academic and fiscal officers. Programs (such as degrees, certificates, concentrations, etc.) are developed by faculty and approved by the Executive Committee, and include proposed coursework, a budget and an assessment plan. Courses and programs are approved at each university, where students enroll, pay a common price which includes tuition and fees, and obtain their degrees. Programs in Agricultural Education, Agricultural Mechanization, Food Safety and Defense, Grasslands Management and Swine Science have been approved to be offered through AG*IDEA. Other programs in various agricultural disciplines are under development. Information regarding the national consortium can be obtained at www.agidea.org.

Key Words: distance education, AG*IDEA, academic programs

897 Using cell phones to engage your audience. P. A. Curtis* and M. O. Kloepper, *Auburn University*, *Auburn, AL*.

Get your audience involved without the expense of proprietary response systems. Two applications that can be used in your class or for your presentation will be showcased. Attendees are encouraged to bring a cell phone to use during this presentation. Learn how to make this conference more engaging and informative for yourself and others.

898 Use of e-portfolios for outcomes assessment in the animal sciences. C. M. Wood*, J. W. Knight, and E. A. Dunnington, *Virginia Tech*, *Blacksburg*.

The Department of Animal and Poultry Sciences (APSC) at Virginia Tech (VT) has been conducting outcomes assessment since 1991. Currently, each degree program must develop a mission statement that relates directly to student learning outcomes; specific learning outcomes that may be revised based upon information collected; direct and indirect measures of the learning outcomes; and findings for measures assessed. Examples of student work are an excellent source of direct measures of learning outcomes but the collection, storage and analysis of such work can be daunting. E-portfolios, an electronic version of traditional collections of student work, are one method of addressing these concerns. E-portfolios, which can be maintained indefinitely, are 2-dimensional matrices into which electronic files are loaded. They are an integral part of Scholar, VT's implementation of Sakai, an open-source educational software package. The APSC assessment e-portfolio consists of 7 columns that correspond to the undergraduate program's specific learning outcomes (communication skills, leadership skills, critical thinking and reasoning, independent learning, subject matter expertise, and knowledge of contemporary issues) plus capstone activities, and 15 rows representing courses and other sources of electronic evidence such as extracurricular accomplishments. Collection of student work began fall semester 2009. A total of 262 students enrolled in 2 courses submitted 3 pieces of evidence: a 4-year plan of study, a resume and a cover letter. Initial feedback from instructors and students indicate that placing files into the e-portfolio is straightforward. Development of procedures for optimizing use of the e-portfolio in outcomes assessment is in progress. We believe that e-portfolios are an excellent model for documenting student learning based on faculty-defined outcomes and for assessing student development over time. Additionally, students have the opportunity to construct their own e-portfolios using the evidence they placed into the APSC matrix.

Key Words: outcomes assessment, student learning, e-portfolios

899 Use of SoftChalk to create professional appearing content that will creatively engage students. M. O. Kloepper*[3,4], P. A. Curtis[3], and D. R. Mulvaney[1,2], [1]*Coll. of Agr., Auburn University*, *Auburn, AL,* [2]*Anim. Sci.*, *Auburn, AL,* [3]*Poult. Sci.*, *Auburn, AL,* [4]*IT Specialist*, *Auburn, AL*.

Creating content for e-learning can be cumbersome, time consuming and challenging for faculty. In addition, less than meritorious results may be obtained after considerable amount of time and effort. Our objective is to discuss the merits and experiences of using SoftChalk as a powerful tool to create and advance web-based learning environments. SoftChalk is a simple and easy to use tool that shows provides easy to use steps for organizing classroom and module content. Output can be customized to look both interesting and professional in a matter of minutes. Educational content can be placed online and accessed by student or other viewers. Packaging educational materials with SoftChalk puts fun and enjoyment into digitizing course content, scientific research results, and expert information. The presenters will show various examples of content created with SoftChalk and enable participants' valuable insight into relevant applications for enhancement of teaching and learning.
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Key Words: Soft Chalk software, e-learning, web-based teaching

900 Using Second Life for poultry science. M. O. Kloepper* and P. A. Curtis, *Auburn University*, *Auburn, AL*.

A 3-dimensional poultry space has been created digitally and includes a farm, egg processing facility, processing line, and more. This teaching resource has been created by using a virtual world platform, Second Life. Usage of 3-D applications for educational purposes is on the rise but many educators are unaware of the potential for utilizing this format. On-site tours of poultry facilities are difficult, if not impossible, to obtain. Virtualization provides an inside look of plant operations safely and comfortably. It provides a method for close inspection of angles not allowed or possible in a real world facility. Imagine *seeing* a piece of equipment in action, from all sides, zooming in and out, as well as up and down, from any perspective that you want by moving your computer mouse. 3-D digital world components are imagined. Consider it an "explosion of creativity". This presentation will showcase the virtual space called Eagle Island in Second Life, highlight its history, animations and 3-D teaching resources, discuss collaborative efforts using the virtual space, and share plans for future endeavors.

901 On-line text, a new technology use in animal science courses. G. M. Hill* and J. E. Link, *Michigan State University*, *East Lansing*.

Meeting the demands of freshmen courses in animal science has resulted in innovation and utilization of new technologies. With the ever changing type of student that enrolls in beginning courses, faculty members are challenged to provide up-to-date materials, a broader look at animal agriculture, and the latest technologies. Faced with the reality that introductory animal science books are limited in number, incomplete for the species to study and not up-to-date, we pursued the opportunity to write our own book that matched our lecture and laboratory lessons and could be improved even within the semester of use. Our on-line publisher is Great River Technologies of Dubuque, Iowa. We began by taking photographs in all our laboratories, creating illustrations to demonstrate difficult concepts, developing ideas for interactive exercises, writing questions for self-study and outlining and writing the text. Photographs needed to be of high quality and resolution for their utilization, and we were required to obtain permission from students in the photos to be used in the text. These photos were not used as a substitute for laboratory periods, but to support the laboratory sessions and provide study materials. The publisher provided a portion of the finished artwork and contacted publishing houses for permission to use illustrations and artwork of others. The publisher contacted bookstores on our campus and arranged for students to purchase an access code from the store or directly from the publisher via credit card. The price was the same for students regardless of purchase location and overall, less than the cost of a textbook. Limitations for such a project include making materials simple enough for the naïve student yet challenging for those with a livestock background, working with artists who have no concept of animal agriculture, allotting time for preparation, and finding areas that are not as completely covered as anticipated.

Key Words: undergraduate education, on-line text

902 Asynchronous distance education in feed science. C. R. Stark and P. R. Ferket*, *North Carolina State University*, *Raleigh*.

The growing demand for courses in the field of animal feed manufacturing, combined with diminishing classroom space initiated the development of a distance education (DE) curriculum in the Feed Science program at North Carolina State University (NCSU). Feed industry businesses are looking for cost effective methods to train middle management and production employees while limiting their time away from the workplace (AFIA, 2007). Feed Manufacturing Technology (FM 425), the first DE course offered in Feed Science at NCSU, has been offered since 2005 over 15 semesters to 201 students, both on- and off-campus. The total enrollment in FM 425 has more than doubled (40 versus 17 students) in the last 5 years (2005 to 2010) as compared with the previous 5 years (2000 to 2004). In addition to the increased enrollment, 34% of the students who enrolled in the DE courses were on-campus. The asynchronous instructional format allowed students the flexibility to view on-line lectures, watch videos, complete assignments, and take exams at their own pace. Students indicated they enrolled in DE courses because the courses were not constrained to a scheduled place or time. The addition of the Feed Mill Operations and Leadership (FM 460) course in the fall of 2008 increased the DE enrollment in the Feed Science curriculum by 28%. The success of these courses has led to the development of 7 new DE courses in the Feed Science curriculum, which can be applied toward an undergraduate or graduate certificate in Feed Science (www.feedmill.ncsu.edu). The Feed Science DE program has a consistent course format within all courses regardless of the instructor. Each learning module contained an introduction, video lecture, lecture notes, assignment, and self test. There was no difference in student evaluation responses between students who took the DE courses versus all the other on-campus courses. The success of these courses confirm that DE can be used to expand and develop specialized programs such as Feed Science, while providing extension and outreach opportunities to the feed industry.

Key Words: asynchronous, distance education, feed science

Animal Behavior and Well-Being: Dairy, Sheep, and Beef

903 Behavioral changes of dairy cows during drying-off using abrupt cessation of milking. K. A. Painter, K. E. Leslie*, and E. H. Tatone, *University of Guelph*, *Guelph, ON, Canada*.

The dry period between successive lactations is crucial for regeneration of productive function of mammary tissue, preparation for high production, and to prevent new intramammary infections (IMI). With continually increasing production levels over time, the stress of abrupt drying-off could be a welfare concern, as well as an increased risk period for new IMI. The objectives of this study were to document standing and lying behaviors through the process of drying-off, and to evaluate the associations between parity (lactation 1 relative to lactation 2 and above) and production level (>27 kg/d compared with <22 kg/d) and changes in these activities. From June to October 2009, a total of 76 cows in a commercial free-stall herd, milking 3 times per day, were enrolled onto this study. Each cow was fitted with a HOBO data logger (HOBO Pendant G Data Logger, Onset, Pocasset, MA) on the outside of the right hind leg, parallel to the floor (longitudinally). The HOBOs were programmed to start data collection at 7am, 2 d before drying-off (d-2), and to continue for 6 d following drying-off (d6). Cows received their last milk-out at the second daily milking (d0, noon). The HOBO recorded time-stamped standing and lying behavior (including lying side) at one minute intervals, allowing for the calculation of total lying time per day. Simple univariable analysis by 2-sample *t*-tests was used to compare production level and parity against total lying time. Upon completion of the full data set, multivariable analysis will be performed. Cows drying-off at high production had significantly lower lying times compared with cows at lower production levels on d1 ($P < 0.05$; 634.71 ± 211.04 vs. 747.04 ± 166.86 min) and d3 ($P < 0.005$; 724.58 ± 138.81 vs. 836.15 ± 116.03 min). Lactation 1 cows also showed significantly ($P < 0.001$) lower lying times of almost 3 h compared with multiparous cows on d1 (572 ± 195.04 vs. 751.61 ± 170.66 min). In conclusion, these data suggest that abrupt cessation of milking at drying-off is associated with changes in standing and lying behaviors, indicative of increased discomfort. These behavioral changes appear to be influenced by production level at the time of drying-off and by parity. Management interventions in the process of drying-off may be warranted.

Key Words: drying-off, behaviour, lying and standing time

904 Short-term overcrowding affects the lying and social behavior of lactating Holstein dairy cows. P. D. Krawczel*[1,2], L. B. Klaiber[1], R. E. Butzler[1], L. M. Klaiber[1], H. M. Dann[1], C. S. Mooney[1], and R. J. Grant[1], [1]*William H. Miner Agricultural Research Institute*, *Chazy, NY,* [2]*The University of Vermont, Department of Animal Science*, *Burlington*.

Reduced access of resources, due to overcrowding, may affect lactating dairy cows′ daily time budgets detrimentally. The objective of this study was to determine the differences in feeding, ruminating, lying, and social behaviors of Holstein dairy cows housed at stocking densities of 100 (1 cow per freestall and headlock), 113, 131, and 142%. Multiparous cows (n = 96) and primiparous cows (n = 40) were assigned to 4 pens in a 4-row barn. Pens were balanced for parity, milk production, days in milk, and somatic cell count. Treatments were imposed by reducing resting and feeding space for 14 d using a 4 × 4 Latin square design. Time spent feeding and ruminating were quantified by 24 h of direct observation beginning at 0800 on d 11. Dataloggers recorded lying behavior (time and bouts) of 12 focal cows per pen at 1-min intervals during the final 5 d of each period. Social aggression was defined as the number of successful displacements from the feed bunk during the 2 h after cows returned to the pen after milking. Displacements were recorded after 9 milkings over the last 4 d of each period. Pen means (n = 16) were analyzed using MIXED procedure of SAS. Feeding (3.7 ± 0.2 h/d) and ruminating (7.2 ± 0.2 h/d) did not differ among stocking densities ($P > 0.5$). Overcrowding did change the location of rumination; a greater percentage (95.1 ± 2.4) of the total rumination ($P < 0.01$) occurred within a freestall at 100% compared with 131% (89.6 ± 2.4) or 142% (87.3 ± 2.4). Lying time was reduced by 0.8 h at 131% and 0.7 h at 142% ($P < 0.02$) compared with 100 or 113%. Lying bouts (11.3 ± 0.6 per d) were not affected by stocking density ($P = 0.57$). Relative to 100% (13.2 ± 2.5 per 2 h), social aggression was greater at 142% (20.4 ± 1.8 per 2 h; $P = 0.03$) and tended to be greater at 131% (15.8 ± 3.5 per 2 h; $P = 0.10$). Decreased lying time and increased aggression at the feed bunk during short-term overcrowding suggests increased stocking densities may alter the time budgets of lactating dairy cows. The long-term ramifications of these changes are unknown and should be addressed to ensure management practices ensure the welfare of lactating dairy cows.

Key Words: dairy cow, stocking density, behavior

905 Early detection of lameness through pedometric activity and lying behaviour of dairy cattle. J. H. Higginson*[1], S. T. Millman[2], G. Cramer[1,3], K. E. Leslie[1], A. M. B. de Passille[4], T. F. Duffield[1], and D. F. Kelton[1], [1]*University of Guelph*, *Guelph, ON, Canada*,[2]*Iowa State University*, *Ames,* [3]*Cramer Mobile Bovine Veterinary Services*, *Stratford, ON, Canada*,[4]*Agriculture and Agri-Food Canada*, *Agassiz, BC, Canada*.

The objective of this pilot study was to examine changes in dairy cow activity around lameness events, a component of a larger ongoing investigation to determine the efficacy of pedometric activity for early lameness detection. The commercial Pedometer Plus system (SAE Afikim, Israel) provides information regarding the number of steps taken, the duration of lying time, and the number of lying bouts. The device was affixed to the hind limbs of 130 lactating cows and data was collected twice daily during milking. Hooves were examined for lesion identification every 3 mo and trimmed every 6 mo. In addition, Between these, lameness cases identified by the producer were evaluated by a veterinarian, treated, and causal factors recorded. To date, 5 cows with new cases of digital dermatitis were identified. Activity and lying behavior were analyzed during 2 time periods - 7 d before lameness identification and exam, and 7 d following exam, with exam day excluded. A paired *t*-test demonstrated a difference in activity between time periods ($P = 0.03$). On average (±sd), cows performed 65.1 (±4.1) steps/hour before lesion identification and 76.2 (±5.6) following identification. The mean number of lying bouts between time periods was not different ($P = 0.79$), with mean lying of 10.0 (±0.7) bouts/day before the lameness exam and 9.9 (±0.6) following the lameness exam. Lying duration also did not differ ($P = 0.54$), with 693.1 (±28.0) minutes/day before the lameness exam and 675.1 (±34.5) minutes/day following the exam. Our preliminary results suggest that during the 7 d before identification of digital dermatitis, cows are less active. Continued enrolment will determine if other hoof lesions show similar changes. Further evaluation of activity around lameness events will determine if early detection through the use of pedometry is possible.

Key Words: lameness, pedometry, activity

906 Behavioral responses to feeding regimens, housing and heat stress in dairy calves. A. L. Adams*, T. H. Friend, G. A. Holub, S. M. Garey, and C. L. Terrill, *Texas A&M University*, *College Station*.

There is concern that accelerated feeding programs may adversely influence calves during periods of environmental heat stress. The objective of this study was to determine the effects of housing, feeding regimens, and heat stress on activity and utilization of shade by dairy calves. Fifty-five Holstein bull calves 1–3 d of age were randomly assigned to 1.85 m^2 individual pens that were either indoors in a climate-controlled environment (n = 28) or outdoors in a covered barn (n = 27) for 7 wk. Within each of the 2 housing treatments, calves were assigned to one of 3 feeding regimens: milk replacer increased by 0.1% of BW weekly, n = 17; consistent amount of milk replacer at 1.1% of BW, n = 18; or milk replacer decreased by 0.1% of BW weekly, n = 20. Calves were fitted with pedometers and released into a 15.24 m × 9.14 m partially shaded (9.14 m × 3.05 m) outdoor open-field test pen for 1 h every 7 d in the early afternoon in July and August. Behavior was classified as active, standing, lying or in-shade at 5-min intervals. Recorded steps, shade use (0 = in-shade, 1 = not in-shade), and mean activity scores (0 = lying, 1 = standing, 2 = active) were analyzed as repeated measures in an autoregressive covariance mixed model. Feed regimen did not affect the number of steps taken, shade use, or activity of the calves. An increase in steps occurred over time with 454 ± 25.35 steps for wk 1 and 717 ± 24.49 steps for wk 7 ($P < 0.0001$). Calves housed outdoors took more steps (618 ± 17.88) than calves housed indoors (559 ± 17.39; $P = 0.0039$). Calves averaged significantly ($P < 0.0001$) fewer steps (465 ± 13.84) during field tests with high (≥83) temperature-humidity index (THI) values than during field tests with low (<80) THI (718 ± 40.14 steps). Calves spent less time in the shade as they aged ($P < 0.0001$), when the THI was low ($P < 0.0001$), and if they were housed outdoors ($P = 0.0011$). Calves housed indoors tended to be more active than calves housed outdoors ($P = 0.094$). These results suggest that accelerated feeding programs do not impose additional thermal stress on calves.

Key Words: calves, behavior, heat stress

907 Behavior of two cow genotypes (Holstein vs. Jersey) in two milk production systems (grazing vs. confinement). A. I. Roca-Fernández*[1], C. P. Ferris[2], E. R. Vance[2], and A. González-Rodríguez[1], [1]*Agrarian Research Centre of Mabegondo*, *La Coruña, Galicia, Spain,*[2]*Agri-Food and Biosciences Institute*, *Hillsborough, Co. Down, UK*.

Diverse milk production systems exist in Europe, ranging from low input grazing systems to high input confinement systems. The impact of these systems on dairy cow behavior has not been extensively examined. The aim of this study was to compare the behavioral activities of 2 cow genotypes (Holstein-Friesian, H-F vs. Jersey × Holstein-Friesian crossbred, Jx) when managed within 2 contrasting milk production systems (grazing, G vs. confinement, C). One hundred 20 spring calving cows (H-F, n = 60 and Jx, n = 60) were balanced on calving date and milk yield and randomly assigned to one of 2 milk production systems (G, n = 60 and C, n = 60) in a block design with a 2 × 2 factorial arrangement of treatments. Cows were scanned on 3 occasions in a 6 week period (P1, end July; P2, middle August; P3, end August) and the behavioral activities of cows were registered at 20-min intervals, between 16.00 and 22.00 h and 7.00–14.00 h. The behavior of each cow was recorded, according to the following activities: lying, eating, standing and ruminating. There were differences ($P < 0.001$) between periods for time spent lying, eating and ruminating in relation to daylight, while time spent standing did not show any difference. Cows on the grazing system spent more time lying and ruminating in P3 (272 and 165 min., respectively) than in P1 (152 and 122 min., respectively) and time spent eating was lower in P3 (485 min.) than in P1 (553 min.). Breed had no effect on any of the behaviors recorded. Nevertheless, a tendency to spend more time eating and ruminating was observed in Jx (354 and 195 min., respectively) than in H-F (343 and 184 min., respectively). System showed an effect ($P < 0.001$) on dairy cow behavior. Cows on the grazing system spent more time grazing (522 min.) than those on the housing system spent eating (175 min.). Cows on the confinement system spent more time lying (405 vs. 212 min., respectively), standing (301 vs. 87 min.) and ruminating (246 vs. 134 min., respectively) than did those in the grazing system. Greater synchrony of dairy cows behavior was observed at pasture than in the confinement system.

Key Words: milk production systems, cow genotypes, feeding behavior

908 Diet palatability influences the feeding behavior of sheep. I. R. Ipharraguerre*[1] and J. J. Villalba[2], [1]*Lucta SA*, *Barcelona, Spain*, [2]*Utah State University*, *Logan*.

The aim of this study was to assess whether the feeding pattern displayed by sheep exposed to a monotonous ration is modified when the same ration is presented in a diversity of flavors. Thirty-five 2-mo old lambs were randomly assigned to 5 groups (7 lambs/group). One group of lambs [Diversity (D)] was fed simultaneously an unflavored ration of alfalfa and barley (75:25) and the same ration mixed (0.2%) with one of 3 flavors: 1) sweet, 2) umami, and 3) bitter. The other 4 groups (Monotony) received just one of the 4 rations [i.e., unflavored control (C); sweet (S); umami (U); and bitter (B)]. All animals were fed their respective rations ad libitum from 0800 to 1600 for 60 d. Feed consumption was measured throughout the study. Data were analyzed as a split-plot design with repeated measures using a mixed-effect model with animal (random) nested within group. On d 55, intake was estimated every 30 min for 8 h. On d 56, scan samples were taken at 5-min intervals to assess the incidence of offered feeds on feeding events. On average, lambs in D consumed 4 to 8% more feed than lambs in the other groups ($P < 0.008$). Lambs in D showed lower intakes than the other groups during the 2 peaks of food consumption: 30 min ($P < 0.008$) and 270 min ($P < 0.007$) after offering the rations. In contrast, lambs in D consumed more feed than lambs exposed to monotonous flavors at 60 ($P < 0.05$), 90 ($P < 0.07$), 120 ($P < 0.10$), and 180 min ($P < 0.05$) post-feeding. No differences among groups, however, were detected in the proportion of scans recorded during the feeding cycle. Thus, differences in total feed consumption were likely supported by changes in the rate, but not the frequency, of feeding events. Within group D, diet preferences were umami > sweet > bitter (33 > 28 > 26 g/kg of metabolic BW; $P < 0.01$) and plain > bitter (31 vs. 26 g/kg of metabolic BW; $P < 0.01$). Exposure to diverse flavors in the same ration has the potential to increase feed intake and foster an even utilization of feed across time by reducing peaks and nadirs of feed consumption compared with exposure to monotonous rations.

Key Words: behavior, flavor, intake

909 Early experience to flavor diversity influences food selection and intake by sheep. J. J. Villalba*[1] and I. R. Ipharraguerre[2], [1]*Utah State University*, *Logan,* [2]*Lucta SA*, *Barcelona, Spain*.

The objective of this study was to determine whether early experiences to flavor diversity or monotony influence intake and preferences for novel feeds by sheep. Thirty-five 2-mo old lambs were randomly assigned to 5 groups (7 lambs/group). One group of lambs [Diversity (D)] was fed

simultaneously an unflavored ration of alfalfa and barley (75:25) and the same ration mixed (0.2%) with one of 3 flavors: 1) sweet, 2) umami, and 3) bitter. The other 4 groups (Monotony) received one of the 4 rations [i.e., unflavored control (C); sweet (S); umami (U); and bitter (B)]. All animals were fed ad libitum from 0800 to 1600 for 60 d. Afterward, all groups received alfalfa hay for 46 d. Following, preference tests were conducted over 5 d by offering simultaneously novel feeds of either (1) high energy content (beet pulp, corn, milo, oats), (2) high protein content (wheat gluten meal, rabbit pellets, soybean meal, Calfmanna), or (3) beet pulp mixed with secondary compounds [condensed quebracho tannins (10%), quillaja bark saponins (2%), and sagebrush terpenes (3%)]. Data were analyzed as repeated measures using a mixed-effect model with animal (random) nested within group. On average, lambs in D consumed more feed ($P < 0.01$) than lambs in the other groups (118, 113, 113, 109, and 109 g/kg of metabolic BW for lambs in D, B, U, C and S, respectively). No differences in ADG were detected among groups for the first 33 d of exposure, but from d 34 to 60 lambs in D grew faster ($P < 0.04$) than lambs in the other groups (0.30, 0.20, 0.22, 0.19, and 0.20 kg/d for lambs in D, B, U, C and S, respectively). Lambs in C preferred beet pulp compared with lambs in U and B ($P < 0.04$); lambs in B preferred oats compared with lambs in D, C, and S; lambs in S preferred corn compared with lambs in B ($P < 0.05$); and lambs in D preferred milo compared with lambs in N and S ($P < 0.06$). Thus, exposure to diverse flavors in the same ration may influence intake and selectivity and contribute to modify initial acceptability and preference for novel feeds by lambs.

Key Words: early experience, flavor, intake

910 Preference in cattle offered a ground switchgrass and alfalfa hay blend flavored with sucrose or citric acid. S. J. Chavez*, S. Freeman, and G. B. Huntington, *North Carolina State University*, *Raleigh*.

Intake of feed can be influenced positively or negatively by flavor. The objective was to evaluate preference for sucrose or citric acid addition to a ground hay blend (switchgrass:alfalfa = 3:1, as fed). Flavors were dissolved in 50 mL deionized water for blending. Sucrose hay (SU) had 100g sucrose added per kg hay. Citric acid hay (CA) had 50 g citric acid added per kg hay. Control hay (CON) had 50 mL deionized water added per kg hay. Hays were mixed 3 d before the experimental period and stored at room temperature. Eleven Angus-cross steers and 1 heifer (initial BW = 283 ± 25 kg) were housed under a roof on expanded metal flooring with access to 6 feed slots designated I through VI, west to east. Cattle were offered 1 kg of supplement (47.5% each, soybean hulls and corn with 5% trace mineralized salt, as fed) at 0800 daily. Orts were removed and weighed at 0800. Cattle were offered 0.6% BW treatment hay at each feed slot and treatments (SU, CA, and CON) were randomly assigned to 2 of the 6 locations at 0830 daily. Cattle were given a 14-d adaptation to CON followed by a 7-d preference trial. Preference was determined by disappearance where greater disappearance was taken to mean animal preference. Cattle preferred SU (3.42 ± 0.04 kg/d) over CON (2.8 ± 0.04 kg/d, $P < 0.01$) and CA (0.32 ± 0.04 kg/d, $P < 0.01$) and preferred CON over CA ($P < 0.01$). Feeding location I was preferred more than III ($P < 0.03$). This difference was seen since CA was randomly assigned 4 out of the 7 d from position III. Cattle searched for SU and consumed SU in entirety in both locations before consuming CON or CA. Cattle consumed SU over CON and CA independent of location. Cattle searched for the SU and consumed SU immediately after SU was presented in both locations. Cattle may search for food that stimulates taste receptor cells for sweetness over other flavors. Adding sweet flavors to cattle feeds would increase intake of forages with lower nutritional values such as switchgrass.

Key Words: cattle, preference, flavor

911 Characterization of feeding behavior traits and associations with feed efficiency in beef heifers fed a high-grain diet. E. Mendes*, G. Carstens, and L. Tedeschi, *Texas A&M University*, *College Station*.

Few studies have characterized meal criterion in beef cattle, which is an estimate of the longest nonfeeding interval that is considered to be part of a meal. Objectives of this study were to quantify meal criteria, and to examine within-animal repeatability of feeding behavior traits and their associations with residual feed intake (RFI) in beef heifers fed high-grain diets. An electronic feed intake system (GrowSafe; DAQ4000E version 9.25) was used to record individual bunk visit frequency (BVF) and duration (BVD) for 62 heifers (initial BW = 286) fed a high grain diet (3.1 Mcal ME/kg DM) for 81 d. A mixture 2-pool distribution model (R mixdist package 0.5–2) was fitted to log10-transformed interval lengths between BVF. The intersection of the 2 distributions, which The intersection of the 2 distributions, which represents intervals within and between meals, was computed as the meal criteria and used to calculate meal frequency (MF) and duration (MD). RFI was calculated as the difference between actual and expected DMI from linear regression of DMI on ADG and mid-test $BW^{0.75}$. The overall means (±SD) for BVF and MF were 50 ± 8.9 and 8 ± 1.5 events/d, respectively; 61 ± 17.3 and 129 ± 26.6 min/d for BVD and MD; respectively, and 6 ± 1.1 for number of bunk visits per meal (BVM). The pooled meal criteria calculated on the 62 animals in this study was 12.5 min. RFI was positively correlated ($P < 0.05$) to BVF (0.42), BVD (0.41), MD (0.32), and BVM (0.44), but not with MF (0.03). Feed behavior traits for period 1 (d 1 to 40) were regressed on feed behavior traits on period 2 (d 41 to 81) to access within-animal repeatability of these traits. The r^2 of the regression equations for BVF, BVD, MF, MD were 0.63, 0.76, 0.73, 0.77, respectively, and for number of bunk visits per meal was 0.55. These results suggest that within animal repeatability of feed behavior traits are high and that they may be useful indicator traits for RFI in beef cattle.

Key Words: feed behavior, residual feed intake

912 Approaches for assessing temperament in calves post-weaning. K. L. Barkley*[1], L. D. Pullen[1], A. M. Kopanko[1], A. E. Tanner[1], S. R. Blevins[1], M. L. Wahlberg[1], C. W. Swecker Jr[1], J. P. S. Neel[2], W. M. Clapham[2], and R. M. Lewis[1], [1]*Virginia Tech*, *Blacksburg,* [2]*USDA-ARS*, *Beaver, WV*.

Cattle under routine management express behaviors that may represent stress or anxiety. Our objectives were to develop reliable measures of calf behavior, and to determine whether these measures change under repeated handling. A factorial design of 2 measurement protocols [regular (R), irregular (I], and 3 recording periods, each 1 mo apart, was used. The R measurements were collected over 3 consecutive d; I measurements were collected on d 1 within each period. Twenty Angus-cross heifer calves, 2 wk post-weaning, were randomly assigned to each protocol. Calves were weighed, calmly moved into a squeeze chute, and their heads caught. Behavior was scored from 1 (docile) to 5 (aggressive) by 3 observers. Heart rate (HR), and blood and fecal samples, were then collected. Exit velocity (EV) was obtained on release from the chute over 2 m. Calves were penned individually with the same human presence, and again scored. Plasma cortisol concentrations were determined by EIA. Data were analyzed with ANOVA. Protocol, period, and their interaction, were compared on d 1. Period, day, and

their interaction were fitted within R. Both scores were included as covariates to assess cortisol. Chute (0.33 ± 0.16; $P = 0.04$) and pen (0.52 ± 0.12; $P < 0.001$) scores and HR (20 ± 5 beat/min; $P < 0.001$) were less and EV slower (0.43 ± 0.09 s; $P < 0.001$) in R than I. Chute score decreased across periods in R but increased in I ($P = 0.03$). In R in a period, chute score declined with d (0.34 ± 0.14; $P = 0.05$), with little change in pen score, EV or HR ($P > 0.17$). Chute and pen score were highly correlated in R (0.56; $P < 0.001$); less so in I (0.31; $P = 0.04$). Plasma cortisol was 39% higher at period 1 than 3 ($P < 0.001$). It increased with chute and pen score ($P = 0.01$). Plasma cortisol in R was 22% higher at d 1 than 3. It increased with chute score ($P = 0.01$). Repeated handling reduced ill temperament and signs of stress. Chute score is quickly assessed, indicative of anxiety, and could be used to monitor husbandry practices.

Key Words: temperament, cortisol, calves

913 Relationship of temperament at calving and distribution of beef cows grazing foothill rangeland. D. W. Bailey*[1], H. C. VanWagoner[2], D. Jensen[2], D. L. Boss[2], and M. G. Thomas[1], [1]*New Mexico State University*, *Las Cruces,* [2]*Montana State University*, *Havre*.

The objective of this study was to determine if docility score measured at calving was related to measures of cattle grazing distribution in foothill rangeland of northern Montana. We hypothesized that cows with aggressive temperaments would travel farther horizontally and vertically from water and use steeper slopes than docile cows. A herd of Hereford and Tarentaise crossed cows (n = 186) and a herd of Angus, Charolais, Hereford, Piedmontese, Salers, and Tarentaise crossed cows (n = 191) were observed at calving and assigned a temperament score (1 = calm and 6 = dangerous and extremely aggressive) for 5 years. Both herds were also visually observed during grazing, and their locations were recorded in multiple pastures with rugged topography for 5 years. Only cows that had 2 or more calves in their lifetime were included the analyses. Mean temperament, number of calves and breed were used to explain differences in the average recorded terrain use with a mixed model analysis. Temperament at calving was not related to horizontal or vertical distance traveled to water and slope use in either herd. For the Hereford and Tarentaise crossed cows, breed and number of calves affected both horizontal and vertical distance traveled to water ($P < 0.05$). Cows with more Tarentaise breeding traveled farther than cows with predominantly Hereford breeding. Tarentaise cows traveled 58 ± 2 m vertically from water while Hereford cows traveled 50 ± 2 m. Cows with 3 or more calves during their lifetime (56 ± 2 m) traveled farther ($P < 0.01$) vertically from water than cows with only 2 calves (48 ± 2 m). For the other herd, vertical distance traveled to water was affected by the number calves ($P = 0.01$) with cows with 4 or more calves traveling farther than cows with 2 or 3 calves. We rejected our hypothesis and concluded that docility at calving was not related to terrain use during grazing.

Key Words: docility, behavior, breed

ASAS Western Section Symposium: Perinatal Programming of Offspring Quality 2: Evidence for impacts of maternal nutrition on livestock production

914 Maternal malnutrition induces metabolic reprogramming in offspring. S. P. Ford*[1], L. Zhang[1], L. A. George[1], Y. Ma[1], N. M. Long[1], A. B. Uthlaut[1], and P. W. Nathanielsz[2], [1]*Center for the Study of Fetal Programming, Department of Animal Science, University of Wyoming*, *Laramie,* [2]*Center for Pregnancy and Newborn Research, University of Texas Health Sciences Center*, *San Antonio*.

Evidence suggests that both maternal undernutrition and overnutrition negatively impacts fetal growth and development and postnatal health in mammals. Maternal nutrient restriction from early to midgestation in ewes (NR ewes) results in fetal IUGR (~30% weight reduction) at midgestation compared with ewes fed to NRC requirements (Control, C ewes). If NR ewes are then fed to requirements from mid gestation to term, their offspring are born at weights similar to C ewes, suggesting accelerated fetal growth rate from mid to late gestation. These offspring exhibit increased appetite, insulin resistance and adiposity during post natal development. By 8 mo of age, these NR offspring are heavier, and have increased carcass fat and reduced skeletal muscle mass compared with C offspring. In contrast, if ewes are overfed from 60 d before conception and throughout gestation (obese, OB ewes) their fetuses are macrosomic (enlarged) at midgestation, and then exhibit reduced growth rates from mid-gestation to term. As with lambs from NR ewes, Lambs from OB ewes exhibit birth weights similar to those of ewes fed to requirements. Also similar to NR offspring, OB offspring develop an increased appetite, insulin resistance, and obesity in early adulthood. Interestingly, fetuses gestated by NR and OB ewes experience similar alterations in pancreatic growth and development throughout gestation. At midgestation, both NR and OB fetuses exhibit marked increases in pancreatic β-cell numbers compared with C fetuses, but by late gestation, β-cells numbers have decreased dramatically to reach numbers much lower than that of C fetuses. This talk will compare and contrast the specific prenatal and postnatal impacts of maternal nutrient restriction and overfeeding on conceptus development and offspring health.

Key Words: maternal malnutrition, fetal development, postnatal health

915 Impacts of maternal nutrition in farm animal species on growth characteristics of their offspring. M. Du*, M. J. Zhu, and S. P. Ford, *Department of Animal Science, University of Wyoming*, *Laramie*.

Meat animals spend about one third of their life inside the uterus, and more importantly, all major developmental events are accomplished during the fetal stage. Proper maternal nutrition is crucial for fetal development and the growth characteristics of offspring. Maternal under-nutrition during mid to late gestation reduces birth weight, muscle weight and fatness of offspring at birth, but increases fatness at slaughter, resulting in a permanent impairment of growth performance of offspring. On the other hand, the impact of maternal over-nutrition on fetal development and offspring growth performance is more complicated depending on whether placental function is impaired. If maternal obesity and over-nutrition impairs the function of placenta, the nutrient delivery to fetuses is limited, resulting in poor fetal development and offspring growth characteristics. One the other hand, maternal obesity and over-nutrition without impairment of placental function provides excessive macronutrients to fetuses, which often results in macrosomia and slightly improves the growth performance of offspring. Inflammation associated with maternal obesity may promote adipogenesis (formation of adipocytes) at the expense of myogenesis (formation of muscle cells) and osteogenesis (formation of bone tissue), increasing the fatness but also the marbling of offspring carcasses

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Key Words: maternal nutrition, growth, offspring

916 Maternal nutrition and developmental programming: Impacts on development and function of the gastrointestinal system in offspring. J. S. Caton*, A. M. Meyer, D. A. Redmer, K. A. Vonnahme, and L. P. Reynolds, *Center for Nutrition and Pregnancy, Department of Animal Sciences, North Dakota State University, Fargo*.

Developmental programming is the concept that a perturbation during a sensitive period of development can have lasting consequences in offspring. Maternal nutrition is one of the primary factors impacting growth and development of the gravid uterus, and altered maternal nutrient supply has resulted in compromised offspring. Growth, development, and vascularization of the gastrointestinal tract are often overlooked but are essential processes underlying nutrient uptake and expenditure, immunological competence, neonatal survival, postnatal growth, and metabolic regulation via a cadre of hormones and growth factors. Tissue vascularization is crucial for nutrient transport both to and from the intestine; thus angiogenesis, or the formation of blood vessels, is critical for proper intestinal function. Data indicate that maternal nutrition can alter vascular measurements in late term fetal, early postnatal, and at market weight in ruminant offspring. Additionally, intestinal development during the perinatal period includes growth via cell proliferation, hypertrophy, as well as changes in vascularization. Fetal intestinal growth, inflammatory responses, and/or vascularity, measured near term, have been altered by changes in maternal nutrient supply. In addition, nutrient digestibilities and enzyme activities have been altered in offspring from nutrient compromised dams. Maternal nutritional effects on intestinal vascularity have been accompanied by changes in mRNA expression of vascular endothelial growth factor (VEGF) synthesis, and soluble guanylate cyclase (endothelial nitric oxide, NO receptor), implying possible regulatory roles of VEGF and NO systems. Nutritional modulation or other therapeutics may provide means to stimulate intestinal blood flow and/or angiogenesis, affording potential opportunity to overcome growth or health challenges in compromised ruminants.

Key Words: developmental programming, intestine, maternal nutrition

917 Programming reproductive tract development. F. F. Bartol*[1] and C. A. Bagnell[2], [1]*Auburn University*, *Auburn, AL*, [2]*Rutgers, The State University of New Jersey*, *New Brunswick*.

Female reproductive tract (FRT) development begins prenatally and is completed postnatally. This developmental program is defined by patterns of gene expression in FRT tissues during organizationally critical fetal and perinatal periods. Data for cattle, sheep and pigs show that transient exposure to steroid hormone receptor-modulating agents from birth (postnatal day = PND 0) can disrupt the normal developmental program and alter the developmental trajectory of FRT tissues with lasting consequences. Data for the pig (*Sus scrofa domesticus*) show that postnatal endometrial development and programming are marked by the onset of estrogen receptor (ESR1) expression in nascent glandular

epithelium and stroma by PND 2. Factors affecting ESR1 expression and activation in porcine uterine tissues between birth and PND 14 affect the uterine developmental program and can alter endometrial function and reduce uterine capacity in adults. Maternal effects on neonatal FRT development can be communicated through signals transmitted in milk via a lactocrine mechanism. Studies involving relaxin (RLX), a prototypical milk-borne morphoregulatory factor in the pig, were conducted to test the lactocrine hypothesis for maternal programming of porcine FRT development. Developmental programs were compared for uterine and cervical tissues obtained on PND 2 or PND 14 from gilts allowed to consume colostrum versus those fed a milk replacer from birth, in the presence and absence of exogenous RLX. Results indicated that a lactocrine-driven mechanism, essential to support normal FRT developmental programs, evolves in the uterus and cervix between birth and PND 2. In the absence of lactocrine signaling during this period, normal uterine and cervical ESR1 expression, as well as that of other markers of RLX action and/or estrogen receptor activation including vascular endothelial growth factor-A and matrix metalloproteinase-9, are markedly ($P < 0.01$) reduced by PND 2 and remain low through PND 14, even when replacer-fed gilts are allowed to consume colostrum after PND 2. Lactocrine signaling deserves consideration as an element of the FRT programming equation.

Key Words: female reproductive tract, lactocrine, programming

Beef Species Symposium: Upcoming Environmental Policies and Their Effects on Beef Production

918 Environmental issues: What every beef producer needs to know. T. McCann Thies*, *National Cattlemen's Beef Association*, *Washington, DC*.

The current environmental regulatory climate in Washington is intense. Effects of animal agriculture operations on the environment are being scrutinized increasingly by the US Environmental Protection Agency, Congress, the courts, and environmental groups. The presentation will discuss the political climate in Washington with regard to environmental issues, and will summarize briefly many of the environmental issues that confront the beef industry.

919 Alberta's experiences with greenhouse gases: The beef protocols. J. Basarab*, *Department of Agricultural, Food and Nutritional Science, University of Alberta*, *LaCombe, AB, Canada*.

Protocols have been developed to lessen green house gases. These protocols include feeding edible oils to cattle, reduced days in the feedlot, reduced age at slaughter and selection for low RFI in beef cattle. How are greenhouse gases quantified using one or two examples? What are the economic returns for reducing greenhouse gases? We are conducting this research to reduce costs, improve production efficiency and ultimately profit.

920 Integration of environmental mandates into ranching and farming operations. P. Genho*, *FMC*, *Salt Lake City, UT*.

From a rancher's perspective, how will they adapt ranch management practices to comply with mandated legislation related to the environment?

921 Telomere maintenance mechanisms in normal, immortalized, and transformed chicken cells. T. H. O'Hare* and M. E. Delany, *Department of Animal Science, University of California, Davis*.

Telomeres protect the ends of linear chromosomes in eukaryotes. A specialized holoenzyme consisting of an RNA and a protein catalytic subunit, telomerase, adds the telomeric TTAGGG repeat to the chromosome ends thus mitigating telomere shortening. A recent study (O'Hare and Delany, 2009) investigated variation within and among the telomeric array profiles of normal, immortalized, and transformed chicken cells. An immortalized chicken embryo fibroblast (CEF) cell line, DF-1, exhibited ~3-fold more telomeric content (17%) as compared with normal chicken cells (5%). Interestingly, DF-1 had been reported to be telomerase-negative (Christman et al., 2005). The current study confirmed that DF-1 cells are telomerase-negative and found that a chemically transformed CEF cell line, OU2, is telomerase-negative. The telomeric profile of this transformed line indicates a content of ~5%. Given their lack of telomerase activity, we hypothesize DF-1 and OU2 are using the alternative lengthening of telomeres (ALT) pathway to maintain or lengthen their telomeres. Gene expression of telomerase components, telomere-regulating, and ALT-related proteins was examined. The expression profiles of DF-1 and OU2 were compared with telomerase-negative mortal CEFs, telomerase-positive virally transformed DT40 cells, and gastrula stage embryos. These results provide evidence supporting the existence of the ALT pathway in DF-1 and OU2 cells.

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Key Words: telomere, telomerase, alternative lengthening

922 Genetic analysis of walking ability and mortality in the turkey. C. D. Quinton[1], B. J. Wood*[1,2], and S. P. Miller[1], [1]*Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, Canada*, [2]*Hybrid Turkeys, Kitchener, Canada*.

Genetic selection for fitness is a potential method to improve overall liveability in the turkey. A method in which fitness can be defined is mortality and the potential to survive to slaughter. In this study the heritability (h^2) was calculated for survival (SURV) to slaughter/maturity (23 weeks) and hip and leg strength (H/L) and their relationship (both phenotypic and genetic) to walking ability (WALK) and bodyweight (BW). The heritabilities of the binary traits were also transformed to a liability scale. Consequently there are heritabilities on both the observed and liability scales. Genetic parameters were estimated with multiple-trait restricted maximum likelihood in ASReml 3.0 using a series of 3-trait animal models. The table shows the results of the analysis with walking score having a moderate heritability similar to body weight. Survival and hip/leg health had lower heritability on the observed scale, but a moderate h^2 on the liability scale. The liability scale heritability estimates were moderate which would predict a good response to selection. All survival traits had high genetic correlations with each other, but negative genetic correlations with weight. Genetic correlations were stronger than corresponding phenotypic correlations. Walking score has good heritability and has high positive genetic correlation with survival, as well as moderate genetic correlations with hip and leg health. As a consequence walking score would be a good indicator trait for selection to improve both survival and hip and leg health.

Table 1. Heritability (h^2), common environment (c^2) and genetic[1] and phenotypic[2] correlations between survival, walking score, hip and leg strength and bodyweight

	SURV3	WALK4	H/L5	BW6
h^2 observed	0.166	0.224	0.080	0.248
h^2 liability	0.190		0.174	
c^2	0.034	0.074	0.041	0.350
Correlations				
SURV	-	0.864	0.808	–0.435
WALK	0.670	-	0.913	–0.372
H/L	0.575	0.660	-	–0.366
BW	–0.070	–0.192	–0.090	-

[1]above diagonal, [2]below diagonal, [3]survival to 23 wks, [4]walking score, [5]hip and leg strength, [6]bodyweight.

Key Words: liveability, turkeys, parameter estimation

923 Factors affecting spermatozoa morphology in beef bulls. C. A. Roberts*, T. W. Geary, M. D. MacNeil, R. C. Waterman, A. J. Roberts, and L. J. Alexander, *USDA-ARS, Fort Keogh Livestock and Range Research Laboratory, Miles City, MT*.

The objective of this study was to evaluate factors affecting sperm morphology of bulls (n = 908) collected at 320 d of age. Bulls were a composite breed (50% Red Angus, 25% Charolais, and 25% Tarentaise) born from 2002 to 2008 to dams fed levels of feed during mid and late gestation that were expected to provide marginal or adequate nutrition while grazing dormant winter forage. After weaning, bulls were fed to appetite (CON) or restricted (REST) to 80% of that consumed by CON on BW basis. Semen samples were collected using an electroejaculator and evaluated using standard BSE procedures. Spermatozoa morphology was evaluated by classifying 100 spermatozoa per bull at 400X magnification into the following categories: normal spermatozoa, knobbed acrosome, head defects, distal midpiece reflex, dag defect, bowed midpiece, proximal droplet, distal droplet, coiled principle piece, and bent principle piece. Each morphological trait, along with scrotal circumference (SC), gross motility, and percent progressive motility was analyzed using MTDFREML and pedigree information from 8163 relatives born from 1974 to 2008 to provide heritability estimates. Heritability estimates for these traits were: SC ($h^2 = 0.67$), normal sperm ($h^2 = 0.18$), dag defect ($h^2 = 50$), bowed midpieces ($h^2 = 0.19$), proximal droplets ($h^2 = 0.37$), bent principle pieces ($h^2 = 0.18$), gross motility ($h^2 = 0.20$), and progressive motility ($h^2 = 0.20$). The moderate heritability of percent normal sperm and several of the other sperm defects suggest that selection for improved sperm morphology is possible. Further analysis with MTDFREML determined genetic correlations between the above traits and pre-weaning gain direct, pre-weaning gain maternal, post-weaning gain, and scrotal circumference. Maternal pre-weaning gain was highly correlated with scrotal circumference ($r = 0.70 \pm 0.24$) but pre-weaning gain direct ($r = 0.29 \pm 0.20$) and post-weaning gain ($r = 0.01 \pm 0.17$) were not. Scrotal circumference and post-weaning gain were not highly correlated with morphology and therefore are not good indicators of spermatozoa morphology. Neither in utero nor postweaning diet affected any of the traits measured.

Key Words: bull, spermatozoa morphology, heritability

924 Bayesian QTL inference and gene identification for first service conception rate in Brangus heifers. S. O. Peters*[1,5], K. Kizilkaya[2,4], D. J. Garrick[2], R. L. Fernando[2], J. M. Reecy[2], Z.-L. Hu[2], R. L. Weaber[3], G. A. Silver[1], and M. G. Thomas[1], [1]*New Mexico State University*, *Las Cruces,* [2]*Iowa State University*, *Ames,* [3]*University of Missouri*, *Columbia,* [4]*Adnan Menderes University*, *Turkey*, [5]*University of Agriculture, Abeokuta*, *Abeokuta, NGR*.

First service conception (FSC) like many binary fertility traits is of low heritability, but strongly impacts production costs in beef cattle operations. The objectives of this study were to conduct a Bayesian-based whole genome QTL scan for FSC in Brangus (3/8 Brahman x 5/8 Angus) heifers and to identify candidate genes from a hypothalamic transcriptome reference resource. Yearling heifers (n = 830 from 67 sires) were estrous synchronized with progesterone-based protocols, artificially bred, then later palpated for pregnancy status (57.3% FSC rate). Heritability was estimated to be 0.21 ± 0.1. Genotypes for each heifer were obtained from BovineSNP50 Infinium beadchips. Simultaneous association of all SNP with FSC were tested in a GenSel Bayes C analysis using a mixture model that treated SNP effects as random with an assumed fraction 0.001 indicating an association. Fixed effects for analysis of FSC included birth year, calving season, contemporary group, and covariates of yearling age and weight. Model frequency >0.01 was assumed indicative of QTL association. Eight regions on chromosomes 6, 8, 26 and 29 were associated with variation in FSC (model frequency ≥0.03). The strongest evidence of association (model frequency 0.17) was a SNP mapped to position 28.6 Mb on BTA 8. Since the hypothalamus is a regulatory tissue of the reproductive endocrine axis, the transcriptome of this tissue was sequenced using the Illumina Genome Analyzer II (RNA-Seq) and aligned with bovine genome (Ver. 4.0) to evaluate presence and level of expression of potential candidate genes among pre and postpubertal heifers. Several annotations were identified within a 1.5 Mb region flanking this SNP on BTA 8 using Alpheus. Five genes with differential hypothalamic expression were identified and ontology of these genes included neuron function and gene regulation. Cumulatively, results warrant fine mapping this region of chromosome 8 to help determine functionality in regulating FSC.
USDA-AFRI: 2008–35205–18751; 2009–35205–05100; NRSP-8 Bioinformatics.

Key Words: candidate gene, fertility, QTL

925 Impact of sire birth weight potential on birth and weaning traits when mated to virgin heifers. G. K. Mantz* and P. Nyren, *North Dakota State University Central Grasslands Research Extension Center*, *Streeter*.

The objective of this study was to examine the effect that mating virgin heifers to sires of varying birth weight potential (BWP) has on birth and weaning traits of offspring. In June, 2008, 98 virgin heifers 13 to15 mo of age were stratified by frame score and weight within frame score. Heifers were assigned randomly to 2 treatment groups. Treatments were based on sire BWP: 1) moderate BWP (MBWP) sires - Angus sires with birth weight (EPD between −1.6 and +0.4 kg, and 2) very low BWP (VLBWP) sires - Lowline sires. Pre-calving heifer weights were obtained 18 February 2009. Calves were born March through May of 2009. Birth weights and a calving difficulty (CD) score (1 = unassisted, 2 = hand pull, 3 = jack pull, 4 = Caesarean, 5 = abnormal presentation) were recorded within 24 h of calving. Calf weaning weights and post-calving dam weights were recorded in October of 2009. Weaning weights were adjusted to a constant 205-d weaning age. There was a calf sex by sire BWP interaction for birth weight ($P = 0.01$) and CD score ($P = 0.03$). Bull calves from MBWP sires were heavier at birth than bull calves from VLBWP sires (40vs. 34 kg; $P = 0.0002$) and had a greater CD score (1.7 vs. 1.1; $P = 0.01$). Birth weights did not differ ($P = 0.92$) between heifer calves sired by the MBWP sires (33 kg) and those sired by VLBWP sires (32 kg). All heifer calves from both sire groups were born unassisted (CD = 1). Calf weaning weight was affected ($P < 0.0001$) by sire BWP, and calf sex ($P = 0.01$). Offspring of MBWP sires were heavier at weaning than those of VLBWP sires, 243 and 213 kg, respectively. Steer calves were heavier at weaning (235 kg) than heifer calves (220 kg). Weaning weight for calves from MBWP and VLBWP sires were 217 and 195 kg, respectively. Dams nursing calves of VLBWP sires lost less weight than dams nursing calves of MBWP sires (28 vs. 43 kg; $P = 0.04$). In summary, using VLBWP sires reduced birth weight and calving difficulty in bull calves and reduced dam weight loss. However, calves sired by VLBWP sires weighed less at weaning than calves sired by MBWP sires.

Key Words: birth weight, calving difficulty, heifers

926 Use of random regression models for the genetic analysis of farrowing survival in pigs. C. Y. Chen*[1], I. Misztal[1], S. Tsuruta[1], W. O. Herring[2], J. Holl[2], and M. Culbertson[2], [1]*Department of Animal and Dairy Science, University of Georgia*, *Athens,* [2]*Smithfield Premium Genetics Group*, *Rose Hill, NC*.

The objective was to compare estimates of genetic parameters for number of stillborns (NSB) in relation to litter size (LS) using random regression models (RRM). Records of a single Duroc population were obtained from 4 nucleus farms from 2004 to 2008. Data from first parity (P1, n = 6,575) litters and second to fifth parity (P2–5, n = 6,259) litters were analyzed separately. Fixed effects included farm-year-season as contemporary groups, parity (for P2–5 only), and fixed cubic regression coefficients on LS with Legendre polynomials. Random effects were additive genetic and permanent environmental effects (for only P2–5). Heterogeneous residual variances were considered in the models. Legendre polynomials (RRM-L), linear splines (RRM-S), and degree 0 B-splines (RRM-BS) with regressions on LS were applied. Parameter sets used for respective models were quadratic polynomial, knots at LS 5, 9, and 13, and intervals of LS 5–7, 8–10, and 11–13 for P1. For P2–5 the same parameters were linear polynomial, knots at LS 6 and 12, and intervals of LS 5–7 and 8–13. Estimates of genetic parameter were similar with the 3 models. For P1, average heritabilities were 0.14, 0.06, and 0.07 in LS 5, 9, and 13, respectively. For P2–5, heritabilities were 0.18, 0.05, and 0.06 with repeatabilities of 0.19, 0.11, and 0.21. For P1, average genetic correlations between LS 5–9, 5–13, and 9–13 were 0.53, −0.29, and 0.65, respectively. For P2–5, correlations averaged for RRM-L and RRM-S were 0.75, −0.21, and 0.50, respectively. The correlation was 0.66 between LS 5–7 and 8–13 for RRM-BS. Based on the analysis, NSB at low and high LS appear to be different traits although genetic parameters for NSB in first and later parities are similar.

Key Words: litter size, pigs, random regression, stillbirth

927 Effectiveness of genetic predictions of Holstein gestation length and relationship to lactation yield for the subsequent lactation. H. D. Norman*, J. R. Wright, and R. H. Miller, *Animal Improvement Programs Laboratory, ARS, USDA*, *Beltsville, MD*.

To determine if genetic evaluations of gestation length (GL) were reliable and repeatable, Holstein bulls used to develop those evaluations were stratified into 7 groups according to predicted transmitting ability (PTA) for service-sire GL based on calvings from 1998 through 2004: ≤ –3.00, –3.00 to –2.01, –2.00 to –1.01, ... 1.00 to 1.99, and ≥ 2.00 d. An independent set of 261,598 first-parity cows later mated to the

same bulls were grouped by the service-sire PTA GL groups (group size of 8,317 to 73,324 gestations), and their GL were examined to determine effectiveness of PTA GL. The model included fixed effects for service-sire group, conception date, conception date squared, and herd-year. Mean GL for mates by service-sire group (from lowest to highest PTA) were 275.3, 276.4, 277.7, 278.7, 279.6, 280.7, and 281.8 d. Yield in the subsequent lactation was also examined for mates by service-sire group. Least squares differences by service-sire group were –84, –79, –14, 15, 28, 50, and 0 kg for standardized milk yield; –2, –3, –1, 1, 1, 1, and 0 kg for fat yield; and –2, –2, 0, 1, 1, 1, and 0 kg for protein yield. The relationship between PTA for service-sire GL and yield appeared to be curvilinear as yield decreased for the ≥2.0 d PTA group. Phenotypic relationship between GL and standardized yield in the subsequent lactation also was examined using 9 cow GL groups: ≤275, 276, 277, ... 282, and ≥283 d. Group size ranged from 17,493 to 64,876 gestations. The model included fixed effects for GL group, conception date, conception date squared, and herd-year. Least squares differences by GL group were −528, –287, –218, –194, –128, –122, –90, –90, and 0 kg for standardized milk yield; –19, –10, –8, –7, –5, –4, –4, –3, and 0 kg for fat yield, and –11, –6, –4, –3, –2, –2, –2, –2, and 0 kg for protein yield. Cows mated to bulls with PTA for longer service-sire GL and cows with longer GL phenotypes were more productive in the lactation following gestation.

Key Words: gestation length, genetic evaluation, lactation yield

928 Estimation of genetic parameters for measures of calf survival and health in a population of Holstein dairy calves in New York state. L. Henderson*[1], F. Miglior[2,3], A. Sewalem[2,3], D. Kelton[1], A. Robinson[4], and K. E. Leslie[1], [1]*Department of Population Medicine, University of Guelph*, *Guelph, Ontario, Canada, N1G 2W1*, [2]*Guelph Food Research Centre, Agriculture and Agri-Food Canada*, *Guelph, Ontario, Canada, N1G 5C9*, [3]*Canadian Dairy Network*, *Guelph, Ontario, Canada, N1K 1E5*, [4]*Department of Animal and Poultry Science, University of Guelph*, *Guelph, Ontario, Canada, N1G 2W1*.

The objectives of this study were to estimate the genetic parameters of calf survival and health for a population of Holstein calves from New York (NY) State, as well as to associate the EBV determined in the current study with traits from on-going genetic evaluations used in Canada and the US. Data were recorded for 7,372 heifer calves at a commercial rearing facility in NY, from arrival at 1 to 7 d of age for the duration of stay at the facility. Performance and disease up to weaning, and mortality before and after weaning, were recorded. Analyzed data were limited to daughters of sires with at least 10 calves originating from farms which had sent at least 5 calves to be raised at the facility. As such, calves from 264 sires and 36 herds were studied using survival analysis and 2-trait model (survival from arrival to weaning and from weaning to exit) for calf survival and 3-trait sire model for calf health (preweaning undifferentiated respiratory disease, umbilical diseases, and bloat). In general, there was increased risk of mortality for calves with very light or heavy weight at arrival, low serum total protein, low weaning weight and for calves born in a difficult parturition. The heritability from the survival analysis was 0.063, where the heritability from the linear model was 0.001 for survival to weaning and 0.036 for survival from weaning to exit. The genetic correlation between the 2 latter traits was 0.58. In the genetic analysis of health traits, the heritability estimates were 0.09 for bovine respiratory disease, 0.14 for umbilical diseases and 0.04 for bloat. The genetic correlation between bovine respiratory disease and umbilical diseases was 0.62. Significant associations between proofs for survival and health traits with proofs for routinely evaluated traits in Canada and the US were found. Results suggest that there are significant differences among Holstein sires for calf survival from weaning to the growing period and for calf health during the preweaning period.

Key Words: calf survival, calf health, multiple-trait model

929 Estimation of genetic parameters for workability traits. A. Sewalem*[1,2], F. Miglior[1,2], and G. Kistemaker[2], [1]*1Agriculture and Agri-Food Canada, Guelph Food Research Center*, *Guelph, ON, Canada*, [2]*Canadian Dairy Network*, *Guelph, ON, Canada*.

The aim of this study was to estimate the genetic parameters of milking temperament for Canadian Holsteins and to assess the correlation with other traits of economic importance. Cows were evaluated for this trait during milking and given a subjective score based on a 5 point linear scale (1 = Very Nervous, 2 = Nervous, 3 = Average, 4 = Calm and 5 = Very Calm). The phenotypic frequency of each score was 1.45%, 9.80%, 49.20%, 35.43% and 4.13%, respectively. The model included the fixed effects of herd-year, season of calving, age at calving, months in milk and random effects of animal and residual. The estimated additive genetic and residual variances were 0.0042 and 0.0285, respectively. The resulting heritability value was 0.128%. Correlations between bull EBV for milking temperament with EBV for production, type and other traits were calculated for the Holstein breed. Correlations were essentially low for production traits and functional herd life (0.038 - 0.048), favorable for most type traits (0.09 – 0.15) as well as milking speed (0.14) but undesirable for type traits related to feet and legs (−0.02), lactation persistency (−0.07), calving ease (−0.11) and somatic cell score (0.18). Low and undesirable correlations were also observed for most fertility traits (−0.026 to −0.114).

Key Words: milking temperament, variance component estimation, breeding value correlations

930 Health treatment rates of Holstein cows selected for large versus small body size. J. C. Becker*, B. J. Heins, G. D. Marx, and L. B. Hansen, *University of Minnesota*, *St. Paul*.

Holsteins selected for large versus small body size since 1966 were evaluated for incidence rates of health treatment from the Northwest Outreach and Research Center, Crookston, of the University of Minnesota. All health treatments were recorded for cows from 1983 to 2005. Treatments were recorded for 12 categories of health disorders. Records were for 544 first lactations, 366 s lactations, and 445 third and greater lactations, and the 3 lactation groups were analyzed separately. A chi-squared test was conducted separately for genetic lines for first, second and third and greater lactations. For first lactation, cows in the small line had significantly ($P < 0.01$) fewer displaced abomasums (5% versus 16%) and significantly ($P < 0.05$) less ketosis (5% versus 9%) than cows in the large line. The small line and large line did not differ significantly for mastitis, locomotion, milk fever, and early reproduction problems during first lactation. For second lactation, cows in the small line had significantly ($P < 0.05$) fewer hoof disorders (15% versus 24%), displaced abomasums (8% versus 2%), and respiratory disorders (0.5% versus 3%) than cows in the large line. The small line and large line did not differ significantly for mastitis, ketosis, milk fever, and early reproduction problems during second lactation. For third and greater lactations, cows in the small line had significantly ($P < 0.01$) fewer hoof disorders (17% versus 38%) than cows in the large line. Cows in the small and the large line did not differ significantly for incidence of mastitis, displaced abomasums, ketosis, milk fever, respiratory disorders, and early reproduction problems during third and greater lactations.

Key Words: body size, health traits, genetics

931 Sequential evaluation of longitudinal conformation data in dairy cows. N. Gengler*[1,2], S. Vanderick[1], and C. Bastin[1], [1]*University of Liège - Gembloux Agro-Bio Tech*, *Gembloux, Belgium*, [2]*National Fund for Scientific Research*, *Brussels, Belgium*.

Current genetic evaluation for Holstein type data in the Walloon Region of Belgium is based on a multi-trait animal model for repeated data and missing traits using a transformation based on multiple diagonalization. Currently used data covers 33 traits observed in all lactations if at least one classification was done for a given cow before it was considered mature. A total of 102,875 records were available for first parity and 30,378 records for second or later parities in January 2010. With a total of 117,013 classified cows, the number of repeated records was 16,240, with repetitions within and across lactations. Based on a request from the field and to make better use of available longitudinal data along an age at classification gradient, research was performed to develop an adapted model. In this study a random regression model was developed that was equivalent to a multi-lactation (first vs. later) model allowing repeated classifications inside parity but with some fixed effects spanning across parities. The random regressions were defined as constant and linear regressions on parity number −1. A 2 step approach was developed, for solving and variance components estimation. In this approach, a model based on the current genetic evaluation model modified to host single-trait random regressions was the first step. The second step consisted in the joint multiple-trait analysis of the meta-data (regression coefficients) provided by the first step. The proposed approach has very interesting potential for the analysis of data with large numbers of traits as trait reduction techniques can be integrated in the procedure.

Key Words: type traits, equivalent model, sequential evaluation

932 Fitness of Boer, Kiko, and Spanish does managed on humid, subtropical pasture in central Tennessee. R. Browning Jr.*[1] and M. L. Leite-Browning[2], [1]*Tennessee State University*, *Nashville*, [2]*Alabama A&M University*, *Huntsville*.

Records for Boer (n = 132), Kiko (n = 92), and Spanish (n = 79) does across 6 yr of production were processed to assess doe fitness traits among meat goat breeds when managed on southeastern US pastures. Does were mated in a complete 3-breed diallel each fall for spring kidding. A total of 1042 doe-yr units were observed with does ranging from 2 to 8 yr of age and managed together in a semi-intensive manner. Herd health records were analyzed for each production year. Does were treated for foot scald and foot rot upon observed lameness. The herd was not vaccinated for foot rot. Breeds differed ($P < 0.01$) for lameness cases treated during the year. Boer required more ($P < 0.01$) treatments for lameness (1.8 ± 0.1 cases/doe) than Kiko (0.6 ± 0.1 cases/doe) or Spanish (0.9 ± 0.1 cases/doe). A larger ($P < 0.01$) proportion of Boer required single (75 ± 5%) or multiple foot treatments (49 ± 4%) annually compared with Kiko (36 ± 5%; 17 ± 4%) or Spanish (45 ± 5%; 24 ± 4%). Does received a tactical anthelminic treatment at parturition. Individual does presenting clinical symptoms of endoparasitism during the year received need-based treatment. Breeds differed ($P < 0.01$) for need-based anthelmintic treatment. Need-based dewormings were more numerous for Boer (0.8 ± 0.1 cases/doe) than for Kiko (0.4 ± 0.1 cases/doe) or Spanish (0.3 ± 0.1 cases/doe). A larger ($P < 0.01$) proportion of Boer required single (53 ± 4%) or multiple need-based dewormings (23 ± 4%) per year compared with Kiko (26 ± 4%; 4 ± 3%) or Spanish (23 ± 3%; 7 ± 2%). Fecal egg counts to assess endoparasite loads 3 mo postpartum were higher ($P < 0.01$) for Boer dams (660 eggs/g) than for Spanish dams (362 eggs/g); Kiko dams were intermediate (500 eggs/g). A smaller proportion ($P < 0.01$) of Boer does weaned 3-mo-old kids (49 ± 3%) and stayed in the herd (64 ± 3%) annually compared with Kiko (78 ± 3%, 85 ± 2%) and Spanish does (77 ± 3%, 84 ± 2%). Significant differences were evident among meat goat breeds for doe fitness under southeastern US pasture conditions.

Key Words: meat goats, breed, fitness

Companion Animals Symposium: Comparative Enrichment: Implications for Health and Behavior

933 The role of training and enrichment. C. Dikeman*, *Omaha's Henry Doorly Zoo*, *Omaha, NE*.

Animal scientists have an extraordinary burden to promote the health and well-being of all animals in their care. With more than 100 million guests visiting zoos, and the US companion-animal population extending to well over 350 million, the role humans play in promoting the health and well-being of companion and exotic animals in captivity is increasingly important. Additionally, an estimated 6–8 million dogs and cats enter US animal shelters annually, with many of those animals surrendered by owners for behavioral problems. Promoting species, or breed appropriate behaviors through proper training and environmental enrichment, regardless of animal housing, should be a paramount concern for all animal scientists working with livestock, exotic animals, laboratory animals, shelter animals, or privately owned pet animals. Improving the psychological well-being of an animal can improve the viability that animal has to a program and could aid in the reduction of owner surrendered animals to shelters. The objectives of this symposium will be to explore the important role that training and environmental enrichment provide to captive and companion animals including shelter animals, laboratory animals, pets, and zoo animals, and to encourage and promote the development of training and enrichment protocols and ideals within animal science and husbandry programs.

Key Words: training, enrichment, behavior

934 Animals make us human: A look at the emotional lives of animals. T. Grandin*, *Colorado State University*, *Fort Collins*.

Some scientists may question if animals have true emotions similar to humans. Research clearly shows that the emotional systems in all mammals are similar. Human psychiatric drugs such as Prozac have similar effects on dogs. All mammals have the same neurotransmitters and similar subcortical brain structures where the emotional systems are located. The basic emotional systems in mammals have been extensively mapped. Unfortunately, most of these studies are in the neuroscience literature that is seldom read by animal scientists and veterinarians. The emotional circuits for fear have been the most studied. Lesioning the amygdala will block both conditioned and unconditioned fear behaviors. Jaak Panksepp has identified 3 other core emotional systems of seeking (approaching a novel stimulus), rage, and panic (separation anxiety). He also lists 3 additional emotional systems of play, lust (sex drive), and care (mother young nurturing behavior). Neuroscientists have located the specific subcortical brain regions that control these emotional systems. Animals in barren environments will often engage in repetitive stereotypical behavior. Figuring out which emotional system is driving their behavior will make it possible to design more effective environmental enrichments. For example, a gerbil will often engage in repetitive digging that still continues after the gerbil is given more substrate to dig in. The digging behavior stops when the gerbil is given a shelter so it is hidden from aerial predators in the sky. This behavior is driven by an instinctual fear of predation. The gerbil futilely keeps digging unless it is given enough substrate to form a hiding place. An understanding of the emotional systems that are driving a behavior will greatly improve animal welfare.

Key Words: environmental enrichment, animal welfare, emotion

935 Bringing out their wild side—Enriching the lives of captive exotic animals. M. S. Edwards*, *California Polytechnic State University*, *San Luis Obispo*.

Enrichment is a dynamic process for enhancing animal environments within the context of a species' behavioral biology and natural history. The goal of environmental changes is to increase the animal's behavioral choices and draw out species–appropriate behaviors, thus enhancing animal welfare (AZA Behavior Scientific Advisory Group, 1999). Application of management techniques encouraging species–typical behavior is not a recent phenomenon among animal care professionals, yet significant expansion in the field began in the 1980s (Mellen and MacPhee, 2001). Not unlike the integration of animal health, reproduction or nutrition sciences into exotic animal husbandry, current application and systematic review of environmental enrichment practices is objectively based in disciplines of ethology, psychology and animal science (Shepherdson, 1998). The inherent value of enrichment to captive exotic animal welfare is recognized by both regulatory and professional organizations. USDA regulation of environmental enhancement to promote psychological well–being of nonhuman primates was adopted in 1991 (9 CFR 3.81). Institutions accredited by the Association of Zoos and Aquariums are required to have a formal written enrichment program that promotes species–appropriate behavioral opportunities (AZA, 2010). Potential enrichment techniques are as diverse as a species′ behavioral repertoire. Success of enrichment efforts are enhanced when approached systematically. Goal definition, program implementation, documentation of response criteria to facilitate objective evaluation and continued refinement are hallmarks of a self-sustaining enrichment program (Mellen and MacPhee, 2001). Complex environments and enrichment techniques are not inconsistent with visitor recreation, wildlife conservation, and conveying an education message. Methods based in enrichment implementation and evaluation have been utilized to enhance visitor experience and advance institutional goals (Kuhar et al., 2010). Natural history and biology define physiological and psychological boundaries within which science-based enrichment, inseparable from animal husbandry, operates.

Key Words: nondomestic, zoo, welfare

936 Improving the lives of laboratory dogs and cats through enrichment and training. B. M. Vester Boler*, *University of Illinois*, *Urbana*.

In 2007, over 22,000 cats and 72,000 dogs were used for animal research in the United States. Current housing guidelines are written for the welfare of these animals, but some undesirable behaviors persist. Providing supplemental enrichment may help lessen unwanted behaviors, such as destructiveness, aggression toward humans and other animals, stereotypies, and self-mutilation. Because the animals are in a research setting, however, toys used for enrichment must meet a specific set of standards, including being able to be cleaned and sanitized, not influencing study results (e.g., consumption during nutritional studies), and safe for the animal to play with while unsupervised. Social interaction within the colony and with humans also appears to be beneficial, leading to decreased stereotypies, less vocalization, reduced stress for the animal and caretakers, and even beneficial effects in cognitive health of aged animals. It is suggested, but not well studied, that training of laboratory animals for routine procedures and as a means of social interaction with humans also may be beneficial. Training of simple commands has been

used in shelters to decrease return relinquishments; as such, laboratory facilities that put their animals up for adoption upon completion of studies may benefit from similar training. In conclusion, more can be done beyond the minimum standards required for laboratory dog and cat housing and socialization that will benefit the animal caretakers and the animals themselves. Finding behavioral and social enrichment activities that meet the requirements of the animal facilities and the research program are vital for sustainability and success.

Key Words: laboratory dogs, enrichment, laboratory cats

937 Do our pets live enriched lives? C. Dikeman*, *Omaha's Henry Doorly Zoo*, *Omaha, NE.*

With over 170 million cats and dogs residing in US households, it seems a contradiction that the question about their husbandry should even be considered a topic for discussion. An estimated 8 million pets enter animal shelters annually with a high percentage of those facing euthanasia. Studies have indicated behavior problems in pets as main causes of owner relinquishments to shelters. Aggression (51%), and inappropriate elimination (43%) were reported as the main causes of owner relinquishments of dogs and cats, respectively (Salman et al., 2000). Both problems may be attributed to the misunderstanding and mismanagement of natural species-appropriate behavioral development. While humans have evolved to share an increasing social bond with these species, we have not mastered the husbandry of living with species of the order Carnivora. While this order is diverse, all carnivores are predatory. Innate carnivorous behavioral patterns include communication, social and territorial, and predatory behaviors (Case 1999, 2003). Carnivores have evolved with keen visual, olfactory, and auditory senses, in addition to musculoskeletal adaptations, that support their predatory ancestry. If one considers the natural history of the canine and feline, including the deliberate breeding to produce breeds displaying unique phenotypes, and temperaments, it becomes clear that our pampered pets live typical lifestyles that fail to support the innate behavioral patterns that naturally dictate their behaviors. Many behavioral problems in pets may be prevented by providing environments that support their species-appropriate natural behaviors. Environmental enrichment is a process for enhancing environments that support behavioral biology (Young, 2003). The concept of providing for psychological well being has been a focus of captive animal management for the last several decades; however, its application in the management and husbandry of domestic pets has not been well studied or applied. Five types of environmental enrichment (social, occupational, physical, sensory, and nutritional) can be utilized in common households to enhance the well-being of our pets, thus promoting the human-animal bond.

Key Words: behavior, enrichment, companion animals

938 Bird Enrichment—Above and Beyond. E. Insalaco*, *Denver Zoo*, *Denver, CO*.

Enrichment is a process through which changes to an environment are made with the goal of modifying behavior in an animal. This usually involves encouraging natural, species specific behavior, or discouraging inappropriate behavior. At Denver Zoo, the purpose of our facility wide behavior program is to ensure that behavioral components are incorporated into all animal care. Advances in enrichment and other behavioral practices are often seen in mammal care programs more often that those of other taxa, including birds. However, there are opportunities for avian enrichment and behavior management that are equally as effective and advantageous as those we have seen in mammalian programming. This presentation will talk about the Denver Zoo behavioral husbandry framework and philosophy, and how it applies to all taxa. In addition, the presentation will focus on behavior programs that have been implemented with several bird species both at Denver Zoo and other facilities, and will look at not only enrichment, but at training and behavior research opportunities as well.

939 Training and enrichment: Stepping into the future. N. Irlbeck*[1,2], [1]*Colorado State University*, *Fort Collins,* [2]*Denver Zoological Gardens*, *Denver*.

Several years ago I had the privilege of working with Dr. Temple Grandin on a project at the Denver Zoo. The goal of the project was to determine vitamin E status of nyala and bongo at the zoo. Temple wanted to develop a crate to restrain the animals so they could be bled. For valid samples the animals needed to be bled in a stress-free state. When requesting permission to work with the 2 antelope, zoo administrators argued with Temple that they were wild animals and that what she wanted to do could not be done. Temple persisted and eventually they acquiesced to letting her try. Temple and her students use operant conditioning to gradually coax the animals into the crate and allow them to be bled. If the animals allowed this behavior without avoidance, they were rewarded with a food candy treat. It worked! Fast forward 15 years and the students of today have grown up in an environment where Animal Planet and Walt Disney are household phrases. Because less than 2% of today's population has anything to do with animal agriculture, these young men and women may have experiences with a dog, cat or at most a horse. And yet, the yearnings to work with animals cannot be denied and under the influence of media many seek to work with exotic species. Because of minimal animal experiences in other than home or family settings, young people tend toward a more anthropomorphic attitude when handling animals. These anthropomorphic tendencies have the potential of creating a more emotional response when working and dealing with animals. Public outcry over horse slaughter is a perfect example. The protection of animals was originally legislated in 1966 under the auspices of the Animal Welfare Act. With the merging of a population of young men and women that view animals as part of their family, along with a greater public awareness of animal handling, the animal-human bond has become increasingly important. There is a need to facilitate a safe interaction between human and animals. Training and behavioral enrichment are just 2 steps on the path to creating a more mentally stimulating environment for animal species.

Key Words: training, enrichment

CSAS Symposium: Issues in North American livestock transport

940 Effects of vehicle design on the welfare and meat quality of pigs under Canadian transport conditions. L. Faucitano*[1], S. Torrey[1], R. Bergeron[2], T. Widowski[2], T. Crowe[4], J. A. Correa[3], J. P. Laforest[3], E. Tamminga[2], and H. W. Gonyou[5], [1]*Agriculture & Agri-Food Canada*, *Sherbrooke, QC, Canada*, [2]*University of Guelph*, *Guelph, ON, Canada*, [3]*Laval University*, *Quebec City, QC, Canada*, [4]*University of Saskatchewan*, *Saskatoon, SK, Canada*, [5]*Prairie Swine Centre*, *Saskatoon, SK, Canada*.

It is generally acknowledged that pot-belly (PB) trailers and some specific compartments within this vehicle are worse than others in terms of animal losses. However, there is no real alternative truck with such a large loading capacity (230 pigs). Furthermore, the effect of each compartment on animal welfare has not been clearly established. The effects of the PB trailer design on the stress response and meat quality of pigs was studied between June 2007 and July 2008 within a large pan-Canadian study on swine transportation. Twenty-three transport trials were conducted in Quebec and in the Prairies in 2 different seasons of the year (summer and winter). In the Quebec trials, a PB trailer was compared with a double-decked (DD) truck equipped with a moving upper deck during 2 h transportation. In the Western trials, the PB trailer alone was evaluated during 8 h transportation. In the Quebec trials, higher ($P < 0.05$) digestive tract temperatures (DTT) were recorded in the PB trailer for pigs located on the top deck while waiting at the farm in both seasons, and in pigs located in the rear compartments of the top and middle decks during transport in summer. Unloading from the PB trailer took longer ($P < 0.001$) than from the DD truck and took longer from the upper deck compartments, especially in summer. Higher pHu values were found in the loin and ham muscles ($P < 0.01$ and $P < 0.001$, respectively) of pigs transported on the PB trailer compared with the DD truck. In the Western trials, higher ($P < 0.05$) DDT were recorded in pigs located in the rear compartments of the top deck and of the belly before departure from the farm. Loading took longer ($P < 0.05$) for the bottom-nose and top deck in summer and for the belly in winter. Unloading took longer ($P < 0.001$) from these same locations, regardless of the season. Loin and ham pHu values were higher and drip loss values lower in pigs located in the bottom-nose ($P < 0.05$). In conclusion, it appears that the effects of PB design on animal welfare and meat quality in pigs are related to the greater exertion required to negotiate the multiple internal ramps and poor ventilation at some locations.

Key Words: transport, stress, pork quality

941 Contributions of research to the practical aspects concerning long-term road transport of horses. C. L. Stull*, *University of California, Davis*.

Road transport is a common practice in many facets of the horse industry including sport and competitive events, breeding programs, marketing and slaughter channels, and biomedical purposes. The physiological and behavioral responses of horses have been recently studied with contributing factors such as duration, space allowance, cross-tying restraint, feed and water availability, injuries, trailer design, and environmental factors. Data collected (1998) on 306 slaughter horses showed these horses to generally be Quarter Horses or Thoroughbred breeds with a mean age of 11.4 + 0.4 years old and mean weight of 432 + 3.3 kg. The number of injuries sustained was 3.5 times greater ($P < 0.05$) in double-deck (29%) compared with single deck semi-trailers (8%). Stress parameters such as cortisol, immune, or body weight showed smaller responses ($P < 0.05$) between pre- and post-transport samples with horses provided with higher floor area (1.4 to 1.54 m^2/horse). As trip duration increased from approximately 6 to 30 h, muscle fatigue and dehydration were incrementally increased, especially during trips over 27 h. Both engineering- and performance-based standards were developed from research studies and implemented in the federal regulations to ensure the humane movement of equines to slaughter facilities within the US and into Canada. The practice of cross-tying horses individually in stalls is common during road transport of race and show horses. A study designed to compare cross-tied horses with horses traveling loose in small compartments for 24 h showed elevations ($P < 0.05$) in cortisol concentrations, white blood cell counts, and glucose concentrations in the cross-tied horses during transport and recovery. The study supports allowing horses to travel loose in small compartments without elevating their heads by cross-tying. Data from these studies and previous studies suggest that long-term road transportation compromises immune function, thus predisposing transported horses to respiratory disorders.

Key Words: equine, transport, stress

942 Cattle transport in North America—Current welfare research and future directions. K. S. Schwartzkopf-Genswein*[1], L. A. González[2], and T. Crowe[3], [1]*Agriculture and Agri-Food Canada*, *Lethbridge, Alberta, Canada*, [2]*University of Manitoba*, *Winnipeg, Manitoba, Canada*, [3]*University of Saskatchewan*, *Saskatoon, Saskatchewan, Canada*.

The transport of live cattle is known to be stressful and therefore can have a direct impact on animal production and welfare, and on food safety and quality. Consequently, there has been increased focus on animal welfare during transport at an international level, in both legislation and trade discussions. Unfortunately few studies assessing the impact of transport on cattle under North American conditions are available from which to provide science-based information to the industry, policy makers and trade personnel. Understanding the objectives, challenges and constraints of current industry practices is integral in designing relevant scientific studies to assess the effects of transport on animal well-being. The combination of human, animal and environmental factors needs to be carefully considered and include: animal handling at loading and unloading, driver experience and training, delays during transport; cattle age, breed, sex, health and physiological status; climate and microclimate, trailer design, loading density, length and condition of transport and condition. All these factors will affect production, body weight loss, morbidity and mortality during and after transport (e.g., lameness and downer animals, incidence of disease), and meat quality and safety. Research is needed to access the inter-relationships between these factors in a systematic fashion. Simulated as well as commercial transport studies that employ animal and microclimate monitoring will aid in facilitating such research.

Key Words: cattle, transport, welfare

943 Conditions within B-train trailers transporting broiler chickens in Western Canada. N. A. Burlinguette, J. M. Watts, L. J. Graff, M. L. Strawford, K. P. C. Hui, T. G. Crowe*, H. L. Classen, and P. J. Shand, *University of Saskatchewan*, *Saskatoon, Saskatchewan, Canada*.

Conditions within commercial trailers transporting broiler chickens were recorded during travel from production site to processing facility. Data were collected for typical commercial trailer vent and tarp settings

for B-train trailers used in Western Canada, over a range of ambient conditions from −20°C to +10°C, on 14 separate occasions. Data loggers, capable of recording temperature and humidity, were positioned throughout the trailers and programmed to record conditions at 1-min intervals. Data were analyzed to characterize the conditions within the trailers and to identify locations where extremes occurred. The difference between the on-truck conditions (temperatures and humidity levels) and the respective ambient conditions were calculated for each sensor and grouped by truck vent and tarp configuration. Temperature and humidity gradients within the trailers were visualized using 3-D mapping software. During the summer, temperatures and humidity levels followed the ambient conditions with modest accumulations of heat and moisture. Minimal gradients in temperature and humidity were present, when both sides of the cargo area were exposed. Gradients in temperature were much more pronounced during the winter, when tarps covered the sides of the loads. While the vent configurations had an effect on the temperatures and humidity levels within the load, some general trends did emerge. When both tarps were lowered (colder ambient conditions), heat tended to accumulate, resulting in a relative warm spot, near the front along the midline of the front trailer. Localized warm conditions developed along the midline, near the rear of the second trailer. Cold regions within the load were restricted to areas adjacent to the side tarps, where cold air could infiltrate into the load, particularly along the sides of the load at the rear and bottom of the front trailer plus the front and bottom of the rear trailer. The air within the load was more humid under cold ambient conditions.

Key Words: transportation, broiler chickens

944 Fatigue: a major cause of commercial livestock truck accidents. J. A. Woods*, *J. Woods Livestock Services*, *Blackie, Alberta, Canada*.

Between 1994 and June 2007, accident reports on 415 commercial livestock truck accidents were tabulated in the United States and Canada. The objective of the data collection was to establish the most common cause of commercial accidents involving livestock and determine if there were specific high risk loads to provide accident prevention education and identify possible future research needs. Data was collected from internet searches, Google alerts, news reports, newspaper articles, industry sources, and government agencies. Tabulated data included time of day, month of the year, animal species and type, position of trailer following the accident, average death loss, location of the accident, number of vehicles involved, cause of accident and trailer style. Not all of the reports contained all of the information. Fifty-six percent of the accidents involved cattle, 27% involved pigs, 11% poultry and the balance were other species. Double deck, "pot belly" trailers, were the most common trailer configurations accounting for 73%. Double, straight deck trailers were involved in 12% of the accidents. October, followed by November were the most common months for accidents, with July documenting the least amount of accidents. Weather had relatively little effect on the number of accidents compared to other factors. Evaluation of the data showed that 59% of the accidents occurred during the early morning hours between midnight and 9:00 am while 80% involved a single vehicle. Driver error was blamed for 85% of the wrecks. The data showed that in 83% of the accidents the trailer rolled over onto their side and of those, 84% tipped over on their right side. This data is consistent with circumstances linked to fatigue related motor vehicle accidents. It was determined that drivers fatigue was the leading cause of commercial livestock truck accidents in North America. Recommendations from this study are to incorporate fatigue management programs into livestock transporter training programs, industry literature and company policies. Future research recommendations include trailer design modifications and loading configurations.

Key Words: accidents, livestock, transportation

945 Renneting properties of milk containing high molecular weight oat β–glucan. N. Sharafbafi*[1], S. M. Tosh[2], M. Alexander[1], and M. Corredig[1], [1]*University of Guelph*, *Guelph, Ontario, Canada*, [2]*Agriculture Agri-Food Canada*, *Guelph, Ontario, Canada*.

The effect of concentration and molecular structure of high molecular weight oat β–Glucan (BG) on renneting properties of concentrated skim milk gels were investigated. Incorporation of BG (0.15, 0.3, 0.6, and 0.9% w/w in permeate) into twice-concentrated skim milk resulted in bulk phase separation of gelling systems as shown by reduction in turbidity parameter (1/l*) and diffusion coefficient using diffusing wave spectroscopy (DWS). However, by controlling the kinetics of gelation and phase separation (using shear in renneted milk before BG addition), it was possible to create casein networks with entrapped BG. $CaCl_2$ was added to reduce time of gelation (TG), and increase textural properties, where high concentrations of BG (≥0.6%) resulted in weakening of protein gel network. The effects of shear and the presence of $CaCl_2$ on microstructure and rheological behavior of the renneted gels containing BG were monitored using DWS combined with small deformation rheology. In addition, BG distribution in the rennet gel network was observed by differential staining technique, (Calcofluor and Rhodamine B, for BG and protein, respectively) using confocal laser scanning microscopy. The results showed that the onset of protein interactions, illustrated by the turbidity parameter, and the aggregation point, measured by the diffusion coefficient, were strongly affected by increase in BG concentration. BG-containing gels exhibited a significantly lower elastic modulus (G′) compared with their control counterparts ($P \leq 0.05$). Increase in BG concentration delayed the TG, and reduced gel firmness due to the non-interacting nature of the BG polymer. In contrast, the addition of $CaCl_2$ reduced the TG and produced a firmer gel in both control and BG added samples. BG addition could improve the texture and nutritional value of calorie-reduced cheeses, whose hard texture has traditionally been a barrier to their production.

Key Words: beta-glucan, gelation, rheology

946 Interactions of milk proteins with tea polyphenols. S. Haratifar*, G. Paliyath, and M. Corredig, *University of Guelph*, *Ontario, Canada*.

Few reports are available on the effects of polyphenols when present in milk. A recent study has claimed that the presence of milk decreases the content and the bioavailability of polyphenols during in vitro digestion (Cilla et al., Food Chemistry, 2009). However, little attention has been paid to the interactions occurring between casein micelles and polyphenols. The objectives of this study were to observe the impact of the protein/polyphenol interaction on the functional properties of milk such as enzyme renneting as well as observing the impact on the tea polyphenol bioavailability. The molecular details of the interactions between tea polyphenols and milk proteins were quantified using reverse phase C18 HPLC. Tea polyphenols strongly interact with casein micelles and result in low recoveries especially at lower concentrations of polyphenols, but it does not necessarily cause low bioavailability. This was confirmed also by measuring in vitro digests. The effect of the interactions of different concentrations of tea polyphenols on rennet induced aggregation of milk was studied. The experiments were carried out using a controlled stress rheometer at a constant strain of 0.01 and frequency of 1 Hz at 30°C. A frequency sweep test was run after the gelling of the samples until 80min to determine the frequency dependence of the elastic (G′) and viscous modulus (G″) of the gels. The gelation point was determined as the onset of the increase in the G′. The results showed that at low concentrations of tea polyphenols (<0.25mg/ml, i.e., below saturation of the casein micelles), the G′ modulus increased similarly to that of control milk (35 min ± 5). At higher concentrations, the polyphenols not only delayed the gelling point of milk to 60 min ± 4, but they also affected the structure formation, as could be noted by a lower G′ of the mixture compared with milk. These experiments clearly identify the need for a better understanding of the effect of tea polyphenols on the functionality of casein micelles, before milk can be used as an appropriate platform for delivery of bioactive compounds.

Key Words: polyphenols, interactions, gelling

947 Anticarcinogenic properties of milk fat globule membrane. R. Zanabria*[1], A. M. Tellez[1,2], M. Griffiths[2,1], and M. Corredig[1], [1]*University of Guelph*, *Guelph, ON, Canada*, [2]*Canadian Research Institute for Food Safety (CRIFS)*, *Guelph, ON, Canada*.

Milk fat globule membrane (MFGM) comprises a tri-layer mixture of glycoproteins, phospholipids and enzymes which protects fat globules from coalescence and enzymatic degradation. Though present in small amounts, MFGM is the main source of polar lipids in milk (65%) and it is one of the major components of buttermilk, the by-product of butter manufacture. Objective of this work was to determine the effect of MFGM on the proliferation of a human adenocarcinoma cell line. Milk was collected using a catheter from healthy animals to minimize bacterial contamination and lipopolysaccharide (LPS) presence, and the cream separated by centrifugation. MFGM fractions were isolated washing the cream twice with endotoxin free water and consecutive freeze-thawing and ultracentrifugation. The bioactivity of MFGM isolate on the HT-29 cell line was tested after verifying LPS-absence using the Chromogenic endpoint test. Two different methods were employed to test the MFGM effect on cell proliferation. The BrdU colorimetric test revealed a dose-dependent DNA synthesis decrease in exponentially growing cells exposed to 10 μg of MFGM protein/mL. Up to 53% inhibition was measured after 72h when 100 μg of MFGM protein/mL was used. The results were corroborated using the Sulforhodamine B proliferation assay. In the latter, the amount of MFGM required to produce the same effect almost doubled (200 μg MFGM protein/mL achieved a 57% reduction) after 48h incubation. When cells were similarly treated with commercially available anticarcinogenic compounds (0.1mM/L melphalan and 20 μmol/ L N-Acetyl-D-sphingosine) the reduction in cell growth was 25 and 40% respectively; hence, showing the potential bioactivity capacity of the raw MFGM fractions. Though the study of the mechanism whereby untreated MFGM exerts its anticarcinogenic activity is still undergoing, the results indicate that MFGM isolates have an inhibitory effect on colon cancer cells, most likely through the extracellular signaling pathways. Analyses are in progress to evaluate apoptosis and/or differentiation as possible causes for these properties along with the effect of milk processing over the MFGM bioactivity.

Key Words: milk fat globule membrane, anticarcinogenic, bioactivity

948 Gelation properties of casein micelles during combined renneting and mesophilic bacterial fermentation: Effect of concentration by ultrafiltration. E. Salvatore*[1,2], M. Alexander[2], A. Pirisi[1], and M. Corredig[2], [1]*Agris Sardegna, Dipartimento per la Ricerca nelle Produzi-*

oni Animali, *Olmedo, Italy*, [2]*Department of Food Science, University of Guelph*, *Guelph, Ontario, Canada*.

The objective of this study was to determine the effect of concentration of milk by ultrafiltration on the rheological and chemical properties of combined cultured and rennet milk gels. Pasteurized skim milk (1X; control) with ≈3.7% of total protein was concentrated by ultrafiltration to produce retentates with protein levels of ≈7.4% (2X), and ≈11.1% (3X). All samples were acidified with a mesophilic lactic culture (0.1 g/L), renneted with liquid rennet at a final concentration of 0.00296 IMCU/mL, and incubated at 30°C. Acidification was monitored by recording the pH continuously over the gelation period, and the development of the gel structure was observed by means of small deformation rheology and diffusing wave spectroscopy (DWS). Furthermore, the levels of soluble Ca^{++} were determined during incubation period. The gelation time, defined as the point when the loss tangent (tan δ) = 1, was between 105 and 109 min, corresponding to a pH value of ≈6.5, and was not significantly different among the samples ($P > 0.05$). When measured by DWS, the gelation point was almost superimposable with that found in the rheological measurements. After gelation, the value of G′ showed a significant increase up to pH 5.64, 5.92, 6.18 for 1X, 2X and 3X respectively, and these values were significantly different among treatments ($P < 0.05$). Significant differences ($P < 0.05$) were also found in the pH at maximum value of tan δ. The values of soluble Ca^{++} suggested that the variations between samples were due to the different rates of release of Ca^{++} from the casein micelles. The results clearly show the details of the changes occurring during a mixed coagulation process and allow for a better understanding of the physical and chemical processes that happen during the making of quark-type cheeses.

Key Words: milk gels, rheological properties, light scattering

949 Production of α-lactalbumin enriched concentrate from serum whey. C. Marella*, P. Salunke, L. E. Metzger, and K. Muthukumarappan, *Midwest Dairy Foods Research Center, South Dakota State University*, *Brookings*.

Whey proteins are known for their valuable functional, nutritional and therapeutic properties. Bovine α-Lactalbumin (α-LA) has high homology to human α-LA and has well documented therapeutic uses. Hence development of α-La concentrate with reduced levels of β-lactoglobulin (β-LG) is of high interest to manufacturers of infant formula and whey protein based therapeutic formula. In production of α-LA enriched WPC from cheese whey, the purity of α-LA in the final product is heavily influenced by the presence of glycomacropeptide. Serum whey produced by microfiltration of milk is largely absent in glycomacropeptide. Production of α-LA enriched concentrate from serum whey should result into higher purity and yield. The objective of the present study was to develop α-LA enriched concentrate from serum whey. Wide pore Ultrafiltration experiments were conducted using four (30, 40, 100 kD polyvinylidene fluoride and 300 kD polyethersulfone) membranes and three levels of operating pressure (138, 207 and 276 kilo Pascal (kPa)). In the process serum whey was concentrated to a volume reduction (VR) of 5 and 10. Purity, yield of α-LA and α-LA/ β-LG ratio were used as the parameters indicative of process efficiency. At VR of 5, purity of α-LA obtained in the permeate stream ranged from 52 – 96% while the yield of α-LA ranged from 15-55%. At VR of 10, there was a marginal decrease of 3-7% in purity and 20 – 35% increase in yield of α-LA. For separation of α-LA from serum whey there appears to be an optimum operating pressure. From the present results, it appears that 207 kPa pressure is optimum resulting into a 10-25% higher yield when compared to the yield obtained at other pressures used in this study. The results from this study will be helpful in production of highly purified α-LA enriched concentrate from serum whey. Regardless of the membrane used in this study, use of 207 kPa operating pressure resulted in α-La enriched product with purity ranging from 52 – 96%.

Key Words: α-lactalbumin, wide pore ultrafiltration, serum whey

950 Evaluation of correlations between chemical compositions and sensory properties in Turkish Set-type yogurts. Z. Guler[1] and Y. W. Park*[2], [1]*Mustafa Kemal University*, *31034 Antakya, Hatay, Turkey*, [2]*Fort Valley State University*, *Fort Valley, GA*.

Food quality of yogurt is affected by many factors, including levels of titrable acidity, free fatty acid, aroma compounds, nutritional values, and sensory properties. Ten most popular brands of commercial Turkish set-type yogurts were collected from retail outlets in Hatay, Turkey to determine correlations between chemical compositions and sensory properties of the products. Free fatty acids (FFA) and volatile compounds (VC) were analyzed using a GC-MS (Agilent GC model 6890) and MS (Agilent Mass Selective Detector 5973 N; Palo Alto, CA, USA). Columns used for FFA and VC separation were DB-FFAP-column (30 m × 0.25mm id × 0.25μm film thickness) and HP-INNOWAX capillary column (30 m × 0.32mm id × 0.25μm film thickness), respectively. Intensities and overall acceptability of sensory attributes were measured on 4-point and 9-point hedonic scales. The results revealed that increased volatile compounds (acetaldehyde, acetic acid) and acidity attributed to sour flavor, resulting in decreased overall acceptability of the yogurts. Aromatic volatiles such as 2-nonanone (fruity, musty), 2-tridecanone (fruity, green) and ethyl acetate (fruity) were negatively correlated, whereas diacetyl, C4 to C12 FFA and texture were positively correlated with overall acceptability. 2-Nanonane was negatively correlated with atypical flavor, since ketones having higher carbon numbers are responsible for heated milk flavor. Butanoic (rancid, cheesy), hexanoic (pungent, sour), octanoic (waxy, goaty), decanoic (rancid, fatty) and dodecanoic (fatty) acids were positively correlated with overall acceptability and formation of the specific aromatic flavors of set-type Turkish yogurts. Yogurt flavor intensity appeared to be closely related to titratable acidity, acetic acid, C4 to C10 content, ratio of acetaldehyde to diacetyl, and to a lesser extent to fat and protein contents.

Key Words: Turkish yogurt, chemical composition, sensory property

951 Wooden vat to produce PDO Ragusano cheese is a living system. G. Licitra*[1,2], L. Tuminello[2], N. Fucà[2], P. Campo[2], S. Lortal[3], and S. Carpino[2], [1]*D.A.C.P.A. University of Catania*, *Catania, Italy*, [2]*CoRFiLaC, Regione Siciliana*, *Ragusa, Italy*, [3]*UMR Science et Technologie du Lait et de l'Oeuf*, *Rennes Cedex, France*.

Tina is the traditional wooden vat daily used for the cheese making process of the P.D.O. Ragusano cheese. A previous study has shown the biofilm microstructure and has demonstrated the safety and efficiency of the *tina* as natural inoculation system in the cheese making process. Ragusano cheese is produced from November to May, when native pastures are available; so the *tina* is not used during the summer period. The aim of the present work was to verify the presence and survival of the biofilm on the inner surface of the dried inactive *tina*. Samples were taken, in October, from 2 dried *tinas* belonging to 2 different farms; the biofilm of those *tinas* had been previously (Lortal et al., 2009) analyzed when the same *tinas* were used for the Ragusano cheese production. By using a sterile blade 2 small wood micropieces (15 × 5 × 1 mm about) were removed from 2 opposite sides of the internal surface of each *tina*. *Tina* samples were analyzed by scanning electron (SEM) and confocal laser scanning microscope (CLSM). SEM and CLSM images showed a rich biofilm constituted by big and close microbial communities immersed in an abundant exopolysaccharide matrix which provides the necessary nutrients to the bacteria and protects them from the external environmental conditions. CLSM images highlighted that biofilm is mainly made of live bacteria. Heterogeneous bacterial colonies cover uniformly the whole surface of the *tina* forming a compact multilayered biofilm with a thickness of about 20 - 30 µm. The biofilm goes through the surface in the external wood vessels which look fully stuffed by bacteria and exopolysaccharide matrix. SEM images showed also the presence of biofilm inside the *tina* sample as far as 400–600 µm from the surface. This study demonstrated that at the end of the summer period a microbial biofilm still survives and maintains an intact and well organized structure.

Key Words: biofilm, wooden vat, Ragusano cheese

952 Survival of *Lactobacillus acidophilus* in Boursin-like cheese after gastric and enteric conditions in vitro. A. M. Liserre*[1], P. B. Zacarchenco[1], K. M. O. dos Santos[2], F. C. A. Buriti[2], L. S. Gonçalves[1], and L. R. Monteiro[1], [1]*Instituto Tecnologia Alimentos. Av. Brasil*, *Campinas, SP, Brasil*, [2]*EMBRAPA, Centro Nacional de Pesquisa de Caprinos e Ovinos*, *Sobral, Ceará, Brasil*.

In this study, Boursin-like cheeses were made from goat's milk at the facilities of EMBRAPA Caprinos (Brazilian Agricultural Research Corporation) in the town of Sobral, Brazil. The objective was the evaluation of the survival of probiotics in the cheese after treatment in simulated gastric and enteric juices. The cheeses added with *Lactobacillus acidophilus* were evaluated after 14 d refrigerated storage to quantify the surviving probiotics after treatment simulating gastrointestinal conditions. For this purpose, cheese samples were added to an acid solution at pH 2.5 containing pepsin (3g/L) for 120 min. Next, the pH was changed to 5.6 for another 120 min and finally changed to pH 7.5 for the last 120 min. During the enteric fluid simulation steps the samples were additionally added with bile in a proportion adequate to obtain a final concentration of 3g/L, so as to simulate small intestine conditions. Probiotic counts in the cheese samples after 14 d storage were 7.74 log CFU/g. After the test simulating gastrointestinal conditions, the counts had been reduced to 4.02, 2.42 and <2.00 log (detection limit) CFU/g in the cheeses exposed to gastric (pH 2.5) and enteric (pH 5.6 and pH 7.5) fluids, respectively. Brazilian legislation requires a minimum of 10^8 to 10^9 viable cells per daily portion of a probiotic product. The portion size of 30g of the cheese contained around 10^8 viable cells before the simulation tests but, after action of the gastrointestinal juices the counts were lower than the detection limit of the test, yielding an unsatisfactory result.

Key Words: probiotic, goat milk, cheese

953 Addition of probiotic bacteria modifies the biodiversity of other lactic acid bacteria in Cheddar cheese. B. Ganesan*[4,3], B. C. Weimer[1], G. Rompato[2], J. Pinzon[1], P. Desai[2,3], C. Brothersen[4,3], and D. J. McMahon[4,3], [1]*University of California*, *Davis,* [2]*Center for Integrated BioSystems, Utah State University*, *Logan,* [3]*Department of Nutrition, Dietetics, and Food Sciences, Utah State University*, *Logan,* [4]*Western Dairy Center, Utah State University*, *Logan*.

Bacteria in cheese face abiotic stresses during manufacture and storage that impact their abilities to produce flavors, survive, and interact with other bacterial populations. Apart from the added starter cultures non-starter lactic acid bacteria (NSLAB) are derived from milk handling, cheese equipment, and human contact. Occasionally, flavor adjunct bacteria are added at the beginning of cheese manufacture to modify the flavor of the product. Probiotic bacteria are added to foods with the goal of reaping the microbes' human health benefits; however, addition to cheese poses new stress conditions that may change the characteristics of the microbe. In this study, probiotic bacteria (lactobacilli and bifidobacteria) were added during Cheddar cheese manufacture to determine their survival during the aging process in different milk fat levels. Starter culture and NSLAB populations were determined using real time-quantitative PCR using primers specific for the different bacterial genera or species of interest. Bifidobacteria were initially added at 2.5×10^6 CFU/g cheese and survived the aging process with a small population reduction after 280 d. Added *Lactobacillus acidophilus* populations (10^7 CFU/g cheese) and NSLAB populations (10^8 CFU/g cheese) increased significantly ($P < 0.05$) by 10 to 100-fold during the same time. Analysis of the added probiotic and starter culture using propidium monoazide for differentiating live and dead bacteria by PCR indicated that these microbes not only survived, but increased in numbers significantly ($P < 0.05$) by 10 to 100-fold over aging independent of fat level. In conclusion, probiotic bacteria are capable of surviving throughout the cheese-making and aging process, indicating that delivery via hard cheeses is possible.

Key Words: lactic acid bacteria, probiotic, survival

954 Production of microcapsules of *Lactobacillus acidophilus* to add in dairy products. A. M. Liserre*[1], P. B. Zacarchenco[1], C. R. Meneze[3], A. E. C. Antunes[2], G. M. B. Q. Cardozo[1], and I. Moreno[1], [1]*Tecnolat/ Instituto de Tecnologia de Alimentos*, *Campinas, São Paulo, Brasil*, [2]*UNICAMP; Universidade Estadual de Campinas - Limeira*, *Limeira, São Paulo, Brasil*, [3]*Universidade de Santa Maria*, *Rio Grande do Sul, Brasil*.

Probiotics have attracted attention because of their benefits to human health. However, studies indicate that probiotics may not survive well in dairy products and during their passage through the gastrointestinal tract, due to stress factors such as acidity, low storage temperature, and presence of lactic and acetic acids, bile salts and digestive enzymes.

Microencapsulation is a technology used to improve viability of probiotic. The objective of this study was the development of *Lactobacillus acidophilus* microcapsules with cellulose acetate phthalate, maltodextrin, glycerol, Hi-maize, Tween 80 and skim milk powder prepared by the spray dryer technique. In vitro release of probiotics from the microcapsules was investigated using citrate-phosphate buffer solution (pH 4.5) and in phosphate buffer solution (pH 6.0 and pH 7.5). Aliquots were removed after 60, 120 and 180 min agitation at 150 rpm at 37°C. The number of released cells was determined by pour plating in MRS LP (37°C/72h) under anaerobiosis. Changes in bead integrity with time at pH 7.5 were monitored by optical microscopy and photographed. The spray dryer technique was efficient to obtain probiotic encapsulated cellulose acetate phthalate based microcapsules. The viability of probiotic were very good showing counts of 5.70, 8.85 and 9.37 log CFU/g after 180 min of dissolution at pH 4.5, 6.0 and 7.5, respectively. Microcapsules promoted a controlled release of probiotics in different pH values, because the highest retention of cells occurred at pH 4.5. Theses microcapsules can be applied to dairy products because at the pH of milk (pH 6.0) the release of probiotics was high.

Key Words: probiotic, microencapsulation, acetate phthalate cellulose

955 Novel immunostimulatory activities of CpG oligodeoxynucleotides from *Streptococcus thermophilus*. T. Shimosato*[1], M. Fujimoto[1], M. Tohno[2], T. Sato[3], H. Otani[1], and H. Kitazawa[4], [1]*Shinshu University*, *Kamiina, Nagano, Japan*, [2]*National Institute of Livestock and Grassland Science*, *Nasushiobara, Tochigi, Japan*, [3]*Yokohama City University*, *Yokohama, Kanagawa, Japan*, [4]*Tohoku University*, *Sendai, Miyagi, Japan*.

We previously reported the strong immunostimulatory effects of a CpG oligodeoxynucleotide (ODN), designated MsST, from the lacZ gene of *Streptococcus (S.) thermophilus* ATCC19258. However, there is no evidence of an anti-inflammatory response after IL-33 increase following treatment with CpG ODNs, which act via TLR9. Therefore, in this study, we focused on induction of IL-33 by CpG ODNs and examined the effects of MsST stimulation on mouse splenocytes and peritoneal macrophages.Here we show that 24 h of stimulation with MsST in mouse splenocytes and peritoneal macrophages strongly induces expression of interleukin (IL)-33, a cytokine in the IL-1 superfamily. Other IL-1 superfamily members, including IL-1α, IL-1β and IL-18, are downregulated after 24 h of stimulation of MsST. We also found that MsST-induced IL-33 mRNA expression is inhibited by the suppressive ODN A151, which can inhibit Toll-like receptor 9 (TLR9)-mediated responses. We speculate that upregulation of IL-33 in response to exposure to an external stimulus such as MsST may serve as an endogenous danger signal that alerts cells in the innate immune system to tissue damage during bacterial challenge. Our findings suggest that IL-33 is an important regulator that acts on macrophages via TLR9. Although our understanding of IL-33 is currently limited, it seems reasonable to suggest that IL-33 might counterbalance the activities of proinflammatory cytokines . In conclusion, we found a novel immunoregulatory mechanism mediated by CpG ODNs that induces IL-33. Understanding how IL-33 mediates immunoregulation via MsST activation should help in the development of therapeutic ODNs for treatment of inflammatory disease by the strong induction of IL-33. Exploiting this property may also prove useful in the design and production of new physiologically functional foods.

Key Words: CpG ODN, IL-33, *Streptococcus thermophilus*

956 Toll-like receptor 2 participates in the intestinal epithelial regulating activity of *Lactobacillus kefiranofaciens* M1 isolated from fermented milk product kefir. Y. P. Chen*, W. S. Hong, T. Y. Dai, I. N. Huang, and M. J. Chen, *National Taiwan University*, *Taipei, Taiwan, R.O.C.*

Toll-like receptors (TLRs) are pattern recognition receptors (PRRs) that recognize microbial components and endogenous ligands. Among different TLRs, TLR2 recognizes the broadest range of microbial component, including lipoteichic acid, peptidoglycan, lipopeptide and so on. TLR2 has been known to manipulate important immune function in many kinds of immune cells. However, the physiological significance of TLR2 expressed in intestinal epithelial cells is unclear. In this report, we found that TLR2 was participated in important regulatory roles of *Lactobacillus kefiranofaciens* M1, which was originally isolated from fermented milk product kefir and showed intestinal protective activity in vitro and in vivo. We cultured intestinal epithelial cell (IEC) line Caco-2 onto permeable transwell insert for 28 d until fully polarization and monolayer formation. We found that apical adding of *Lb. kefiranofaciens* M1 increased both the apical and basolateral production of intestinal restitution chemokine CCL-20 in IEC monolayer in a dose dependent and time course manner. The CCL-20 production was further blocked by using TLR2 specific neutralizing antibody. In the experimental colitis model, we used dextran sodium sulfate (DSS) to damage intestinal epithelium and to induce colitis in both wild type and TLR2 knockout mice. *Lactobacillus kefiranofaciens* M1 could ameliorate DSS-induced colitis in wild type mice group by assessing stool consistency, bleeding score, colon length shortening, histological scoring and *ex-vivo* cytokine production pattern of colon segment, while it had no such effect in TLR2 knockout mice group. In summary, *Lb. kefiranofaciens* M1 can regulate IEC restitution chemokine CCL-20 production in vitro and ameliorate DSS-induced colitis in vivo through TLR2. The data indicates that TLR2 plays an important role of *Lb. kefiranofaciens* M1 in regulating intestinal homeostasis.

Key Words: toll-like receptor, probiotics, intestinal epithelial cell

957 Inhibitory effect of Taiwanese ropy fermented milk in an ovalbumin-induced allergy mouse model. I. N. Huang*[1], T. Y. Dai[1], S. Y. Wang[2], and M. J. Chen[1], [1]*Department of Animal Science and Technology, National Taiwan University*, *Taipei, Taiwan*, [2]*Experimental Farm, National Taiwan University*, *Taipei, Taiwan*.

Taiwanese ropy fermented milk (TRFM) has a sticky consistency, which is made with the microbial action of mesophilic lactic acid bacteria (LAB). In our previous studies, we isolated and identified microorganisms from TRFM using a combination of polymerase chain reaction-denaturing gradient gel electrophoresis (PCR-DGGE) and 16S rDNA sequencing. In this study, we assayed the anti-allergic abilities of TRFM and its dominant microorganisms (*Lactococcus lactis* ssp. *cremoris* and *Kluyveromyces marxianus*). The in vitro results depicted that both *L. lactis* ssp. *cremoris* and *K. marxianus* could induce Th1 (TNF-α, IL-6) and Treg (IL-10) cytokines in RAW 264.7 macrophages and murine splenocytes, which might inhibit the Th2 response and IgE production. The OVA-sensitized animal test demonstrated that oral administration of both strains generally tended to reduce serum total IgE in OVA-sensitized BALB/c mice compared with the control groups. In conclusion, the data presented clearly indicate the anti-allergic activities of TRFM microorganisms. Suppression of IgE production by oral feeding of *L. lactis* ssp. *cremoris* and *K. marxianus* probably occurs because of elevation of Th1 and Treg cytokines leading the skewness of Th1/Th2 balance toward Th1 dominance.

Key Words: allergy, lactic acid bacteria, yeast

Lactation Biology 2

958 Regulation of mammary epithelial cell proliferation and gene expression by *Semen Vaccariae* active monomer. Z. Y. WAN, H. L. TONG, Q. Z. LI, and X. J. GAO*, *Key Laboratory of Dairy Science of Education Ministry, Northeast Agricultural University*, *Harbin, China*.

Semen Vaccariae is a traditional Chinese herb that is widely used to increase lactation. However, the underlying changes in gene expression that drive the increased milk production by *Semen Vaccariae*, especially the specific active monomer, remain an open question. Our lab has successfully separated active monomer dibutyl phthalate (DBP) from *Semen Vaccariae* to study its role in lactation. A model DT CASY Cell Counter was used to study the effect of increasing concentrations of DBP on proliferation and viability of primary cultured dairy cow mammary epithelial cells (DCMEC) harvested from a lactating cow at d 140 (n = 3). QRT–PCR and Western blot were used to study changes in mRNA and protein of *prlr, erα, akt1, socs2, pparγ* and *elf5*at 6, 12, 24, 36, 48, and 72 h. miRNAs (21,125b,143 and 195) and secretion of β–casein and lactose were detected by qRT–PCR analysis and RP-HPLC. Each assay was performed in 5 independent experiments using 3 different treatments and the data were analyzed with SPSS by ANOVA. The results showed that DBP (0.5 mg/ml) increased proliferation and viability of DCMEC significantly ($P < 0.05$). DBP acted similarly to prolactin (PRL). It increased the expression of *prlr, erα, akt1* and *elf5*, but repressed the expression of *pparγ*. DBP promoted the expression of *socs2* mRNA, but inhibited the expression of *socs2* protein. Both DBP and PRL repressed the expression of miRNA–125b, miRNA–143 and miRNA–195 in DCMEC. DBP repressed the expression of miRNA–21, while the influence of PRL on miRNA–21 was uncertain. Both DBP and PRL enhanced the expression of β–casein ($P < 0.05$) and the secretion of lactose ($P < 0.05$) significantly. In conclusion, *Semen Vaccariae* active isomer increased proliferation and secretion of milk components by DCMEC. This is the first demonstration that miRNA expression can be changed by DBP and PRL. Further studies to uncover the lactogenic targets of DBP will help to shed light on the genetic mechanisms of mammary gland development and lactation.
This work was supported by the Innovation Team of the Northeast Agricultural University (Grant No. LXT005–1–2).

Key Words: *Semen Vaccariae*, dibutyl phthalate, lactation

959 Deletion of thyroid hormone responsive spot 14 exacerbates the anti-lipogenic affect of *trans*-10, *cis*-12 conjugated linoleic acid (CLA) in the mammary gland. K. J. Harvatine*[1], Y. R. Boisclair[2], and D. E. Bauman[2], [1]*Penn State University*, *University Park,* [2]*Cornell University*, *Ithaca, NY*.

Inhibition of milk fat synthesis by fatty acid (FA) intermediates originating from ruminal biohydrogenation has been extensively studied in the cow and more recently in the mouse. In both species, *trans*-10, *cis*-12 conjugated linoleic acid (CLA) reduces milk fat concentration and markedly reduces milk fat concentration of de novo synthesized FA. During CLA treatment mammary lipogenic capacity is decreased by a coordinated downregulation of genes involved in milk fat synthesis. We also identified downregulation of thyroid hormone responsive spot 14 (S14) in mammary tissue of both the cow and mouse during CLA treatment. The functional role of S14 in CLA-induced inhibition of fat synthesis was tested using wild-type (WT) and S14 null mice in a randomized block design with a 2x2 factorial arrangement of treatments (genotype x CLA). Starting at 6–8 d of lactation, S14 null and WT dams nursing 6–8 pups received oral doses of water (control) or 20 mg/d of CLA for 5 d. Pups and dams were weighed daily. On the last day of treatment dams were milked and killed. The effect of genotype, CLA, and genotype by CLA interaction was tested. Milk fat of S14 null mice was 25% lower than that of WT dams ($P < 0.001$) and CLA treatment reduced milk fat concentration in both genotypes ($P = 0.03$). However, there was a marked interaction of genotype and CLA treatment for milk concentration of de novo synthesized FA ($P < 0.001$), where the WT dams reduced milk concentration of FA less than 16 carbons in length by 27% while S14 null mice reduced FA less than 16 carbons by 72%. In agreement, mammary lipogenic capacity measured as ^{14}C glucose incorporation into lipids by mammary tissue explants was decreased 23% in WT dams and 82% in S14 null dams. Mammary lipogenesis of S14 null dams is hyper-responsive to CLA treatment demonstrating a possible indirect effect of S14 on regulation of lipogenesis. Therefore, S14 may modify the activity of a second CLA responsive mechanism.

Key Words: milk fat, conjugated linoleic acid, lipogenesis

960 The role of SREBP-1 in lipogenesis in bovine mammary epithelial cells. L. Ma* and B. A. Corl, *Virginia Polytechnic Institute and State University*, *Blacksburg*.

Sterol regulatory element binding proteins (SREBPs) are a family of transcription factors that regulate lipid metabolism. There are 3 isoforms, SREBP-1a, SREBP-1c and SREBP-2, among which SREBP-1a and SREBP-1c regulate fatty acid synthesis. The objective of this study was to determine the role of SREBP-1 in lipogenesis in bovine mammary epithelial cells. Bovine mammary epithelial cells (MACT) were used in this study. After reaching 80% confluence in a flask, cells were trypsinized and reseeded to plates at a density of $2X10^4$ cells/cm^2. After incubation in base medium (DMEM+10% FBS) overnight, cells were transfected using small interfering RNAs (siRNA), against SREBP-1 (SSI), Cyclophilin B as positive control (POS), a non-targeting sequence as negative control (NEG), and no siRNA as untreated control (UNT), according to protocol (Dharmacon Inc.). Cells were harvested for mRNA measurement after 24 h, for measurement of protein and acetate incorporation after 72 h. After treatment with SSI at concentrations of 5, 25, 50, 75, and 100 n*M*, the expression of SREBP-1 mRNA was reduced 76%, 84%, 90%, 91%, and 92%, respectively. In POS, the expression of Cyclophilin B mRNA decreased 74%, 90%, 95%, 94%, and 96%, respectively. SSI reduced precursor SREBP-1 protein (10, 586, 705, and 505 ± 241 for SSI, POS, NEG, and UNT, respectively; $P < 0.07$) and mature form of SREBP-1 (0, 376, 453, and 260 ± 85 for SSI, POS, NEG, and UNT, respectively; $P < 0.05$) compared with controls. Acetate incorporation also decreased to 0.31 nmol/4 h with SSI at 5 n*M*, compared with 0.41, 0.56, and 0.43 ± 0.02 nmol/4 h, for POS and NEG, and UNT, respectively ($P < 0.01$). SSI at 5 n*M* reduced SREBP-1 mRNA and protein by 76% and 98%. When SREBP-1 decreased, there was a significant decrease in acetate incorporation, thus SREBP-1 might regulate milk fat through the de novo fatty acid synthesis pathway.
This project was supported by National Research Initiative Competitive Grant no. 2009–35204–05358 from the USDA National Institute of Food and Agriculture.

Key Words: SREBP, small interfering RNA, bovine

961 Effects of t10,c12 CLA dose on mammary gland development, adiposity, and inflammation in mice. M. R. Foote*, S. L. Giesy, G.

Bernal-Santos, D. E. Bauman, and Y. R. Boisclair, *Cornell University*, *Ithaca, NY*.

The t10,c12 CLA isomer has been shown to have a wide range of potential health benefits including anticarcinogenic and antiadipogenic effects in animal models. Despite evidence of beneficial effects in the rat, dietary t10,c12 CLA was recently shown to impair mammary gland development and to accelerate mammary tumorigenesis in the mouse. The level of dietary t10,c12 CLA (0.5% of the diet) in this study was typical of levels shown to result in white adipose tissue inflammation and insulin resistance, 2 factors known to promote mammary cancer. To evaluate the possibility that lower t10,c12 CLA doses might inhibit lipogenesis without detrimental effects on mammary development, FVB wild-type mice received a diet containing 0%, 0.1%, 0.2%, or 0.5% t10,c12 CLA (n = 8 to 10 per treatment) from 24 d to 49 d of age. As expected, the 0.5% CLA dose resulted in increased hepatic triglyceride content and weight and increased plasma insulin ($P < 0.05$). In addition, the 0.5% dose caused abnormal mammary gland development (i.e., reduced ductal elongation combined with ductal hyperplasia) in parallel with dramatic mammary gland inflammation characterized by increased expression of monocyte chemoattractant protein 1 (MCP-1), egf-like module containing, mucin-like, hormone receptor-like 1 (EMR-1), tumor necrosis factor α (TNF-α), and interleukin 6 (IL-6) ($P < 0.05$ for all). The 0.1% CLA dose did not affect any of these metabolic and inflammatory end-points or any indices of mammary gland development ($P > 0.05$ for all). The 0.1% CLA dose, however, was as effective as the 0.5% dose in decreasing gonadal fat weights and fatty acid synthase expression in adipose tissue ($P < 0.05$). Our results establish that a low dose of t10,c12 CLA decreases adiposity without impeding mammary gland development or causing inflammatory and metabolic complications. These results show, for the first time in the mouse, that the positive effects of t10,c12 CLA on adiposity can be dissociated from negative effects on mammary development, metabolism, and inflammation.

Key Words: CLA, mammary gland

962 Impact of time of milk storage in the udder on fat. M. Dutreuil[1,2], C. Cébo[3], J. Guinard-Flament[2,1], and C. Hurtaud*[1,2], [1]*INRA UMR1080 Production du lait*, *Saint-Gilles, France*, [2]*AGROCAMPUS OUEST UMR1080 Production du lait*, *Rennes, France*, [3]*INRA Unité GABI*, *Jouy-en-Josas, France*.

Our objective was to study the effect of duration of milk storage on milk fat globule (MFG) secretion to better understand relationships between milk yield, milk fat and MFG secretion. Four milking frequencies were studied in 6 dairy cows averaging 118 ± 22 dim: 2 milkings/d separated by 11- and 13-h intervals (2M11–13) or by 4- and 20-h (2M4–20) and 1 milking/d (1M24). The experimental trial was a double Latin square 3 × 3 with 2 wk periods. In post-experiment, milking frequency of 36-h (1M36) was repeated twice. Compared with 2M11–13, 1M24 reduced milk and milk fat yields and increased fat content, without any effect on the size of MFG which agrees with previous research. 2M4–20 had no significant effect on milk fat yield and content but tended to increase the size of the MFG. Lipolysis, measured on morning milk, was weaker with 1M24. Milk fatty acid composition was not modified by milking frequency. When data were analyzed according to kinetics of milk storage duration (from 4 to 36-h), the highest fat content and the largest diameters of MFG were obtained on milks from 4- and 36-h milking (respectively 62.8 g/kg and 4.15 µm and 57.7 g/kg and 4.09 µm). Such observations could have 2 origins: the richness in residual milk of the 4-h milk and the coalescence of MFG related to the long storage duration in the 36-h milk. Independently, for each duration of milk storage, there was a relationship between MFG size and fat yield (R^2 from 0.31 to 0.81). Conversely, the relationship between MFG size and fat content was confirmed whatever duration of milk storage ($R^2 = 0.55$). Speed of secretion of milk fat (storage of 4 h excluded) was also well correlated with MFG size ($R^2 = 0.62$). For the 36-h milk, this relationship was also observed but with a significantly different slope suggesting a phenomena of MFG coalescence in response to the increased intra-mammary pressure. Duration of milk storage induces changes in MFG size under factors which interact.

Key Words: milk fat, milk storage, milk fat globule

963 IGF-I regulates the expression of GLUT12 in bovine mammary epithelial cells. Y. Shao* and F.-Q. Zhao, *Department of Animal Science, University of Vermont*, *Burlington*.

Insulin-like growth factor-I (IGF-I) is a potent mitogen for mammary epithelial cells and plays an important role in mammary development. Glucose is an energy source for mammary epithelial cell proliferation and glucose uptake is mediated by facilitative glucose transporters in mammary epithelial cells. The objective of this study was to investigate the role of IGF-I in regulating the expression of the main glucose transporters GLUT1, GLUT8 and GLUT12 in bovine mammary epithelial cells. In the first experiment, Mac-T cells were treated for 12 h with increasing concentrations of IGF-I (20, 50, 100, 200 and 400 ng/mL). mRNA levels of GLUT1, GLUT8, GLUT12 and IGFBP3 were determined by real-time PCR. IGFBP3 mRNA increased 6- to 13-fold in all groups treated with 50 ng/mL or higher concentrations of IGF-I compared with non-treatment group ($P < 0.001$), indicating that Mac-T cells are responsive to IGF-I. There were no treatment effects on GLUT1 and GLUT8 mRNA, but mRNA levels of GLUT12 decreased by 75% in all groups treated with 50 ng/mL or more IGF-I relative to control group ($P < 0.001$). In the second experiment, Mac-T cells were treated with 100 ng/mL of IGF-I for 3, 6, 12, 18, 24 and 48 h. Interestingly, mRNA of GLUT12 decreased to 21–35% after 3 to 12 h treatment but returned to the same levels as in the non-treatment group after 48 h. In summary, these data indicate that IGF-I may regulate the expression of GLUT12, but not GLUT1 and 8 in bovine mammary epithelial cells.

Key Words: glucose transporter, IGF-I, mammary epithelial cells

964 Mammary mitochondrial function is associated with lactation Performance in inbred mice. J. Wei*, S. Kiser, J. George, D. Anderson, and D. Hadsell, *Baylor College of Medicine*, *Houston, TX*.

Milk production in dairy cattle is influenced by genetics. In rodent models of lactation, oxidative metabolism and mitochondrial number/activity are increased dramatically with secretory activation. In addition, different inbred mice have different abilities to support litter gain through lactation implying that genetic background regulates milk synthesis capacity. However, comparison of mammary mitochondrial function among these inbred mice has not been studied. We hypothesized that variation in lactation capacity of different mouse strains is due to difference in mammary mitochondrial function. The FVB and C57BL/6 (C57) mice representing higher and lower lactation performance were used to assess mammary mitochondrial function and biogenesis. Lactation performance was assessed by crossfoster litter weight gain for the first 8 d of lactation. Mammary tissue was collected at Day 10 postpartum. mRNA levels of mitochondrial associated genes and mitochondrial DNA (mtDNA) copy number were measured using quantitative PCR (qPCR). Litter gain was higher with the FVB dams (26.81 ± 0.64g) than with the C57 (22.01 ± 1.82g) ($P = 0.026$). Mammary mitochondrial ATP synthesis activity was 68% higher in FVB mice compared with C57 ($P < 0.001$). Mammary mtDNA copy number per cell was

70% higher in the FVB compared with the C57 ($P < 0.05$). Mammary mRNA levels of Ppargc1a (131.73%), Nrf1 (49.63%), Gabpa (51.34%), Tfb1m (71.65%), Tfb2m (92.37%), Nnt (5052.74%), Sirt1 (79.83%), and Sod2 (34.63%), in the lactating mammary gland were all higher ($P < 0.05$) in FVB mice compared with C57. Mammary mRNAs for Tfam (65.61%) and Ucp3 (61.07%) were lower ($P < 0.05$) in the FVB mice. Significant difference in the expression levels of these transcriptional factors regulating mammary mitochondrial biogenesis and ATP synthesis activity implicates their important roles in lactation performance. The lower expression of the mammary Ucp3 and Tfam in the FVB mice may also suggest novel regulatory mechanisms of mammary mitochondrial functions in lactation.

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Key Words: lactation, mitochondria, mammary

965 Temporal changes in the mammary mitochondrial proteome of the mouse suggest that increases in a limited number of proteins are necessary to support increased ATP synthesis during early lactation. D. Hadsell*[1], W. Olea[1], R. Matsunami[2], and D. Engler[2], [1]*Baylor College of Medicine*, *Houston, TX,* [2]*The Methodist Hospital Research Institute*, *Houston, TX*.

The regulation of mammary mitochondrial biogenesis and function across the lactation cycle is not well understood. This study employed differential in-gel electrophoresis coupled with MALDI-tof/tof mass spectrometry to relate changes in mammary cell mitochondrial function during lactation to changes in the proteins that comprise this organelle. Our hypothesis was that changes in mammary cell mitochondrial biogenesis and function during lactation would directly correlate with coordinated changes in the proteins that make up the oxidative phosphorylation (OXPHOS) pathway and that some of these proteins might also be linked to PPARGC1α and AMP kinase. Markers of mammary mitochondrial biogenesis and function were measured in mammary tissue and mitochondria collected from lactating mice at d 2, 8, 14, 21, 28, and 35 postpartum. Mitochondrial ATP synthesis activity increased ($P < 0.05$) during early lactation and then declined with prolonged lactation. Staining of mammary tissue sections for succinate dehydrogenase activity indicated that mitochondrial number increased ($P < 0.05$) 5-fold during early lactation. Western blotting for the transcriptional co-activator PPARGC-1α and immunofluorescent staining for phospho AMP kinase demonstrated that these proteins were most abundant on d 2 postpartum. Analysis of the proteome identified 154 proteins that changed ($P < 0.05$) throughout the lactation cycle. Of these, only 3 members (NDUFAF3, UQCRB, and ATP6V1B2) of the OXPHOS pathway were increased during early lactation. In contrast, 23 OXPHOS proteins increased ($P < 0.05$) during mid lactation, while most of these same proteins decreased ($P < 0.05$) during late lactation. There were 6 proteins within the data set that could be directly linked to PPARGC1α through analysis for interacting networks. The results suggest that the increased ATP synthesis activity of the mammary mitochondria during early lactation results from changes in only a limited number of rate limiting proteins.

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Key Words: mammary, mitochondria, proteome

Meat Science and Muscle Biology Symposium: Impact of Pre- and Post-Slaughter Handling on Meat Quality

966 Handling of pigs and the effect on muscle metabolism prior to harvest. M. J. Ritter* and S. N. Carr, *Elanco Animal Health*, *Greenfield, IN*.

Market weight pigs are subjected to numerous stressors during the marketing process from loading at the farm to stunning at the packing plant. These stressors have important implications for animal well-being and fresh pork quality traits. The objectives of this presentation are to review: 1) pre-harvest stressors in pigs; 2) common measures of stress during handling and transportation; and 3) effects of pre-harvest stressors on metabolic changes and fresh pork quality traits. Pre-harvest stressors can be encountered during loading, transportation, unloading, lairage, and movement to the stunning area. Although the majority of the work in this area has focused on animal handling procedures, other areas of interest include the mixing of unfamiliar pigs, transport floor space, transport time, lairage time, and environmental conditions. Genetics, previous experiences, and the physical condition of the animal will impact how pigs respond to these stressors. Measures of stress during handling and transportation include: body temperature, heart rate, respiration rate, blood acid-base balance (pH, lactate, bicarbonate, and base-excess), stress hormones (cortisol, epinephrine, and norepinephrine), enzyme activity (creatine kinase and lactate dehydrogenase), and muscle glycolytic potential. The magnitude of the change in these parameters is dependent upon stressor intensity, duration, and frequency. For example, recent work by Hambrecht et al. (2005) and Ritter et al. (2009) reported that multiple concurrent pre-harvest stressors have additive effects on body / carcass temperature, blood lactate, and muscle lactate values in market weight pigs. It is well documented that aggressive handling immediately before harvest increases early postmortem temperature and the rate of pH decline in muscle, resulting in pork with high drip loss (Hambrecht et al., 2004a; 2004b; 2005). However pre-harvest stressors that reduce muscle glycogen during loading at the farm may have beneficial effects on ultimate pH and water-holding capacity (Edwards, 2009). Therefore, improvements in pre-harvest handling do not always translate to improvements in fresh pork quality traits.

Key Words: pig, pre-harvest stress, pork quality

967 Pre-slaughter stress in ruminants and its relationship to meat quality. D. M. Ferguson*[1] and R. D. Warner[2], [1]*CSIRO Livestock Industries*, *Armidale, NSW, Australia*, [2]*Victorian Department of Primary Industries*, *Werribee, VIC, Australia*.

The production of meat that consistently meets consumer expectations requires vigilance and control at all points in the supply chain. In particular, control is required during the critical period from farm or pen to slaughter as the inevitable stress that all livestock experience can result in losses to meat quality. Livestock are exposed to multiple and often novel stressors, some repeated (e.g., handling), during the pre-slaughter phase. Animals can vary enormously in their response to these stressors, depending on their prior experience and genetic predisposition to stress. The variable nature of pre-slaughter stressors and the animalsâ€ response presents major challenges to the design of studies quantifying the impacts of these on animal welfare and meat quality. Furthermore, it creates difficulties in the development of control strategies to mitigate these impacts. The stress-mediated depletion of muscle glycogen and the subsequent dark-cutting condition in meat has been well documented and is perhaps indicative of significant pre-slaughter stress. Despite improved pre-slaughter management, there is still evidence of acute increases in the incidence of dark cutting in consignments of cattle. These spikes cannot be explained by changes in pre-slaughter practices or other known stress mediating factors. Recent research in ruminants has revealed that pre-slaughter stressors can also negatively affect meat quality traits such as sensory panel scores and water holding properties independent of any change to ultimate pH or rate of pH fall. In this paper, we review the impacts of pre-slaughter stress on beef and sheepmeat quality traits and discuss recent developments in strategies to minimize the occurrence and effects of pre-slaughter stress.

Key Words: ruminant, pre-slaughter stress, meat quality

968 Impact of early pre- and post-mortem processing on poultry meat quality. S. Barbut*, *University of Guelph*, *Guelph, Ontario, Canada*.

Over the past decade there have been some major changes in the way poultry is handled. Three of the main ones have been the introduction of mechanical catching on a large commercial scale, controlled atmosphere stunning (CAS), and electrical stimulation (ES). Although the changes have been introduced to reduce manual labor, increase efficiency, address animal welfare issues, and in the case of ES also to shorten time to deboning, one of the major drivers is still meat quality. Efforts have also been directed to improve transportation conditions, restrict feed withdrawal and rest period after transportation; all can contribute to reduce stress and improve to meat quality. These factors are very important in general and also because some birds are known to be more susceptible to stress and show the pale, soft and exudative (PSE) syndrome which up to now is not dealt with by genetics. The new generation of mechanical catchers can handle a large number of birds and reduce wing and other damages if done correctly. CAS is becoming more popular in Europe but it should be remembered that meat quality issues are strongly depended on the method used (single vs multiple phase, gas mix) and way birds are handled. Electrical stunning is still the most common method but variations between high and low voltages / frequencies as well as the use a two phase stunning can be seen around the world. Most new plants are using ES (i.e., not common a decade ago), and together with an appropriate chilling regimen can allow broiler meat deboning with 3-4 hrs. The review will focus on how such developments have been made based on better understanding of meat science, animal physiology, and animal welfare.

Key Words: poultry, meat, stress

969 Processing practices and perceived pork quality. T. Ngapo*, *Agriculture and Agri-Food Canada*, *St Hyacinthe, Quebec, Canada*.

It is well known that potentially good sensory quality of pork brought to slaughter can readily be destroyed by post-mortem processing, but can the quality be further improved? Control of post-slaughter processes, such as, chilling regimens and aging, are vital to both realizing a good eating experience and to achieving a product of consistently good sensory quality. Pork is a relatively tender meat and achieves about 80% of its maximal tenderness in 5 d, twice as fast as that of beef. Consequently many of the post-mortem processes currently used were developed on the basis that an aging period is not required longer than the time to get the meat from slaughter to plate, estimated at about 6 d in North America. These processes have little changed in the last few decades,

but consumer perceptions have, with complaints of blandness leveled against modern lean meat. Accordingly, studies with the specific objective of improving the sensory quality of pork have come to the forefront of meat research in the last few years as avenues for improvement, rather than maintenance, of sensory quality are now being sought. Hence, this bibliographic review of the impact of early post-mortem processing on perceived quality aims to provide insight into potential sources of amelioration of the eating quality of fresh pork. These processes include suspension, chilling, boning, electrical stimulation and aging.

Key Words: pork, post-mortem processing, quality

Nonruminant Nutrition: Feed Additives

970 Benefits of a synthetic antioxidant on improving growth performance in broiler chicks. J. Zhao*, F. Yan, C. Atwell, D. Macaraeg, M. Vazquez-Anon, J. D. Richards, R. J. Harrell, S. Carter, and T. Hampton, *Novus International Inc.*

This study examined the benefits of a synthetic antioxidant (AOX, AgradoPlus, Novus International Inc., St. Charles, MO) on improving performance in broilers. A total of 1152 ROSS 308 male birds were randomly allotted to one of the 4 dietary treatments with 12 pens per treatment and 24 birds per pen. The trial was a 2x2 factorial design with 2 types of soybean oil (fresh vs. oxidized) with or without AOX (0.025%). Oxidized soybean oil was produced by bubbling oxygen in a heated container up to 48 h to reach a target peroxide value (PV) of 200mEq/kg and 6 mEq/kg in the final diets. In the starter phase (d0–10), feed efficiency was significantly impaired with oxidized oil treatments ($P = 0.001$). Birds fed AOX gained more ($P < 0.05$) and ate more ($P < 0.05$) regardless of oil type (interaction, $P > 0.10$). In the grower phase (d10–23), birds fed oxidized oil gained less, ate less, and had lower overall performance index ($P < 0.05$) than birds fed fresh oil. Dietary AOX eliminated the negative effects of oxidized oil on performance ($P < 0.05$). The best performance was observed on birds fed fresh oil with AOX. Overall (d0–39), oxidized oil decreased feed efficiency (6%, $P < 0.001$), weight gain (7.5%, $P < 0.001$), and feed intake (2.3%, $P = 0.11$) compared with birds fed fresh oil. Birds fed AOX ate more ($P = 0.01$) regardless of oil type (interaction, $P = 0.34$), and gained more ($P < 0.001$) especially in birds fed oxidized oil (interaction, $P = 0.05$). The final body weight was 2.848, 2.876, 2.637, and 2.743 kg for birds fed fresh oil without and with AOX and for birds fed oxidized oil without and with AOX, respectively. In summary, oxidized oil impaired weight gain, feed intake, and feed efficiency. Birds fed AOX had better weight gain and feed efficiency regardless of oil type, and the benefits of AOX were more profound in oxidized oil groups.

Key Words: antioxidant, broiler, performance

971 Probiotic, prebiotic and yeast supplementation in broiler diets from 1 to 42 days of age: 1. Productive performance and economic efficiency. S. A. Riad[1], H. M. Safaa*[1], F. R. Mohamed[1], S. S. Siam[2], and H. A. El-Minshawy[3], [1]*Animal Production Department, Faculty of Agriculture, Cairo University*, *Giza 12613, Giza, Egypt*, [2]*Poultry Breeding Department, Animal Production Research Institute*, *Dokki, Giza, Egypt*, [3]*Ministry of Agriculture*, *Dokki, Giza, Egypt*.

A total of 630 Arbor Acres broiler chicks at one-day old was used to study the effect of probiotic, prebiotic and/or yeast supplementation on the productive performance traits and economic efficiency. Chicks were divided randomly into 6 treatments and housed at deep litter in an open house system. Each treatment replicated 3 times (35 chicks per replicate). Treatments were as follows: T1 (control; chicks fed corn-soy basal diet) and in the other treatments diets were supplemented with 1g probiotic/kg diet as *Lactobacillus acidophilus* (T2), 1g yeast/kg diet as *Saccharomyces cervisiae* (5×10^{12} CFU/g; T3), 1g prebiotic/kg diet as mannan-oligosaccharide (T4), 1g probiotic+1g prebiotic/kg diet (T5) or 1g yeast+1g prebiotic/kg diet (T6). Basal diet contains 23.1% CP and 3103 Kcal AME/kg for the starter diet (0–21 d) and 20.0% CP and 3207 Kcal AME/kg for the finisher diet (21–42 d). Body weight at 42 d was heavier ($P \leq 0.0001$) by about 29.5, 21.2, 12.4, 11.3 and 9.9% than control in the T6, T5, T4, T3 and T2, respectively. Moreover, feed conversion ratio was 2.08, 1.80, 1.84, 1.82, 1.63, 1.61 for T_i (i = 1, 2, ... 6, respectively). For all traits, the best values were obtained in T6 followed by T5 then T4. Also, T6 gave the best relative economic efficiency (14.86% more than control group). It could be recommended from this study to supplement the biological additives to broiler diet from 0 to 42 d of age as above mentioned because it has a positive effect on the broiler performance and the economic efficiency.

Key Words: probiotic, prebiotic, yeast, broiler performance, economic efficiency

972 Starter feed supplementation level effects of coated sodium butyrate (ADIMIX) on growth performance of broilers. R. D. Malheiros* and P. R. Ferket, *North Carolina State University*, *Raleigh*.

Dietary supplementation of butyric acid (BA) has been shown to support enteric development and intestinal health of neonatal animals, but BA′s benefit to overall growth performance is variable because of its volatility in finished feed. ADIMIX (Nutriad, Inc.) is a coated sodium butyrate product (30% activity) that is less volatile and has more favorable handling characteristics for feed manufacturers than the concentrated BA. Commercial broilers were randomly assigned to 32 floor pens containing 30 birds each and provided feed and water ad libitum until 49 d. Starter feed (pellet-crumbled) treatments consisting of 4 dietary supplementation levels of ADIMIX (0, 0.015, 0.03, and 0.06% BA) were subjected to 8 replicate pens per treatment from 1 to 14 d. Subsequently, all birds were fed pelleted grower and finisher diets that did not contain ADIMIX. Body weight (BW) and feed intake was determined at 7, 14, 21, 42, and 49 d and feed/gain (FCR) was calculated. At 3, 8, and 14 d, 4 birds/treatment were sampled for gut histology evaluation. There were no treatment effects on mortality rate. BW at 14 d increased linearly ($P < 0.01$) as the level of BA increased (457 g vs 470 g for 0 vs 0.06% BA), but no effects on 1–14 d FCR was observed. Histomorphometic analysis was associated with early treatment effects on BW. The positive starter feed treatment effects were observed throughout the experiment, with 0.015% BA (0.05% ADIMIX) resulting in a 3% and 2% improvement in 42 d BW ($P < 0.02$) and 49 d BW ($P < 0.10$), respectively. A linear improvement in 1–42 d FCR by up to 3% was also observed as the level of BA increased in the Starter feeds. Dietary supplementation of BA as ADIMIX in starter feeds has a lasting positive effect on broiler growth performance.

Key Words: broilers, butyric acid, growth performance

973 Investigation on the effects of antibiotic growth promoters alternatives on broiler performance. M. Shivazad*[1,2], N. Ghazvini[2], and S. N. Mousavi[2], [1]*University of Tehran*, *Tehran, Iran*, [2]*Varamin-Pishva branch, Islamic Azad University*, *Varamin, Iran*.

A study was conducted to evaluate the effects of organic acid (butyric acid and propionic acid), probiotics (*Pediococcus acidilactici*), prebiotics (mannanoligosaccharides) and formalin as potential alternatives to antibiotic growth promoters (AGP) in broiler chickens. Dietary treatments included an antibiotic free diet (CTL-), a positive control (CTL+) containing antibiotic (Avilamycin) and an antibiotic free diet containing butyric acid (Baby C4), Mannanoligosaccharides (BioMOS), Propionic acid (Formycin Gold), Probiotics (Bacto cell) or Formalin (37% formaldehyde). Feed intake was not affected by dietary treatments. Addition of Avilamycin significantly improved weight gain during 1–14 d but the effect was not continued. Birds fed BioMos and butyric acid were significantly heavier than negative controls during 14–28, 28–42 and 1–42 d ($P < 0.05$). Butyric acid treatments improved FCR throughout

the experiment. Avilamycin and probiotics improved FCR for d 1–14 and 1–42. BioMos had highest breast meat percentage among all treatments ($P < 0.05$). Dietary treatments had no significant effect on jejunum morphology (villus length, villus width and crypt depth). The results of this study indicated that addition of butyric acid and MOS to the diet could be an alternative to the use of antibiotics as growth promoters in broiler production.

Key Words: broiler, antibiotic growth promoters, probiotics

974 Dietary supplementation of *Spirulina platensis* in Austra-White chicken improves proximate composition of meat. A. Kollanoor Johny*[1], K. P. Sreekumar[2], S. C. Nair[2], and P. Kuttinarayanan[3], [1]*Department of Animal Nutrition, College of Veterinary and Animal Sciences, Kerala Agricultural University*, *Mannuthy, Kerala, India*, [2]*Department of Animal Physiology, College of Veterinary and Animal Sciences, Kerala Agricultural University*, *Mannuthy, Kerala, India*, [3]*Center of Excellence in Meat Science and Technology, College of Veterinary and Animal Sciences, Kerala Agricultural University*, *Mannuthy, Kerala, India*.

Spirulina platensis, a blue-green alga is generally regarded as a rich source of protein, fats, vitamins and minerals. Although there are a few studies indicating its potential to enhance color of egg yolk and meat, the effect of Spirulina on the proximate composition and minerals including zinc and iron, of chicken meat has not been explored. The study was undertaken to determine the effect of dietary Spirulina on the proximate composition of chicken meat. Twelve, Austra-White male (egg-type) chicken were divided randomly into 2 groups of 6 birds each; control and experimental and were reared in battery cages with ad libitum access to feed and water. They were fed iso-nitrogenous and iso-caloric standard layer rations with the experimental group receiving 2.5% of dried Spirulina powder for a period of 6 mo, starting from the third month of age. At the completion of the trial, birds were sacrificed to collect meat and blood samples for proximate, mineral and serum analyses. The experiment was replicated 2 times. Spirulina-fed group showed significant improvement ($P < 0.05$) in total protein, fat and ash content of the meat samples. The concentrations of zinc, iron, magnesium, manganese, sodium, and potassium in meat did not differ between the groups, however, the serum concentrations of zinc and iron in the spirulina-treated group were significantly higher ($P < 0.05$) compared with that in the control. Analysis of plasma lipid profile revealed significant lowering of plasma total lipids and cholesterol ($P < 0.05$). Results of the study indicate that dietary supplementation of *Spirulina platensis* improves the proximate composition of chicken meat.

Key Words: *Spirulina platensis*, Austra-White chicken, meat, minerals

975 Increased fiber digestion and decreased fecal output in pigs fed fibrolytic bacteria. C. Ziemer*[1], S. Arcidiacano[2], A. Ragauskas[3], and M. Morrison[4,5], [1]*National Laboratory for Agriculture and the Environment, ARS, USDA*, *Ames, IA,* [2]*U.S. Army Natick Soldier Center*, *Natick, MA,*[3]*Institute of Paper Science and Technology, Georgia Institute of Technology*, *Atlanta, GA,* [4]*Department of Animal Science, Ohio State University*, *Columbus,* [5]*CSIRO Livestock Industries*, *St. Lucia, QLD, Australia*.

Fiber digestibility increases when pigs are fed for longer periods of time, suggesting adaptation of intestinal microbiota with increased concentrations of fiber utilizing bacteria. We investigated whether feeding fiber utilizing bacteria to pigs would result in improved fiber digestion and reduce fecal output. Treatments were arranged as a 2 × 4 factorial with 2 diets and 4 bacterial treatments, with random assignment of pigs. Pigs, housed as 2 groups of 24, were fed either conventional or 20% distillers dried grains with solubles + 10% soybean hulls diet ad libitum with free water access. Treatments consisted of no bacteria (A) or one of 3 *Bacteroides* isolates (B, C and D); isolated from fecal enrichments with cellulose and xylan. Bacteria were fed to pigs once daily (0900 h) using a 50:50 mixture of bacteria in growth medium and food grade glycerol (dosage of 10^{10} bacterial cells/d). After 3 weeks, 24 pigs, at a time, were moved into metabolism crates for 11 d. On d 7 to 11 total dietary intake, fecal output, and urinary output were measured and feed, feed refusals and feces were sampled to determine nutrient digestibilities. Blood was taken on d 1 and 11 to analyze plasma for energy metabolites. Data were analyzed as 2 × 2 × 4 randomized block design with 2 groups of pigs, 2 dietary treatments and 4 bacterial treatments; no interactions were significant and these were removed from final model. Initial pig BW averaged 61.1 kg, after 50 d the final pig BW averaged 103.6 kg. Feed intake was not affected by diet or bacterial treatment. The effects of increased fiber in the diet were as expected. Treatment B resulted in the most desirable effects when fed to pigs. Fecal output (g/d, $P = 0.13$) and fecal output/intake (g/g, $P = 0.07$) were decreased when treatment B (by 19.8% and 19.4%, respectively) was fed compared with no bacteria (A). Plasma glucose (mg/dL, $P = 0.10$) and cholesterol (mg/dL, $P = 0.14$) were increased in pigs fed B compared with no bacteria (A) by 5.3 and 10.4%, respectively. Bacterial treatment B demonstrated promise as a method to improve utilization of high fiber diets fed to pigs while maintaining performance.

Key Words: pig, fiber digestion, fecal output

976 Effects of dietary resveratrol supplementation on egg production and egg yolk lipid peroxidation. K. Sahin*[1], F. Akdemir[2], C. Orhan[1], M. Tuzcu[3], A. Hayirli[4], and N. Sahin[1], [1]*Department of Animal Nutrition & Nutritional Disorders, Faculty of Veterinary Medicine, Firat University*, *Elazig 23119, Turkey*, [2]*Department of Animal Nutrition & Nutritional Disorders, Faculty of Veterinary Medicine, Dicle University*, *Diyarbakir 21100, Turkey*, [3]*Department of Biology, Faculty of Science, Firat University*, *Elazig 23119, Turkey*, [4]*Department of Animal Nutrition & Nutritional Disorders, Faculty of Veterinary Medicine, Atatürk University*, *Erzurum 25240, Turkey*.

Resveratrol, a polyphenol derived from red grapes, berries, and peanuts, have anti-inflammatory, antioxidant, and immunomodulatory activities. The objective of this study was to investigate the effects of dietary resveratrol supplementation on performance and serum and egg yolk antioxidant status in quails (*Coturnix coturnix japonica*). A total of 150 5-wk-old quails were allocated randomly to 3 dietary treatments: basal diet and basal diet supplemented with 200 and 400 ppm resveratrol. Each diet was offered to 10 cages of 5 birds in each, for 12 wks. Serum and egg samples were collected at the beginning (wk 4) and end (wk 16) of the experimental period for tumor necrosis factor (TNF-α), malondialdehyde (MDA), vitamin A and vitamin E. Data were subjected to ANCOVA using the MIXED Procedure. There was no treatment effect on feed intake and egg production as well as egg quality. There was no dietary resveratrol supplementation effect on serum and egg yolk vitamin A levels. Serum MDA (0.56 vs. 0.88 mg/l, $P < 0.03$) and TNF-α (18.24 vs. 21.43 pg/ml, $P < 0.008$) levels were lower and serum vitamin E level (5.72 vs. 3.56 mg/l, $P < 0.008$) was higher for quails supplemented with resveratrol than for quails fed the basal diet. Serum MDA ($P < 0.02$) and TNF-α ($P < 0.05$) levels decreased linearly and serum vitamin E level ($P < 0.01$) increased linearly with increasing dietary resveratrol supplementation. Egg yolks from quails supplemented with resveratrol contained less MDA than those from

quails fed the basal diet (0.21 vs. 0.15 μg/g, $P < 0.002$). In response to increasing dietary resveratrol level, egg yolk MDA content decreased linearly ($P < 0.0003$). To our knowledge, this is the first experiment dealing with antioxidant and anti-inflammatory effects of resveratrol in poultry. In conclusion, inclusion of resveratrol up to 400 ppm into quail diets enhanced antioxidant status of birds and improved egg stability, which could be important to consumers.

Key Words: resveratrol, antioxidant status, Japanese quail

977 The effect of feeding Original XPC to turkey breeder hens and progeny on starter poult performance and early breast muscle development. P. R. Ferket*[1], R. D. Malheiros[1], M. J. Wineland[1], J. L. Grimes[1], and D. T. Moore[2], [1]*North Carolina State University*, *Raleigh,* [2]*Diamond V, Inc.*, *Cedar Rapids, IA*.

This study investigated the use of a *Saccharomyces cerevisiae* fermentation product in turkey breeder diets and subsequent progeny diets. A commercial breeder farm provided 2 diets to Hybrid Converter breeder hens starting at 29.5 weeks of age before the onset of lay: control diet or the control diet containing 0.075% XPC. At approximately 33.5 weeks of age, eggs were collected from both breeder flocks and transported to NC State University where they were incubated. Male poults were randomly divided at hatch into 4 treatments with 10 pens/treatment and 15 poults/pen. Treatments were arranged as a 2X2 factorial, consisting of 2 dietary XPC levels for breeders (0 and 0.075%) and 2 dietary XPC levels for progeny (0 and 0.125% 1–42 d and 0.0625% 43–63 d). Poults were raised in a curtain-sided, floor pen facility, and provided feed and water ad libitum. Body weights (BW) and feed consumption was determined at 21, 42, and 63 d and feed/gain (FCR) calculated. At 14 and 42 d, 4 poults/treatment were sampled for breast muscle yield. There were no significant ($P > 0.05$) breeder effects or breeder × progeny treatment interaction effects on BW or FCR throughout the experiment. However, the positive effects of dietary XPC supplementation on the growth performance of progeny was highly significant ($P < 0.0001$). BW of progeny fed XPC was greater than controls at 21 d (579 g vs. 509 g, $P < 0.0001$), 42 d (2595 g vs. 2417 g, $P < 0.0001$) and 63 d (6057 g vs. 5480 g, $P < 0.0001$). However, FCR of progeny fed XPC was better than controls only from 1 to 21d (1.59 vs. 1.71 $P < 0.0001$). Dietary XPC supplementation increased % breast muscle yield at 14 d (15.22% vs. 12.31%, $P < 0.0001$), but no significant effects were observed on % breast muscle at 42 d. Feeding poults XPC during the starter phase improves feed intake and body weight gain for the entire period and improves feed conversion and breast muscle yield early in the phase.

Key Words: turkeys, fermentation product, growth performance

978 Use of a *Bacillus amyloliquefaciens* probiotic in broiler farms. J. J. Mallo*[1], M. I. Gracia[2], P. Honrubia[1], and G. Sedano[3], [1]*Norel SA*, *Madrid, Spain*, [2]*Imasde Agroalimentaria SL*, *Madrid, Spain*, [3]*Nutyser SL*, *Burgos, Spain*.

Ten farms involving 2,240,000 male and female broilers were used to evaluate the efficacy of a probiotic (Ecobiol; EU Zootechnical Feed Additive number 4b1822; containing $1x10^9$ CFU of *B. amyloliquefaciens* CECT 5940 per g) on animal performance. The probiotic was added to the feed at a ratio of 1 kg/ton. Feeds were presented in pelleted form and analyzed for the probiotic concentration. In 9 farms, the former productive results of the farms were used as control, and they were compared with the productive results of the farm when the probiotic was added to the feed. In one farm, 3 buildings (10,000 broilers each) received the control feed and 3 buildings received the probiotic. In this farm, samples of feces were taken to analyze lactobacilli and coliform bacteria (CFU/g) at d 7 and 35. The experimental data were tested for homogeneity, pooled and combined in a meta-analysis. Parameters analyzed were final body weight (g), feed conversion (feed/gain) and mortality (%) for the whole period. At the end of the experimental period broilers fed the probiotic showed better feed conversion (−3.0%, 2.01 vs. 1.95 g/g; $P = 0.0262$) and less mortality rate (−36%; 8.3 vs. 5.3%; $P < 0.0001$) than controls. No significant differences were observed in body weight (2,632 vs. 2,678 g; $P = 0.3701$). Probiotic supplementation of diets increased Lactobacilli counts of feces at 7 d (8.14×10^8 vs. 1.73×10^9 CFU/g; $P = 0.0013$) and at 35 d of age (2.46×10^8 vs. 5.45×10^8 CFU/g; $P = 0.0024$). Coliform bacteria counts were significantly decreased by the use of the probiotic at 7 d (5.74×10^7 vs. 2.94×10^7 CFU/g; $P = 0.0268$) but only numerically at 35 d (1.56×10^7 vs. 9.74×10^6 CFU/g; $P = 0.1627$). It is therefore concluded that the probiotic tested improves feed conversion and reduces mortality in farms, possibly because of a better intestinal balance.

Key Words: probiotic, *Bacillus amyloliquefaciens*, broiler

979 Chemical and nutritive composition of low-fiber canola: The effects of seed coat color and enzyme supplementation. W. Jia*[1], M. Mogielnicka[1], A. Rogiewicz[1], G. Rakow[2], D. Hickling[3], and B. A. Slominski[1], [1]*University of Manitoba*, *Winnipeg, Manitoba, Canada*, [2]*Agriculture and Agri-Food Canada*, *Saskatoon, Saskatchewan, Canada*, [3]*Canola Council of Canada*, *Winnipeg, Manitoba, Canada*.

Canola breeding programs undertaken to improve meal quality without compromising oil content in the seed has led to the development of yellow-seeded *Brassica napus* and *B. juncea* canola. The objective of the current study was to evaluate the chemical and nutritive composition of meals derived from black- and yellow-seeded *B. napus* canola and canola-quality yellow-seeded *B. juncea*. In comparison with its black-seeded counterpart, meal derived from yellow-seeded *B. napus* canola contained more protein (49.8 vs. 43.8% DM), more sucrose (10.2 vs. 8.8% DM) and less dietary fiber (24.1 vs. 30.1% DM). Lower fiber content in yellow-seeded *B. napus* canola was reflected in lower content of lignin with associated polyphenols (3.7 vs. 7.1% DM). *B. juncea* canola showed intermediate levels of crude protein, sucrose and dietary fiber (47.4, 9.2 and 25.8%, respectively). Seed fractionation study demonstrated that the reduction in fiber content of yellow-seeded *B. napus* was a consequence of a bigger seed size, which averaged 3.9, 2.9 and 2.5 mg/seed, respectively, for yellow- and black-seeded *B. napus* and *B. juncea* canola, a lower contribution of the hull fraction to the total seed mass (11.0 vs. 15.9 and 13.7 g/100 g of seed), and a lower fiber content of the hull fraction (5.0 vs. 9.1 and 8.2 g/100 g of seed). The nutritive value of canola meal samples was investigated with broiler chickens fed corn/soybean meal-based diets containing 30% of meals from 3 to 17 d of age. A significantly higher ($P < 0.05$) total ileal digestibility of amino acids (88.8%) was observed in birds fed the yellow-seeded *B. napus* diet when compared with those fed diets containing black-seeded *B. napus* (83.5%) or *B. juncea* (84.2%) canola. In a second study, meal AME_n values for yellow- and black-seeded *B. napus*, and *B. juncea* were determined with broiler chickens (from 14 to 19 d of age) and were 2190, 1904, and 1736 kcal/kg DM, respectively. Enzyme addition significantly increased the AME_n values from 1943 to 2249 kcal/kg DM, on average, with the most pronounced effect observed for *B. juncea* canola (from 1736 to 2356 kcal/kg DM).

Key Words: canola meal, chemical composition, nutritive value

980 Pre-hatch colonization of the chick gut with probiotic bacteria. J. E. de Oliveira*[1], J. M. B. M. van der Vossen[2], A. M. T. Ouwens[2], E. Hangoor[1], and T. A. Scott[1], [1]*Provimi*, *Velddriel, the Netherlands*, [2]*TNO*, *Zeist, the Netherlands*.

Poultry are believed to hatch with minimal amounts of intestinal bacteria present. Gut microflora is believed to be established during or after hatch. This is considered to be a key event with consequences that affect not only the bird's health and performance, but also relates to food safety risks with establishment of food borne pathogens, particularly into the ceca. The current view is that establishment and maintenance of "good" or probiotic microbiota can minimize or prevent overgrowth of pathogens. This study was designed to test the viability to colonize the chick intestine with probiotic bacteria before hatch. Embryonized (E17) chicken eggs were in ovo inoculated with medium containing *B. subtilis* (P1) or *E. faecium* (P2), and compared with embryos from non-inoculated eggs (control). Number of bacteria was calculated as cell equivalents (CE) based on amount of bacterial DNA determined by qPCR at 48 h after inoculation in the embryo's gizzard content, and at hatch (96 h after inoculation) in the ceca content. Ceca results were also confirmed by plate culturing. P1 inoculation greatly increased bacteria number compared with the controls in both, the gizzard (1×10^5 vs. 3×10^2 CE/mL, respectively, $P < 0.01$) and the ceca (4.5×10^4 vs. 3×10^3 CE/mL, $P < 0.05$). Similar increase was found for P2 in both, the gizzard (4×10^5 vs. 4×10^3 CE/mL, $P < 0.05$) and in the ceca (8×10^7 vs. 1×10^7 CE/mL, $P < 0.01$). Culturing of ceca contents showed that P1 inoculation significantly increased the number of total bacteria colonies compared with the control (respectively, 3×10^9 vs. 6×10^7 CFU/mL, $P < 0.05$), with P2 showing intermediate value (1×10^9 CFU/mL). Based on these findings we concluded that the chick intestine can be colonized with probiotic bacteria before hatching. Future research will focus in determining if chicks that hatch with gut probiotic bacteria are less susceptible to pathogenic bacteria such as *Salmonella*, *Campylobacter* and *Clostridia*.

Key Words: probiotic, gut colonization, chicken

981 Methionine hydroxy-analogue as antioxidant defence enhancer. Q. Swenen[1,3], J. Buyse[1], P.-A. Geraert[2], Y. Mercier*[2], N. Everaert[1], A. Stinckens[1], H. Willemsen[1], L. Yue[1], and E. Decuypere[1], [1]*K.U. Leuven*, *Laboratory for Livestock Physiology, Immunology and Genetics, Department of Biosystems. Kasteelpark Arenberg 30, 3001 Leuven, Belgium*, [2]*Adisseo France S.A.S*, *F-92160 Antony, France*, [3]*University of Hasselt*, *Center for Environmental Sciences, Agoralaan building C, 3590 Diepenbeek, Belgium.*

DL-Methionine (DLM) and the DL-methionine hydroxy-analog (HMTBA) are 2 bio-available methionine sources commonly used in the poultry feed industry. Previous studies on absorption and metabolism demonstrated that when compared with DLM, HMTBA metabolism produces more cysteine (Martin-Venegas et al., 2006) which is implicated in glutathione synthesis, one of the major intracellular antioxidant defense mechanisms. The present experiment involved 4 groups of broilers fed different diets: high (23%) or low (18%) dietary protein level and 2 methionine sources (DLM or HMTBA 0.25%) in a factorial design. As expected, the high protein level led to an improved zootechnical performance compared with that on the low protein diet. Whatever the protein level considered, higher slaughter weights were obtained with HMTBA than with DLM. Oxidative status was assessed in plasma by superoxide dismutase (SOD), uric acid and lipid peroxidation and in liver by total, as well as reduced and oxidised glutathione levels. Results showed that irrespective of the dietary protein level, HMTBA-fed birds were characterized by a higher plasma SOD activity compared with that of DLM-fed birds. Moreover, higher plasma levels of uric acid and lower lipid peroxidation were observed with the high protein-HMTBA combination compared with all other treatments. Hepatic concentrations of reduced glutathione as well as total glutathione were significantly higher in the low protein-HMTBA treatment compared with all other treatments. This work allows concluding that HMTBA, besides being a viable alternative dietary supplement for DLM, also improves both extra- and intracellular antioxidant status.

Key Words: methionine sources, antioxidant, glutathione

982 Comparative in vitro antimicrobial activity and mechanism of bovine lactoferricin-derived synthetic peptides. Y. Liu*, Y. Xie, F. Han, Y. Gao, C. Luan, and Y. Wang, *Zhejiang University*, *Hangzhou, Zhejiang, China*.

Lactoferricins are positively charged, highly basic peptides exhibiting multifunctional immunoregulation of antibacterial, antifungal, antiendotoxin, and antiviral activities. Lactoferricin B (LFcinB), a 25 residue peptide derived from N-terminal part of bovine lactoferrin, causes depolarization of the cytoplasmic membrane in susceptible bacteria, but the exact mode of action of LFcinB is not fully understood. In the present study, synthetic bovine lactoferricin and 2 derivatives with 15–residue and 11–residue peptides were prepared to investigate their antimicrobial nature and mechanism. The antimicrobial properties of the peptides were measured against *Escherichia coli* ATCC25922, *Escherichia coli* K88, *Staphylococcus aureus*, *Salmonella typhimurium*, *Salmonella choleraesuis* and *Pseudomonas aeruginosa* and hemolytic activity of these peptides were examined using the erythrocytes of pig. We found that 15-residue and 11-residue bovine lactoferricin almost maintained the same level of growth inhibition as LFcinB against tested bacteria in the minimal inhibitory concentrations (MIC) range of 16–128 μg/mL and the minimal bactericidal concentrations (MBC) range of 64–256 μg/mL. Also, the 11-residue lactoferricin was found to have the lowest hemolytic activity compared with the intact peptide. The mechanism of lactoferricin on *E. coli* and S. aureus was investigated by imaging the cells with scanning electron microscopy (SEM). After 1 h of exposure to MIC of LFcinB, a profound effect on the cell morphology of *E. coli* was observed. Compared with the control, the LFcinB-exposed cells became filamentous and elongated. The cells increased over 4-folds in length, and did not appear to be dividing in a regular manner. S. aureus cells exposed to MIC of LFcinB for 1 h appeared to be significantly smaller and somewhat paler than the cells not exposed to LFcinB. These results showed that LFcinB has a minor permeabilizing effect on the cytoplasmic membrane of both gram-positive and gram-negative bacteria, indicating a possible intracellular target.

Key Words: bovine lactoferricin, antimicrobial activity, mode of action

983 Microbial programming in the gut of neonatal pigs. D. Petri* and A. G. Van Kessel, *University of Saskatchewan*, *Saskatoon, Canada*.

To investigate possible long-term effects of first colonizing bacteria on post weaning gut commensal microbiota composition, a gnotobiotic study was conducted using 27 germ-free piglets derived by caesarian

section. Pigs were assigned to one of 4 isolators and were inoculated with either *L. delbrueckii* (L), *S. infantarius* (S), *C. perfringens* (C) or *E. coli* (E). Piglets were conventionalized on d 7 with sow feces, merged and transferred to group pens. On d 20 of age, piglets were weaned and on d 28 samples of digesta were collected from the stomach, jejunum and colon. Using 16S rRNA gene-based molecular methods, analysis of anal swabs taken on d 4 confirmed monoassociation of S, C and E pigs and di-association with *E.coli* for L pigs. Data was analyzed as a 2x2x4 factorial ANOVA (gender, litter, treatment; SPSS17 GLM function with Tukey's HSD). A significant gender effect ($P = 0.03$) was observed for ADG between d 7 and d 28. DNA was extracted from contents and qPCR used to quantify bacteria as a percentage of log10 total bacteria 16S rRNA gene copies per g of contents. In the stomach, Bifidobacterium spp. were significantly lower ($P = 0.05$) in E vs. L (60.4% vs. 70.8%) and showed a trend ($P = 0.07$) toward a gender effect. Enterobacteria tended ($P = 0.08$) to be lower in L (90.6%) vs. C (96.0%). In the jejunum, enterobacteria were not different between E (85.0%) and L (86.7%) but these were lower ($P < 0.01$ and $P = 0.02$, respectively) than in C (92.7%). Clostridium cluster 1 spp. in E (97.0%) were significantly lower ($P = 0.03$) than in L (109.0%). Bifidobacterium spp. tended ($P = 0.07$) to be lower in C (54.4%) than L (66.1%). Lactobacillus spp. also showed a significant gender effect ($P < 0.01$) and a trend ($P = 0.06$) toward Lactobacillus spp. levels in treatment S (93.4%) being lower than in treatment L (98.5%). Enterobacteria showed a trend ($P = 0.07$) toward a litter effect. In colon a gender by treatment interaction ($P = 0.02$) was observed for Bifidobacterium spp. Early postnatal microbial colonization pattern and gender affect postweaning gut microbial profile.

Key Words: intestinal microbiota, qPCR, gnotobiotic

984 Efficacy of water-soluble antioxidants on chicken embryos challenged by hypoxia. J. E. de Oliveira*[1], Y. Li[2], H. Willemsen[2], E. Decuypere[2], and T. A. Scott[1], [1]*Provimi*, *Velddriel, the Netherlands*, [2]*Department of Biosystems*, *K.U. Leuven, Belgium*.

Searching for natural antioxidants (AO) is challenging because many sources, doses and conditions fail to demonstrate consistent results in vivo. Chick embryo models can be used as tools to indicate bioavailability and bioactivity of feed additives. This trial was designed to investigate the effect of in ovo administration of increasing doses of vitamin E analog Trolox (VEA) or grape extract (GRP) on development and antioxidant capacity (AOC) of chick embryos. Chicken eggs were challenged at 14 d of incubation (E14) by partially sealing egg shell pores to induce mild hypoxia. Embryos were challenged by hypoxia as a way to induce oxidative stress. At E17, a group of 120 eggs was assigned to one of the following treatments: control (CTR, no AO); injection with VEA at 3 concentrations (10, 30 or 100 ppm); injection with GRP at 2.5, 12.5 or 25 ppm, or injection with the combination of VEA 10 ppm and GRP 2.5 ppm (COMB). Sixteen embryos from each treatment were sampled at E18 and E19 to measure embryo yolk-free body mass (YFBM), yolk-sac mass (YKM), and liver mass (LM). Liver samples were analyzed for levels of superoxide dismutase (SOD), catalase (CAT), reduced glutathione (GSH), and glutathione disulphide (GSSG) to indicate AOC. VEA 10 and 30 ppm significantly increased YFBM in both ages compared with CTR ($P < 0.01$), with all other treatments showing intermediate values. There was no treatment effects on YKM or LM. Liver AOC showed VEA 30 ppm and GRP 12.5 ppm with higher CAT then CTR ($P < 0.01$), with other treatments showing intermediate values. SOD results at E18 showed GRP 25 ppm, COMB, and VEA 100ppm having significantly higher values then CTR ($P < 0.05$), with other treatments showing intermediate values. For GSH at E18 there were differences only among VEA levels, with VEA 10 ppm being significantly lower than CTR ($P < 0.01$). No differences were found for SOD or GSH at E19, or for GSSG at both ages. We concluded that hypoxia-challenged chick embryos are good models to test AO, and that VEA 30 ppm, GRP 12.5 ppm and COMB improved growth and liver AOC of challenged chicken embryos.

Key Words: antioxidants, chick embryo, hypoxia

985 Growth response, carcass evaluation and hematology of broilers fed graded levels of enzyme treated cocoa bean shell based diets. M. D. Olumide, O. A. Ogunwole*, and O. A. Adebiyi, *Department of Animal Science, University of Ibadan, Ibadan, Nigeria*.

Cocoa bean shell (CBS) is a waste from cocoa processing industries in Nigeria and it constitutes a serious disposal problem. Previous trials revealed that addition of enzyme reduces the theobromine (anti-nutrient in CBS). Hence, this study focused on evaluating the growth response, carcass characteristics and hematological parameters of broilers fed graded levels of enzyme treated CBS based diets. A total of 150 birds at 1d of age were allotted to 5 dietary treatments (3 replicates/treatment, 10 birds/replicate) in a completely randomized design. The treatments were: A (0% CBS-control diet); B (5% CBS with enzyme); C (10% CBS with enzyme); D (15% CBS with enzyme) and E (20% CBS with enzyme). Each of the diet was fed ad libitum to the experimental birds. The trial lasted 8 weeks. The feed intake, weight gained, carcass characteristics and hematological indices were then evaluated. There were significant differences ($P < 0.05$) in feed intake, weight gain and carcass characteristics of broilers fed the experimental diets. The results revealed that enzyme treated CBS can effectively replace up to 15% maize in the diets of broilers without any adverse effects.

Key Words: broiler, cocoa bean shell, hematology

986 Evaluation of the efficacy of Myco-Ad in preventing aflatoxin toxicity in broiler chicks.. C. A. Mallmann[1], P. Dilkin[1], L. Giacomini[1], R. H. Rauber[1], and D. Zaviezo*[2], [1]*Universidade Federal de Santa Maria, Laboratorio de Analises Micotoxicologicas (LAMIC)*, *Santa Maria, RS, Brasil*, [2]*Special Nutrients*, *Miami, FL*.

The dietary use of 0.25% Myco-Ad has been proven to effectively prevent the toxic effects of aflatoxin B1 (AFB), ochratoxin and T-2 toxin in broilers. Studies were conducted to evaluate the AFB adsorption capacity of Myco-Ad and its efficacy in preventing the deleterious effects of high levels of AFB in broiler chicks; as part of the regulatory anti-mycotoxin additives (AMA) approval process in Brazil. Three hundred day-old Cobb male chicks were placed in battery cages randomly distributed into 5 treatments with 6 replications each and fed a basal corn-soy diet containing or exceeding NRC recommendations. All ingredients used were tested free of mycotoxins contamination. Treatments were: 1 basal diet; 2 basal + 0.5% Myco-Ad; 3 basal + 2.8 ppm AFB; 4 basal + 2.8 ppm AFB + 0.25% Myco-Ad and 5 basal + 2.8 ppm AFB + 0.5% Myco-Ad. AFB was obtained from a culture material containing 96.4% AFB; 1.61% Aflatoxin B2 and 1.99% Aflatoxin G1 produced in LAMIC. Myco-Ad adsorption capacity of 1 ppm AFB was above 95% and 97% at 0.25 and 0.5%, respectively. Results at 21 d of age indicated that broiler fed 2.8 ppm AFB contaminated diet presented significant ($P \leq 0.05$)lower feed intake (31%), smaller body weight (29%), heavier liver weight (56%) and lower plasma protein levels (54%) than chicks fed the control diet. The addition of Myco-Ad (0.25–0.5%) significantly($P \leq 0.05$) improved feed intake (32–40%), body weight (24–33%), liver size (17–30%) and plasma proteins (19–33%) observed in chicks fed the AFB contaminated diet. The addition of 0.5% Myco-Ad to the chick diet did not show any statistical difference in performance, relative liver weight

or total plasma proteins compared with the control diet, demonstrating its lack of interference with the absorption of nutrients. These results indicated that 0.25% Myco-Ad was effective in preventing the toxic effects of AFB in broiler chicks; and therefore met the requirements for AMA registration in Brazil.

Key Words: Myco-Ad, aflatoxin

987 Efficiency of feed additives to reduce the effects of chronic exposure to aflatoxin and deoxynivalenol on growth and immune status of pigs. A. C. Chaytor*[1], M. T. See[1], J. A. Hansen[2], A. L. P. de Souza[2], D. C. Kendall[2], T. F. Middleton[3], and S. W. Kim[1], [1]*North Carolina State University*, *Raleigh*, [2]*Murphy-Brown LLC*, *Rose Hill, NC*, [3]*AgProvision LLC*, *Kenansville, NC*.

Three feed additives with potential ability to detoxify mycotoxins were tested to determine the effects on growth and immune responses of pigs fed diets containing aflatoxin (AF, 180 μg/kg) and deoxynivalenol (DON, 900 μg/kg) for 42 d. Gilts (n = 225, 8.8 ± 0.4 kg BW) were allotted to 5 treatments: PC (positive control without AF and DON); NC (negative control with AF and DON); A (NC + a clay based additive); B (NC + a clay and yeast cell wall based additive); and C (NC + a clay and enzyme based additive). Each treatment had 15 replicates with 3 pigs per pen. Feed intake and BW were recorded weekly, and blood was sampled on d 28 and d 42. On d 42, pigs were killed to obtain liver, kidney and spleen. Pigs in NC had smaller ($P < 0.05$) body weight (24.6 kg) and ADG (374 g) than PC (26.6 kg and 423 g) but were not different from others (25.4 kg and 393 g). Pigs in NC tended to have a smaller ADFI (753 g, $P = 0.090$) and gain:feed (0.495, $P = 0.052$) than PC (816 g and 0.520) but were not different from others (775 g and 0.507). On d 42, pigs in NC had a greater ($P < 0.05$) monocyte count (1432/μL) than PC (968), A (1053), and B (952). Pigs in NC tended to have a greater basophil count (158/μL) than PC (91, $P = 0.088$), but were not different from others. Pigs in NC tended to have a greater serum IgG (1.02 mg/mL) than PC (0.89, $P = 0.074$), and A (0.83, $P = 0.010$). Pigs in NC had a greater ($P < 0.05$) serum IgM (0.2 mg/mL) than PC (0.17) and A (0.17), and tended to have a greater (0.093, $P = 0.099$) serum IgM than B (0.18) and C (0.18). Serum TNF-α was not affected by dietary treatments. Pigs in NC had a greater ($P < 0.05$) % liver weight (14.9%) than PC (12.3%) and B (12.7%). Collectively, feeding 180 μg/kg AF and 900 μg/kg DON to pigs for a 42 d period reduced growth performance and increased immune challenges. Use of these feed additives tended to ameliorated the immune challenges but without affecting the growth performance.

Key Words: alfatoxin, deoxynivalenol, pigs

988 Discrepancies between in vitro and in vivo fumonisin binding with organoclays. J. N. Broomhead*, *Amlan International*, *Chicago, IL*.

An in vitro binding and an in vivo chicken study were conducted to test the efficacy of 2 experimental and 1 commercial organically modified clays (OMC) in binding fumonisin B_1 (FUM). In vitro mycotoxin binding was conducted at physiological conditions of the stomach (pH 3.0) followed by the intestine (pH 6.5) at 1000:1 binder-to-toxin ratio. The in vivo study consisted of 200 d-old male broiler chicks assigned to 8 treatments with 5 replicate pens of 5 chicks each. The 3 OMC were either fed alone (0.5% dietary inclusion) or in combination with 70 ppm FUM supplied from naturally contaminated corn. Chicks were placed in battery-brooders and fed experimental diets for 21 d. On d 21, 3 birds per replicate were killed with CO_2, weighed, and livers removed and weighed from 3 birds per pen for determination of relative liver weight. After weighing, the livers were frozen and then 2 livers per pen were later analyzed for sphinganine (SA) and sphingosine (SO) concentration. In vitro FUM binding results were high and did not vary greatly between OMC (85 to 96% FUM bound). Replacing the normal dietary corn with FUM contaminated corn (70 ppm dietary FUM) reduced ($P < 0.005$) body weight gain (BWG) and feed intake, and increased ($P < 0.0001$) liver SA and SA:SO ratio. Relative liver weight and feed conversion were not significantly affected by treatments ($P > 0.05$). Inclusion of one of the experimental clays to the FUM diet significantly decreased ($P < 0.0005$) BWG and increased ($P < 0.0001$) SA and SA:SO ratio compared with the FUM, alone, treatment. In conclusion, none of the OMC ameliorated the toxic effects of FUM to the broilers. Also, the in vitro FUM binding procedure used may not be a good predictor of in vivo efficacy and in vivo studies should always be conducted to validate in vitro results.

Key Words: fumonisin, in vitro, in vivo

989 Comparison study of alternative cryoprotectants for cryopreserving bull spermatozoa. M. M. Awad*, *Animal Production Dept. Faculty of Agriculture, Suez Canal University*, *Ismailia, Egypt*.

Mammalian spermatozoa experience osmotic stress when the glycerol is added to the cells before freezing and removal from the cells after thawing. To minimize osmotic damage, alternative cryoprotectants, having lower molecular weights and greater membrane permeability than glycerol, were evaluated to determine their effectiveness for cryopreserving bull spermatozoa. The primary goal of this study was to compare glycerol as the most common cryoprotectant of bull spermatozoa to ethylene glycol and methyl as alternative cryoprotectants. Bull semen was diluted with tris-egg yolk extender containing 3% glycerol, 3, 2 and 1% ethylene glycol and 3, 2 and 1% methyl. Bull semen was frozen in pellets form using the cold surface of cattle fat. Computer assisted sperm analysis (CASA) assay was used to study the post-motility properties of bull spermatozoa. Bull spermatozoa exhibited higher percentages ($P < 0.01$) of all motile spermatozoa properties when frozen in extender containing 3% glycerol compared with 3, 2 and 1% ethylene glycol or 3, 2 and 1% methyl cryoprotectants. It is concluded that glycerol concentrations of 3% in the extender is the most suitable cryoprotectant for cryopreservation of bull spermatozoa.

Key Words: cryopreservation, bull spermatozoa

990 Effects of anti-lipid peroxidation supplements on frozen-thawed boar spermatozoa. B. D. Whitaker*, R. Taupier, and S. J. Casey, *Ferrum College*, *Ferrum, VA*.

This study evaluated the effects of 2 anti-lipid peroxidation supplements when added to the thawing and incubation medium of frozen-thawed boar spermatozoa. Semen pellets were thawed and incubated for 1 h in media with either 1.0 m*M* α-tocopherol or diethylenetriamine (DETA, nitric oxide analog). After incubation, the acrosome reaction was inducted using calcium ionophore A23187 and acrosomes were evaluated using Wells-Awa staining. The amount of spermatozoa with fragmented DNA was evaluated using silver staining after single-cell gel electrophoresis. The 1.0 m*M* DETA supplementation had a significantly higher ($P < 0.05$) percentage of acrosome reacted spermatozoa (84.4 ± 4.1%) compared with the control (78.3 ± 4.2%) and the 1.0 m*M* α-tocopherol supplementation (78.0 ± 3.9%). There was no difference between the control and the 1.0 m*M* α-tocopherol supplementation. The control had a significantly higher ($P < 0.05$) percentage of spermatozoa with fragmented DNA tails (59.3 ± 4.3%) compared with the 1.0 m*M* DETA (28.7 ± 4.1%) and the 1.0 m*M* α-tocopherol supplementation (28.0 ± 3.8%). There was no difference between the 1.0 m*M* DETA and the 1.0 m*M* α-tocopherol supplementation. These results indicate that supplementing with either 1.0 m*M* DETA or α-tocopherol during semen thawing protects against DNA fragmentation and increases the percent of spermatozoa capable of completing the acrosome reaction.

Key Words: swine, antioxidant, sperm

991 Reproductive performance of sows inseminated with various doses of frozen-thawed semen. K. S. Fisher*[1], T. S. Stewart[1], P. H. Purdy[2], H. D. Blackburn[2], W. L. Singleton[1], B. L. Sparks[1], P. J. Gunn[1], and G. A. Bridges[1], [1]*Purdue University*, *West Lafayette, IN,* [2]*National Animal Germplasm Program, NCGRP, ARS, USDA*, *Fort Collins, CO*.

Genebanks have a limited supply of frozen-thawed boar semen (FTS), thus it is critical to determine the optimal dose of FTS required for reproductive proficiency. Crossbred sows (n = 106) were used in 3 replicates to determine the efficacy of 4 doses of FTS with a single AI. After weaning, estrous detection was conducted using a boar and sows received a single transcervical insemination 24 h following the onset of estrus. At AI, sows were randomly assigned to receive FTS from 1 of 2 boars (boar 1, n = 36; boar 2, n = 61) at a post-thawing dose of 0.25 (n = 24), 0.50 (n = 25), 0.75 (n = 24), or 1.0 (n = 24) × 10^9 motile cells. Thirty d after AI, sows were slaughtered and viable fetuses and corpora lutea were counted. The effects of replicate (REP), boar, dose, and all interactions on pregnancy rate and number viable fetuses were evaluated using the Glimmix and Mixed procedures of SAS. Pregnancy rate did not differ among semen doses (0.25- 25%, 0.5- 44%, 0.75- 54%, 1.0- 42%), but was decreased ($P < 0.05$) for boar 1 (22.2%) compared with boar 2 (52.5%). The number of viable fetuses recovered was decreased ($P < 0.05$) for boar 1 (4.6 ± 1.4) compared with boar 2 (8.6 ± 0.7). There was a REP x dose interaction ($P < 0.05$) for number of fetuses. The 1.0 and 0.75 doses resulted in the greatest number of fetuses in REP 1 and REP 3, respectively, with no difference among doses in REP 2. Across replications, a linear effect of dose on viable fetuses was observed ($P < 0.05$) and a tendency for a quadratic effect ($P < 0.1$). To ascertain the dose most appropriate to use if semen was limited, the total viable fetuses per sow inseminated was multiplied by the number of potential doses available if only 1 × 10^9 motile sperm cells existed. Although only non-significant differences among doses were found (0.25- 0.91 ± 2.1, 0.50- 3.4 ± 1.7, 0.75- 4.8 ± 1.7, 1.0- 3.3 ± 1.7), results suggested, from the perspective of maximizing both the number of sows that can be inseminated with a limited supply of semen and reproductive proficiency, that the optimal dose of semen to utilize per insemination was between 0.50 and 0.75 × 10^9 motile sperm cells.

Key Words: germplasm preservation, semen, swine

992 Analysis of proteomic changes during sperm capacitation associated with sperm fertility. Y. J. Park*, S. A. Oh, W. S. Kwon, S. J. Yoon, Y. H. Kim, E. A. Mohamed, Y. A. You, and M. G. Pang, *Department of Animal Science & Technology and BET Research Institute, Chung-Ang University*, *Ansung, Gyeonggi-Do, Korea*.

Spermatozoa are required to undergo the processes of capacitation before fertilization. Since spermatozoa are transcriptionally silent, the functional metamorphosis of these cells during capacitation is accomplished entirely by post-translational modifications. Despite the importance of this process, very few studies have attempted to define the precise nature on the molecular level. The objective of this study was to characterize the supposed differences in fertility with respect to capacitation-related proteins. We undertook differential proteome profiling before and after capacitation of spermatozoa from fertile bulls with extreme non-return rates (NRR): a low fertility group (45.10±4.95) and a high fertility group (82.45±6.26). For identification of capacitation related proteins associated with fertility, capacitation was induced by 10 μg/mL heparin for 20 min and was confirmed by chlorotetracycline assay where significantly increasing in capacitated sperm was observed. Two-demensional gel electrophoresis (2-DE) was carried out with triplicate samples of pooled spermatozoa before and after capacitation from 3 low and 3 high fertility bulls. Protein expression levels were compared using PD-Quest software. The marked difference in spot intensity was arbitrarily set as a >3-fold difference following analysis data from the software manufactures. Twelve protein spots showed differences

between high and low fertility groups and seven of these proteins were identified by LC/MS-MS. Glyceraldehyde 3-phosphate dehydrogenase, phosphatidylethanolamine-binding protein 1, bovine mitochondrial F1-ATPase complexed with Aurovertin B and actin-related protein T2 were more expressed in high fertility group. On the other hand phospholipid hydroperoxide glutathione peroxidase, ropporin and enolase 1 were more expressed in high fertility group. These proteins are in correlation with sperm physiology, and these proteins may be used as sperm fertility markers.

Key Words: fertility, capacitation, proteome

993 Prognosis of bull fertility using sperm penetration assay. Y. J. Park*, S. A. Oh, S. J. Yoon, W. S. Kwon, Y. H. Kim, E. A. Mohamed, Y. A. You, and M. G. Pang, *Department of Animal Science & Technology and BET Research Institute, Chung-Ang University*, *Ansung, Gyeonggi-Do, Korea*.

The prediction of sperm fertility is of paramount importance for breeding animal herds when artificial insemination is applied. While the fertility assays provide valuable quantitative data, they yield limited information concerning the functional competence of the spermatozoa. The objective of this study was to standardize a method for predicting in vivo fertility in bulls using the in vitro penetration assay. To increase the assay sensitivity, each step in the procedure was standardized. We found that maximum penetration of hamster zona-free oocytes (SPA) obtained from heparin-treated (10 μg/mL) sperm cells for 20 min ($P <$ 0.05). The SPA result showed significant correlation with historic average non-return rate (NRR) ($P < 0.05$). To determine the normal range for the SPA, lower limits of the sperm fertility index from SPA were established as 2.55 to cut-off more than 70% NRR using the receiver operating characteristic curve. The overall accuracy was 93.33% for the low and high NRR, sensitivity and specificity were 92.86 and 93.75 respectively. The protocol increases the potential to discriminate between bulls with good and poor fertility. Although the conditions for the capacitation and penetration of the spermatozoa are greatly different from the in vivo situation, nevertheless the test provides meaningful information on the bull fertility.

Key Words: sperm, fertility, sperm penetration assay

994 Semen quality index of broiler breeder cockerels subjected to different collection techniques. A. Ijaz*, M. U. Sohail, H. Rehman, M. Aleem, A. Riaz, and M. S. Yousaf, *University of Veterinary and Animal Sciences*, *Lahore, Pakistan*.

Present study aims at evaluating 3 different semen collection techniques; abdominal-massage, live-mount and dummy-mount technique, in broiler breeder cockerels. Six cockerels (50 week old), randomly selected from a natural breeder farm, were kept in individual floor pens. After one week of acclimatization, cockerels were trained for semen collection using the abdominal-massage technique and dummy-mount technique. Thereafter, the cockerels were subjected to abdominal-massage, live-mount and dummy-mount technique in phases for 14 d each, with 2 weeks period of rest among techniques. Semen was daily collected from 6 cockerels pooled. Semen was evaluated for number of semen ejaculates, semen volume per ejaculate, visual appearance of semen, sperm motility and sperm concentration. Visual appearance of semen was indexed as watery, milky or opaque. Diluted semen was placed on pre-warmed slide and examined under microscope for motility. Sperm concentration was estimated using Neubauer hemocytometer. Data regarding semen volume, visual appearance, sperm motility and concentration were analyzed using ANOVA, while data regarding number of ejaculates were subjected to chi-squared test. Live-mount technique gave higher ($P < 0.01$) number of ejaculates and volume per ejaculate (44, 0.26 ± 0.24) compared with abdominal-massage technique (26, 0.04 ± 0.01) and dummy-mount technique (37, 0.15 ± 0.03). Visual appearance index of semen, sperm motility and sperm concentration remained unaffected ($P > 0.05$) independent of the techniques employed. In conclusion, live-mount technique is better for cockerel semen collection compared with abdominal-massage and dummy-mount technique.

Key Words: cockerel, semen, collection method

995 Effect of supplemental sialic acid on the fertility of in vitro stored turkey semen. J. A. Long* and T. Conn, *Beltsville Agricultural Research Center*, *Beltsville, MD*.

The fertility of turkey semen stored for longer than 6 h in vitro is dramatically lower than that of fresh semen. Previously we have shown that physiological changes occur on the sperm membrane when turkey semen is held for 24h at 4°C. In particular, the carbohydrate content of the sperm glycocalyx undergoes significant alterations, including loss of terminal sialic acid residues. The objective of the present study was to determine if the glycocalyx can incorporate exogenous sialic acid and whether incubation with sialic acid in vitro will improve the fertility of stored turkey semen. Semen was collected from toms and extended with Beltsville Poultry Semen Extender supplemented with 0, 60, 70, 80, 90 or 100 μg/ml of sialic acid. At 30 min intervals for up to 3h, aliquots were removed, stained with LFA (a sialic acid-specific lectin), counterstained with propidium iodide (PI) and assessed by cell flow cytometry. The mean fluorescence intensity (MnFI) of viable (PI negative) sperm was compared with control sperm samples at each interval. Significantly higher MnFI occurred at 30 and 60 min ($P < 0.05$) in the presence of sialic acid; however, further increases in MnFI were not noted at later time points. A dose-response effect ($P < 0.05$) occurred for the 60, 70 and 80 μ/ml treatments only. Twelve-week fertility trials were conducted using semen held at 4°C for 24h with and without sialic acid. Of the 5 doses evaluated, 80 μg/ml supported the highest fertility rates (mean 81.2 ± 9.1%) for the first 6 weeks of insemination. Taken together, these data suggest a possible strategy for improving the fertility of in vitro stored turkey semen.

Key Words: glycocalyx, NANA, semen storage

996 Vitrification of bovine blastocysts: Effects of cooling with an aluminum block submerged in liquid nitrogen versus liquid nitrogen cooled air and lowering sodium and calcium concentrations in vitrification media. S. G. Kruse* and G. E. Seidel, *Colorado State University*, *Fort Collins*.

Our objective was to improve procedures for vitrifying bovine blastocysts produced using standard in vitro procedures. In Experiment 1, we studied a new base medium with lowered sodium and calcium concentrations based on the hypothesis that this would result in a lower chance of sodium and calcium toxicity. Base media contained either 1) normal concentrations of sodium (120 m*M*) and calcium (2 m*M*) (CONT; n = 151) or 2) 60 m*M* sodium choloride + 60 m*M* choline chloride and 0.5 m*M* calcium (LOW; n = 139). Blastocysts were exposed to 5 M ethylene glycol made in CONT or LOW base medium (V1) for 3 min at 22°C and moved to 6.5 M ethylene glycol + 0.5 M galactose + 18% Ficoll made in CONT or LOW base medium (V2) at 22°C and immediately loaded into 0.25 mL straws. After 35 s, embryos were vitrified by either 1) standard cooling in liquid nitrogen cooled air (AIR) for 1 min or 2) cooling via contact of straw walls with columns drilled into an aluminum block immersed in liquid nitrogen (BLK) for

2 min, and then directly plunged into liquid nitrogen. Embryos were warmed by holding straws in air at 22°C for 10 s, placing them in a water bath at 37°C for 20 s, mixing embryos with 1.0 M galactose diluent in the straw for 2 min and expelling into CONT or LOW base medium. Embryos were recovered, rinsed through holding medium, and cultured in chemically defined medium for 24 h before evaluation. Post warming survival did not differ ($P > 0.1$) between base medium (CONT = 22.5%; LOW = 25.9%). Experiment 2 was conducted as Experiment 1 (some overlap of embryos used) except the AIR (n = 134) versus BLK (n = 138) comparison was made. There was no difference ($P > 0.1$) in survival due to vitrification method (AIR = 32.1%; BLK = 31.9%). We recommend use of the BLK vitrification method as it is both easier to use and more consistent.

Key Words: blastocyst, vitrification, bovine

997 Efficacy of embryo transfer in lactating dairy cows during summer using fresh or vitrified embryos produced in vitro with sex-sorted semen. B. M. Stewart[1], J. Block[2,4], P. Morelli[1], A. E. Navarrette[1,3], M. Amstalden[3], L. Bonilla[4], P. J. Hansen[4], and T. R. Bilby*[1,3], [1]*Texas AgriLife Research and Extension, Texas A&M System*, *Stephenville*, [2]*OvaTech, LLC*, *Gainesville, FL*, [3]*Texas A&M University*, *College Station*, [4]*University of Florida*, *Gainesville*.

Objective of the study was to determine whether transfer of fresh or vitrified embryos produced in vitro with sex-sorted semen could improve pregnancy rates during summer in lactating dairy cows versus artificial insemination (AI). Lactating dairy cows (n = 722) were enrolled during summer at 2 commercial dairies in Texas. Cows were randomly assigned to one of 3 treatments: AI (n = 227), embryo transfer-vitrified (ET-V; n = 279) or embryo transfer-fresh (ET-F; n = 216). Embryos were produced in vitro using sex-sorted semen and cultured in BBH7 culture medium until d 7 after insemination. For vitrification, grade 1 expanded blastocysts were vitrified using the open-pulled straw method. Fresh embryos were grade 1 blastocysts and expanded blastocysts. Cows were submitted to an estrous synchronization protocol and either time-AI or AI following detected estrus (day of estrus = d 0). On d 7, cows were ultrasounded for presence or absence of a corpus luteum (CL). A vitrified or fresh embryo was transferred to cows with CL in ET-V and ET-F groups. Cows were synchronized if progesterone was <1 ng/mL on d 0 and presence of CL on d 7. There was no treatment by farm interactions. At initial pregnancy diagnosis (40 ± 7 d), proportion of cows pregnant was greater ($P < 0.01$) for ET-F versus both ET-V and AI for all cows (42.1 vs. 29.3 and 18.3%) and synchronized cows (45.5 vs. 30.9 and 22.9%). Also, proportion of cows pregnant was greater for ET-V than AI among all cows ($P < 0.01$) and tended ($P = 0.10$) to be greater among synchronized cows. At second pregnancy diagnosis (97 ± 7 d), proportion of cows pregnant among all cows was greater ($P < 0.05$) for ET-F and ET-V versus AI (36.4 and 25.7 vs. 17.0%) and ET-F was greater ($P < 0.05$) than ET-V. Among synchronized cows, proportion of cows pregnant was greater for ET-F than ET-V and AI (39.4 and 27.0 vs. 21.2%); there was no difference between ET-V and AI. There was no effect of treatment on embryo loss. Transfer of vitrified and fresh embryos produced in vitro using sex-sorted semen can improve fertility in lactating dairy cows during summer.

Key Words: embryo, heat stress, dairy

998 The importance of fibroblast growth factors on bovine embryo development in vitro. S. D. Fields*, P. J. Hansen, and A. D. Ealy, *University of Florida*, *Gainesville*.

The objective was to test the hypothesis that fibroblast growth factors (FGF) regulate early embryonic development. The first 2 experiments were performed to determine if embryo-derived FGFs are required during development. In Exp 1, bovine embryos were produced in vitro and cultured in modified synthetic oviductal fluid (mSOF) containing either 20 μ*M* SU5402, an FGF receptor inhibitor, or carrier (0.2% DMSO) at D 0 or 4. There was no effect of SU5402 on cleavage rate at Day 3. SU5402 reduced ($P = 0.04$) the percent of oocytes that were blastocysts on D 7 compared with controls when added at D 0 (5.9 ± 2.1 vs. 16.9 ± 2.4) but not when added at Day 4. Exp 2 tested if blocking FGF action at the blastocyst stage would affect subsequent cell number. D 8 blastocysts were placed into individual culture drops of mSOF containing 0.2% DMSO or 20 μ*M* SU5402. SU5402 decreased ($P = 0.04$) the number of cells at D 11 (211.1 ± 27.5 vs. 297.8 ± 25). Exp 3 was performed to test if supplemental FGF2 would enhance development to the blastocyst stage. Embryos were cultured in mSOF containing 0, 5, or 100 ng/mL FGF2. There was no effect of FGF2 on cleavage or percent of oocytes that were blastocysts at D 7 or 8. For Exp 4, 8–16 cell embryos were placed in fresh mSOF containing 0, 5, or 100 ng/mL FGF2 at D 5 after insemination. There was no effect of concentration of FGF2 on percent of oocytes that were blastocysts at D 7 or 8, number of trophectoderm cells or inner cell mass cells, or the ratio. Effects of higher concentrations of FGF2 were examined in Exp 5. Embryos received 0 ng/mL of FGF2 or 500 ng FGF2 at D 0, D 4, or D 0 and 4. There was no effect of FGF2 on cleavage. Addition of FGF2 at both D 0 and 4 (27.4 ± 1.3) increased ($P \leq 0.03$) the percent of oocytes that became blastocysts on D 7 compared with control (19.7 ± 1.3) or FGF2 on D 4 (20.4 ± 1.3), but did not differ from FGF2 treatment on D 0 (23.2 ± 1.3). In summary, FGFs are important for normal blastocyst development. One of these, FGF2, increased the competence of embryos to become blastocysts at high concentrations.
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Key Words: fibroblast growth factor-2, embryo

999 Changes in cotyledonary vascular architecture with advancement of placentomal (PLAC) type during gestation in the ewe. S. Hein*[1], A. Uthlaut[1], P. W. Nathanielsz[1,2], and S. P. Ford[1], [1]*Center for the Study of Fetal Programming, Dept. of Anim. Sci., University of Wyoming*, *Laramie,* [2]*Center for Pregnancy and Newborn Research, Dept. of OB/GYN, University of Texas Health Sciences Center*, *San Antonio*.

PLAC advance morphologically from Type A to Types B, C, or D during the second half of gestation in sheep in association with exponential fetal growth. Several research groups have attempted to understand the changes in the cotyledonary vascular bed with advancing PLAC type using routine histological evaluation of individual PLAC sections which fail to provide a 3 dimensional view of the vascular architecture, leading to conflicting results. We utilized vascular casting to visualize cotyledonary capillary bed 3-dimensional structure. Six multiparous ewes of similar age and body condition were necropsied at d135 gestation and a Type A, B, C, and D PLAC collected from each. The cotyledonary arterial vasculature of each PLAC was perfused with Biodur (Heidelberg, Germany), forming a flexible vascular cast. The surrounding tissue was removed by storage in a 5% KOH solution for 4–6 weeks. The vascular cast images were then visualized on a tabletop Scanning Electron Microscope (TM-1000), and analyzed for capillary area density (CAD, cotyledonary capillary area/cotyledonary area) and capillary diameter (CD) using ImageJ (NIH). Data are M Â ± SEM; differences determined by ANOVA. Cotyledonary CAD and CD (Table 1) and arteriole branching increased as PLAC progressed from type A

to type D. The cotyledonary villous capillary trees of later stage PLAC (C and D) extend for greater distances along villi, became increasingly organized, and consolidated into large nodes. These changes suggest an increased capacity for maternal to fetal nutrient transfer with PLAC advancement in late gestation.

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Table 1. CAD and CD of Differing Placentome Types

	A	B	C	D	P-value
CAD (%)	58.25±1.54^{a}	59.88±1.78^{a*}	64.16±1.54^{b*}	67.12±1.26^{b}	a,b<0.05, *<0.10
CD (μm)	8.18±0.36^{a}	7.59±0.42^{a}	9.31±0.36^{b}	10.70±0.30^{c}	a,b,c<0.05

Key Words: placentomal type, cotyledonary vasculary, sheep

Production, Management and the Environment: Beef 2

1000 Effects of anabolic implants on growth and carcass traits of feedlot steers and heifers: A meta-analysis. C. D. Reinhardt*[1] and L. R. Corah[2], [1]*Kansas State University*, *Manhattan,* [2]*Certified Angus Beef*, *Manhattan, KS*.

Data from 82 studies (60 steer and 22 heifer studies) were compiled and analyzed to evaluate the effects of anabolic implants on feedlot performance and carcass traits. Dependent variables in the model included ADG, G:F, DMI, dressing percentage, HCW, and marbling score. Categories created for type and dosage of active compound were: low dose primarily estrogenic hormone (E2; LOW), moderate dose E2 (MOD), intermediate dosage combination E2 + trenbolone acetate (TBA; INT), and full-strength TBA or E2 + TBA (HIGH). Treatment categories were: no implant, single MOD, single HIGH, delayed HIGH, initial and terminal MOD, initial and terminal INT, initial LOW and terminal HIGH, initial MOD and terminal HIGH, initial INT and terminal HIGH, and initial and terminal HIGH. Implant treatment was the fixed effect in the model, and trial was a random effect. Increasing the implant dosage (potency of individual implants or reimplant vs. single implant) increased ADG, G:F, and HCW in both steers and heifers ($P < 0.01$). Increasing implant dosage in steers decreased marbling score ($P < 0.01$) but did not affect yield grade ($P = 0.11$). Increasing implant dosage in heifers decreased yield grade and marbling score ($P < 0.01$) so that when marbling score was adjusted to a common yield grade, there was no effect of implant on marbling score ($P = 0.52$). The percentage of Prime and Choice carcasses increased at a decreasing rate with increased marbling score, fitting the equation: Percent Prime + Choice = (sin[-2.2144 + 0.00548 * Marbling score]) * 100; (R2 = 0.86). Implants reduce marbling content of steers, but high-potency implant programs will have a decreasing impact on quality grade in cattle with high average marbling score compared with cattle with low average marbling score.

Key Words: carcass, feedlot, implant

1001 Factors affecting *Certified Angus Beef* acceptance in spring-born, black-hided beef calves. G. D. Fike*[1], M. E. King[1], L. R. Corah[1], and W. D. Busby[2], [1]*Certified Angus Beef LLC*, *Wooster, OH*, [2]*Iowa Tri-County Steer Carcass Futurity*, *Lewis*.

Logistic regression was used to determine factors affecting *Certified Angus Beef* (CAB) acceptance in black-hided beef calves (n = 966) born during the springs of 2002 to 2007 at a central Missouri ranch. After weaning, all calves were fed, implanted and managed similarly each year in a southwest Iowa feedlot and were harvested when visually determined to have one cm of fat cover. Calves born in 2006 were excluded from the analysis because percent Angus of the calf could not be determined. For categorical variables, the odds ratio (OR) for each variable category was the odds of calves in that category qualifying for the CAB program compared with calves in the reference category (OR = 1). The OR for continuous variables was the odds of calves qualifying as CAB for each unit increase in the continuous variable. Gender and percent Angus of the calf significantly affected CAB acceptance. Steers were 0.59 times as likely to qualify as CAB as heifers. Calves that were 0–25% or 26–50% Angus were 0.45 and 0.38, respectively, times as likely to meet CAB requirements as were calves that were 51–100% Angus. CAB acceptance tended ($P = 0.06$) to be influenced by time of birth within the calving season. The oldest calves (born during the first 21 d) tended to be twice as likely to be CAB than the youngest calves (born >63 d into the calving season). As adjusted final weight (OR = 1.014) and back fat thickness (OR = 2.93) increased, the odds of CAB acceptance were higher. The odds of CAB acceptance were lower in calves with higher feedlot ADG (OR = 0.35) and heavier delivery weight/d of age (OR = 0.003). These data indicate that CAB acceptance is affected by gender, percent Angus, delivery weight/d of age, ADG, back fat thickness and adjusted final weight and tends to be influenced by time of birth in spring-born, black-hided beef calves.

Key Words: CAB acceptance, spring-born beef calves, percent Angus

1002 Effect of time of birth within the spring calving season on performance and carcass traits of beef calves fed in the Iowa Tri-County Steer Carcass Futurity. G. D. Fike*[1], M. E. King[1], L. R. Corah[1], and W. D. Busby[2], [1]*Certified Angus Beef LLC*, *Wooster, OH*, [2]*Iowa Tri-County Steer Carcass Futurity*, *Lewis*.

Calves (n = 1,369) from a central Missouri ranch born from 2002 to 2007 were used to determine the effect of birth sequence within a spring calving herd on feedlot performance and carcass traits. After weaning, all calves were fed, implanted and managed similarly each year in a southwest Iowa feedlot in the Iowa Tri-County Steer Carcass Futurity program and were harvested when visually determined to have 1 cm of fat cover. Calving sequence periods were defined as: d 1–21 (early = E); d 22–42 (mid-early = ME); d 43–63 (mid-late = ML); d > 63 (late = L). The effect of birth sequence on continuous outcomes was quantified using one-way ANOVA. Chi-squared analysis was used to determine the effect of birth sequence on rates. E calves were heavier at feedlot delivery than ME, ML and L calves (328.2, 321.7, 310.8 and 291.4 kg, respectively; $P < 0.05$). Adjusted final and hot carcass weights were greater for E than for L calves (554.2 vs. 538.6 kg and 341.1 vs. 332.5 kg, respectively; $P < 0.05$), but were similar to ME and ML calves. The percentage of Angus in the E calves was greater than ME, ML and L calves (49.3, 44.9, 39.4 and 43.3%, respectively; $P < 0.05$). Disposition scores were lower for E and ME calves than for L calves ($P < 0.05$). ADG for E calves was less than ML calves (1.46 vs. 1.53 kg/d; $P < 0.05$), but not different from ME or L calves. L calves had better feed efficiency than E and ME calves (6.72, 7.14 and 7.03 kg/kg, respectively; $P < 0.05$). Marbling scores were greater for E and ME calves than ML and L calves ($P < 0.05$). The percentage of calves grading USDA Choice decreased as calves were born later in the calving season ($P = 0.009$), and *Certified Angus Beef* (CAB) acceptance rate followed a similar pattern in black-hided calves ($P < 0.0001$). Calves born during the first 21 d of the spring calving season had heavier delivery, adjusted final and carcass weights; greater marbling scores and a higher percentage grading Choice and CAB than their latest born counterparts.

Key Words: beef calves, carcass and performance, CAB acceptance

1003 Effects of roughage source and dried corn distiller's grains concentration on feedlot performance and carcass characteristics. C. L. Maxwell*[1], M. S. Brown[1], N. A. Cole[2], B. Coufal[1], J. O. Wallace[1], J. Simroth-Rodriguez[1], and S. Pratt[1], [1]*West Texas A&M University*, *Canyon,* [2]*USDA ARS Conservation and Production Research Laboratory*, *Bushland, TX*.

Physical attributes of roughages used in finishing diets may impact the extent of ruminal digestion of dried distillers grains (DDG) and growth performance. Crossbred steers (n = 380) were adapted to a common finishing diet, blocked by BW, implanted with Revalor-S (120 mg of

trenbolone acetate and 24 mg of estradiol), and assigned to treatments of roughage source (sorghum-sudan hay [SH] or sorghum-sudan silage [SS]) and DDG concentration (0 or 20% of diet DM). Cattle were housed in 40 soil-surfaced pens with at least 16.7 m^2 of pen space and 30.5 cm of bunk space/animal. Roughages were included on an equal NDF basis. All diets contained 3.4% non-protein N from urea (1.2% urea) and cottonseed meal was utilized as a protein source in 0% DDG diets. Cattle were fed twice/d for 108 d (initial BW = 410 ± 13 kg). Steers fed 20% DDG ate 4.1% more DM than steers fed 0% DDG (10.42 vs. 10.85 kg, $P = 0.007$), but SS or SH did not influence DMI ($P = 0.55$). Overall shrunk ADG on a live basis was not altered by treatment ($P > 0.57$). Gain efficiency on a live basis was not altered by SS or SH ($P = 0.77$), but steers fed 0% DDG were 2.8% more efficient than steers fed 20% DDG ($P = 0.008$). There was a roughage source × DDG interaction for carcass-adjusted ADG and gain efficiency, dressing percentage, hot carcass weight, and LM area ($P < 0.08$). Adjusted ADG was increased 7% by 20% DDG with SS ($P = 0.05$), but not with SH ($P = 0.39$). Gain efficiency was reduced ($P = 0.03$) 4.8% by 20% DDG with SH, but was not altered ($P = 0.71$) with SS. Dressing percentage was reduced by 20% DDG with SH (63.0 vs. 62.4, $P = 0.02$) and increased by 20% DDG with SS (62.4 vs. 63.3, $P < 0.001$). Hot carcass weight was not altered by DDG with SH, but was increased 8 kg by 20% DDG with SS. The LM area was increased by 20% DDG with SS ($P = 0.02$), but not with SH ($P = 0.29$). Marbling score was higher when DDG was fed with SS or SH (380 vs. 390, $P = 0.06$). Results suggest that rate of gain on a carcass basis can be improved by feeding DDG with SS, but performance can be reduced when DDG is fed with SH.

Key Words: feedlot cattle, growth performance, dried distiller's grains

1004 The relative importance of weaning management and vaccination history on finishing performance and carcass characteristics of beef calves. M. J. Macek*[1], K. C. Olson[1], J. R. Jaeger[2], T. B. Schmidt[3], D. U. Thomson[1], J. W. Iliff[1], and L. A. Pacheco[1], [1]*Kansas State University*, *Manhattan,* [2]*Western Kansas Agricultural Research Center*, *Hays,* [3]*Mississippi State University*, *Starkville*.

Angus × Hereford calves (n = 437; average initial BW = 208 ± 25 kg) were stratified by BW, sex, and age and assigned randomly to 1 of 3 weaning treatments that corresponded to length of time between maternal separation and shipping to a feedlot: 45, 15 or 0 d. Within each weaning treatment, calves were assigned randomly to 1 of 2 BRD-vaccination treatments: vaccinated 14 d before maternal separation and again at weaning (PRE) or vaccinated on the d of arrival at the feedlot and again 14 d later (POST). On a common shipping date, calves were transported 3 h to an auction market and held for 12 h. Calves were then transported 1 h to a feedlot. All calves were fed the same diets ad libitum during the weaning (PRESHIP), receiving, and finishing phases of the experiment. Steers were fed to a harvest endpoint of 11.5 mm subcutaneous fat over the 12th rib and harvested in 3 groups. Calves weaned 45 d PRSHIP required fewer ($P = 0.02$) days on feed than calves weaned 15 or 0 d PRESHIP. Calf ADG during finishing was greater ($P < 0.01$) for 45- and 15d calves than for 0-d calves, whereas ADG was similar ($P = 0.26$) between PRE and POST. Consequently, 45-d calves had greater ($P < 0.01$) harvest BW than 15- or 0-d calves. Carcass weight tended to increase ($P < 0.02$) as the length of the weaning period increased. Marbling score, USDA yield grade, 12th-rib fat thickness, REA, and KPH were similar ($P \geq 0.22$) between weaning and vaccination treatments. Likewise, incidence of liver abscesses was similar ($P < 0.47$) between weaning and vaccination treatments. Incidence of lung lesions was not affected ($P > 0.81$) by weaning treatment; however, POST tended ($P < 0.09$) to have greater incidence of lung lesions than PRE. Ranch-of-origin weaning for 45 d was associated with increased carcass weight but similar growth performance during finishing and carcass merit compared with weaning for 15 d. PRESHIP BRD vaccination did not improve growth performance or carcass merit of ranch-direct cattle relative to BRD vaccination deferred until feedlot arrival.

Key Words: carcass merit, preconditioning, weaning

1005 Effects of degree of respiratory disease vaccination on health and growth performance of ranch-direct beef calves during weaning and receiving. M. J. Macek*[1], J. R. Jaeger[2], T. B. Schmidt[3], D. U. Thomson[1], J. W. Bolte[2], L. A. Pacheco[1], N. A. Sproul[1], L. R. Hibbard[1], G. J. Eckerle[1], and K. C. Olson[1], [1]*Kansas State University*, *Manhattan,* [2]*Western Kansas Agricultural Research Center*, *Hays,* [3]*Mississippi State University*, *Starkville, MS*.

Angus × Hereford calves (n = 430; initial BW = 230 ± 31.8 kg) were stratified by sex, age, and BW and assigned randomly to 1 of 4 treatments: 0, 1, 2, or 3 BRD vaccinations before feedlot placement (NOVACC, VACC1, VACC2, or VACC3, respectively). Calves were removed from their dams 29 d before feedlot placement; they were weighed, vaccinated for clostridial diseases, treated for internal and external parasites, and placed in a ranch-of-origin weaning facility. Calves on VACC1, VACC2, and VACC3 treatments were given an initial BRD-vaccination at that time. Calves were revaccinated according to their respective treatments at 14-d intervals during the ranch-of-origin weaning phase of the experiment (PRESHIP). On a common shipping date, calves were transported 3 h to an auction market and held for 12 h. Calves were then transported 1 h to a feedlot. During the PRESHIP period, NOVACC calves tended ($P = 0.06$) to have greater incidence of undifferentiated fever than VACC1, VACC2, or VACC3 calves. Consequently, NOVACC calves had greater ($P < 0.01$) drug-therapy costs PRESHIP than other treatments. Calf ADG, DMI, and G:F during the PRESHIP period were similar ($P \geq 0.61$) between treatments. Upon arrival at the feedlot, calves were weighed and assigned to a receiving pen based on treatment. Calf BW was similar ($P \geq 0.48$) between treatments at feedlot placement, 27 d post-receiving, and 55 d post-receiving; moreover, calf ADG during receiving was similar ($P < 0.92$) between treatments. Degree of BRD vaccination had no affect ($P \geq 0.71$) on DMI or G:F during the receiving period. Incidence of undifferentiated fever among VACC2 calves was greater ($P < 0.01$) than that among NOVACC, VACC1, or VACC3 calves during the receiving period; therefore, drug-therapy costs of VACC2 cattle were greater ($P < 0.01$) than that of NOVACC, VACC1, and VACC3 cattle. Vaccination for BRD, regardless of degree, improved health of calves during the PRESHIP period but not DMI, ADG, or G:F. Degree of BRD vaccination influenced calf health during receiving but not DMI ADG, or G:F.

Key Words: beef calves, health, preconditioning

1006 Influencing steer performance through maternal nutrition. A. F. Summers*[1], K. H. Ramsay[2], and R. N. Funston[1], [1]*University of Nebraska West Central Research and Extension Center*, *North Platte*, [2]*Rex Ranch*, *Ashby, NE*.

A 2-yr study was conducted to determine the effects of maternal nutrition on male progeny. Two locations of a commercial ranch in the Nebraska Sandhills were used with crossbred spring-calving multiparous cows at one location (yr1 = 754; yr2 = 700) receiving higher levels of supplement (HN) and cows at the second location (yr1 = 673; yr2 = 766) being fed lower levels of supplement (LN). Cows were managed in a year-round grazing system with HN cows receiving the equivalent of

1.1 kg/d supplement (28% CP) and LN cows receiving 0.4 kg/d supplement delivered 3 times weekly from December through February and then meadow hay through calving in March and April. After weaning, a random group (yr 1 = 100, yr 2 = 100) of male progeny from each management regimen were placed in a feedlot and slaughtered 218 d later. There were significant ($P < 0.05$) interactions between yr x treatment for performance and carcass characteristics. There was no difference ($P = 0.17$) in initial BW between HN and LN calves. Re-implant and final BW were greater ($P = 0.09$; 0.07) for HN calves compared with LN calves (437 vs. 428 ± 3 kg; 625 vs. 614 ± 4.4 kg). Calf ADG tended ($P = 0.12$) to be greater for HN calves. Calves from yr1 had greater ($P < 0.01$) ADG from initiation to re-implant, whereas yr2 calves had greater ($P = 0.02$) ADG from re-implant to slaughter. Steer HCW and marbling score were greater ($P = 0.07$; 0.05) for HN calves. Steer 12-th rib fat, LM area, final yield grade, and percent USDA Choice were similar ($P > 0.10$) among treatments. Final yield grade and percent grading USDA Choice were greater ($P < 0.01$) for yr2 calves compared with yr1. The proportion of HN calves and yr2 calves grading USDA quality grade of modest or greater was greater ($P = 0.07$; < 0.01) compared with LN calves (21 vs. 11%) and yr1 calves (24 vs. 8%), respectively. Level of dam nutrition during the last trimester of gestation influenced subsequent steer progeny final BW, HCW, and percent USDA average Choice or greater in this study.

Key Words: maternal nutrition, carcass quality, beef cattle

1008 Incidence of quality defects in market beef and dairy cows and bulls sold through livestock auction markets in the Western United States. J. K. Ahola*[1], H. A. Foster[3], D. L. VanOverbeke[4], K. S. Jensen[2], R. L. Wilson[2], J. B. Glaze[2], T. E. Fife[2], C. W. Gray[2], S. A. Nash[2], R. R. Panting[2], and N. R. Rimbey[2], [1]*Colorado State University*, *Fort Collins,* [2]*University of Idaho*, *Moscow,* [3]*Independent Contractor, California Beef Council*, *Sacramento,* [4]*Oklahoma State University*, *Stillwater*.

The incidence of Beef Quality Assurance-related defects in market beef and dairy cows and bulls selling at auction was determined during 2 seasons in 2008. Traits were evaluated by 9 trained personnel during sales at 10 livestock auction markets in Idaho (n = 5; beef and dairy), California, (n = 4; dairy only), and Utah (n = 1; beef and dairy). Overall, 18,949 unique lots (8,213 beef cows, 1,036 beef bulls, 9,177 dairy cows, and 523 dairy bulls,) consisting of 23,479 head (9,299 beef cows, 1,091 beef bulls, 12,429 dairy cows, and 660 dairy bulls,) were evaluated. Market cattle weighed 548 ± 103.6 kg (beef cows), 751 ± 176.1 kg (beef bulls), 658 ± 129.7 kg (dairy cows), and 731 ± 150.8 kg (dairy bulls). Mean BCS for beef cattle (9-point scale) was 4.7 ± 1.24 (cows) and 5.3 ± 0.94 (bulls), and for dairy cattle (5-point scale) was 2.6 ± 0.76 (cows) and 2.9 ± 0.56 (bulls). Some 16.5% of beef cows and 4.1% of beef bulls were thin (beef BCS 1 to 3) while 34.8% of dairy cows and 10.4% of dairy bulls had a dairy BCS of 2.0 or less. Among beef cattle, 85% of cows and bulls were considered to not be lame. However, 45% of dairy cows and 26% of dairy bulls were considered lame. Hot-iron brands were observed in 60.6% of beef cows and 57.3% of beef bulls, but only in 27.9 and 29.1% of dairy cows and bulls, respectively. Some stage of ocular neoplasia was observed in 0.6% and 0.3% of beef cows and bulls (respectively) and 0.25% of dairy cows and 0.0% of dairy bulls. Cattle classified as visibly sick included 0.84% of beef cows, 2.95% of dairy cows, 0.10% of beef bulls, and 1.15% of dairy bulls. Lots that were no-saled included 0.15% of beef cow lots, 1.5% of dairy cow lots, and no bull lots. Results suggest that incidence rates of quality defects among both market beef and dairy cattle selling at auction in the Western United States are substantial.

Key Words: auction market, Beef Quality Assurance, market cows

1009 Effects of quality defects in market beef and dairy cows and bulls on selling price at auction in the Western United States. J. K. Ahola*[1], H. A. Foster[3], D. L. VanOverbeke[4], K. S. Jensen[2], R. L. Wilson[2], J. B. Glaze[2], T. E. Fife[2], C. W. Gray[2], S. A. Nash[2], R. R. Panting[2], and N. R. Rimbey[2], [1]*Colorado State University*, *Fort Collins,* [2]*University of Idaho*, *Moscow,* [3]*Independent Contractor, California Beef Council*, *Sacramento,* [4]*Oklahoma State University*, *Stillwate*.

The relative effect of Beef Quality Assurance-related defects observed in market beef and dairy cows and bulls on selling price at auction was determined during 2 seasons in 2008. The BQA-related traits were evaluated by 9 trained personnel among 18,949 lots (23,479 head) offered for sale at 10 livestock auction markets in Idaho, California, and Utah. The mean sale price ± SD (per 45.45 kg) for market beef cows, beef bulls, dairy cows, and dairy bulls was $45.15 ± 9.42, $56.30 ± 9.21, $42.23 ± 12.26, $55.10 ± 9.07, respectively. Linear regression models were developed based on type and(or) sex to evaluate the effect of each quality-related trait on selling price. Dummy variables were used to test for observer bias, regional differences, and selected traits. Premiums and discounts were determined in comparison to a par animal. Compared with a BCS of 5 (9-point scale), beef cows with less condition were discounted ($P < 0.0001$), while slight premiums ($P < 0.05$) were estimated for BCS 6, 7 and 8 cows. Compared with BCS 3.0 dairy cows (5-point scale), more body condition resulted in premiums ($P < 0.001$), while dairy cows with a less-than-desirable BCS of 2.0 or 2.5 were discounted ($P < 0.0001$). Beef cows weighing less than 455 kg were discounted ($P < 0.0001$) compared to cows weighing 545 to 635 kg, and heavier beef cows received ($P < 0.05$) a premium. Compared to dairy cows weighing 636 to 727 kg, cows less than 636 kg were discounted ($P < 0.0001$) while heavier cows (727 to 909 kg) received premiums ($P < 0.01$). Both beef and dairy cows with any amount of visible lameness were discounted ($P < 0.0001$). Cancer eye in the precancerous stage tended (P = 0.05) to discount beef cows and heavily discount ($P = 0.002$) market dairy cows; while the cancerous stage extremely discounted ($P < 0.0001$) all cows. Animals that were visibly sick were discounted ($P < 0.0001$) substantially. Results suggest that improving BCS and BW increases sale price on a per kg basis. However, visibly sick animals, or those with severe quality defects, were discounted considerably.

Key Words: auction market price, Beef Quality Assurance, market cows

1010 Performance of medium and small frame steers under pasture and pasture-feedlot finishing. G. K. Mantz* and P. Nyren, *North Dakota State University Central Grasslands Research Extension Center*, *Streeter*.

This study evaluated the performance of Medium Frame (MF) and Small Frame (SF) steers under 2 finishing systems: 1) Full-season pasture finishing; and 2) Early-season grazing followed by feedlot finishing. Forty yearling steers were frame-scored. Frame scores 4, 5, and 6 were classified as MF and frame scores 2 and 3 classified as SF. Day 1 (14 May 2009) the steers were placed in 6 native range pastures, 3 supplied with a salt-limited, sunflower screening-oat supplement and 3 non-supplemented. Each pasture contained approximately equal numbers of MF and SF steers (average BW 373 and 297 kg, respectively). Frame within pasture was the unit of replication. On d 48 all steers were weighed and half of the MF and SF in each pasture (chosen at random within frame and pasture) were removed for feedlot finishing and divided into 2 pens of MF and 2 pens of SF steers with pens as unit of replication. Pasture-

finish steers were removed from pasture on d 152, weighed and scanned by ultrasound for percent intramuscular fat (IMF). Feedlot steers were harvested when ultrasound indicated 4.00% IMF or 12.8 mm of back fat. The first 48 d on pasture, supplementation did not affect ADG (P = 0.40) and ADG for MF and SF steers was 1.0 and 0.8 kg, respectively (P = 0.17). For pasture-finish steers in the d 48 to d 152 period, ADG was greater in supplemented than control pastures (0.9 vs. 0.7 kg; P = 0.002) and ADG was greater for MF than SF steers (0.9 vs. 0.7 kg; P = 0.001), but no frame by supplement interaction was found (P = 0.81). Pasture-finish steers average IMF of 3.7% was not impacted by frame (P = 0.70) or supplement (P = 0.78). In the feedlot, MF steers tended to have greater final BW (614 vs. 511 kg; P = 0.14) and hot carcass weight (372 vs. 310 kg; P = 0.14) than SF steers. However, MF and SF steers did not differ in ADG (1.5 vs. 1.4 kg; P = 0.27), days on feed (123 vs. 131 d; P = 0.66) DM G:F (0.116 vs. 0.119; P = 0.94) or yield grade (2.8 vs. 2.6; P = 0.40). All feedlot steers produced USDA choice carcasses. Results show MF and SF steers can both perform well under pasture and pasture-feedlot finishing systems.

Key Words: feedlot, frame size, pasture finishing

1011 Comparing the environmental impact of the US beef industry in 1977 to 2007. J. L. Capper*, *Department of Animal Sciences, Washington State University*, *Pullman*.

Historical livestock production is commonly perceived to be inherently more environmentally sustainable than modern agricultural practices. This study modeled the environmental impact of the 1977 US beef industry, which produced 10.6 billion kg beef from 38.7 million head slaughtered, compared with that of 2007 (11.9 billion kg beef produced from 33.7 million head). The deterministic environmental impact model integrated resource inputs and waste outputs from animal nutrition and metabolism, herd population dynamics and cropping parameters using a life cycle assessment approach. Rations were formulated according to NRC for growing animals (steers, heifers) at breed-appropriate bodyweights and growth rates; and for the supporting population (cows, bulls, herd replacements). System boundaries extended from the cow-calf operation to arrival at the slaughter plant, thus all operations and transport within these limits were included. Resource inputs included feedstuffs, water, land, fertilizers and fossil fuels. Waste outputs included manure and greenhouse gas emissions. The total animal population required to produce one billion kg of beef in 2007 was reduced by 27% compared with 1977. The decrease in population size conferred reductions in total feed energy, feedstuffs and land use of 10%, 17% and 27% respectively. Water use per billion kg beef was reduced by 15% between 1977 and 2007. Compared with the 1977 beef industry, fossil fuel energy for beef production was reduced by 11% per unit in 2007. Methane and nitrous oxide emissions per billion kg beef produced in 2007 were reduced by 17% and 13% respectively. The total carbon footprint (expressed as CO_2-equivalents per billion kg beef) was therefore reduced by 14% in 2007 compared with 1977. This analysis clearly demonstrates that improvements in US beef industry productivity conferred by advances in slaughter weight, growth rate, nutrition and management have considerably reduced the environmental impact of modern beef production, thus improving the sustainability of livestock production.

Key Words: beef production, environmental impact, carbon footprint

Production, Management and the Environment: General

1012 A mobile modified atmosphere killing unit for small flock depopulation. A. B. Webster* and S. R. Collett, *University of Georgia*, *Athens*.

In addition to having methods for depopulation of commercial poultry flocks to contain outbreaks of serious avian disease, there is need to have an efficient and humane method to dispose of small flocks that might fall within an affected area. A modified atmosphere killing (MAK) chamber mounted on a trailer to be pulled by a pickup truck was designed for small flock depopulation. The atmosphere inside the chamber is controlled automatically using gas sensors. A portable gasoline generator drives the electronic systems so no external electrical supply is required. The chamber (152.5 cm W × 152.5 cm L) has a total interior volume of about 2.1 m^3, with a 1 m^3 section to hold birds below gas injection nozzles distributed 44.5 cm above the floor around the perimeter of the chamber. The chamber rises to a height of 51 cm to provide sufficient head space to load birds through 4 doors, 2 on each side of the chamber. The loading doors can be sealed shut and the trailer sanitized by a disinfectant solution pumped from a self-contained 114 L tank before the trailer leaves the premises to deliver a killed flock to a disposal site. A hydraulic lift facilitates dumping of carcasses. The MAK trailer was tested in several trials using spent layer breeder hens, spent laying hens, and turkey hen broilers. CO_2 levels during loading were targeted at 45–50%. The highest rate of loading was 2.8–3.4 s per bird during trials with the spent layer breeders. Since the floor capacity of the chamber is about 100 birds, this rate of loading is unlikely to cause birds to be overlain by others before onset of unconsciousness. Chamber temperature and RH during turkey trials ranged from 24 to 29 C and RH from 55 to 85%. Maximum loads ranged from 305 to 440 hens (total wt. 567–609 kg), and 79 turkeys, (555–560 kg). In its final configuration, the MAK unit was able to maintain effective stunning/killing atmospheres during use. Loading could be continuous when CO_2 was used but N_2 required birds to be killed a layer at a time to prevent piling of conscious birds.

Key Words: depopulation, poultry, small flock

1013 Overview of lighting in Kentucky broiler houses. D. G. Overhults[1], A. J. Pescatore[1], I. Lopes[1], G. Morello[1], J. P. Jacob*[1], J. Earnest, Jr.[1], M. Miller[2], and R. S. Gates[3], [1]*University of Kentucky*, *Lexington,* [2]*Kentucky Poultry Federation*, *Winchester,* [3]*University of Illinois*, *Champaign*.

Floor level illuminance was measured in the brood area of 37 broiler houses on 25 farms in 5 different production complexes in Kentucky. A light meter was used to measure light intensity under both "bright" and "dimmed" light conditions that were typically used during flock growout. Measurements were taken between light fixtures at each of the 4 water lines and at the center line of the house. All houses had lights installed above the 2 feed lines. Some houses had additional lights at the center line of the house. In general, lighting type and intensity was inconsistent from farm to farm. A variety of incandescent (IN), compact fluorescent (CFL), cold cathode (CC), and high pressure sodium (HPS) bulbs were used. Fixture spacings over the feed lines varied from 10 to 30 feet. Bulb sizes varied from 5 W CFL to 100 W IN. Two complexes used only CFL lights, usually with 2 alternating size bulbs in each light string. Dimming was accomplished by turning off the larger size bulbs. Various electronic dimmers were used to dim CC and IN bulbs. Under bright light conditions, average light intensity was 11.0 lx, but the range was large. Bright light intensities ranged from 3.2 to 49.5 lx, with the intensity on most farms being concentrated in the mid to lower part of that range. The highest intensity occurred in a house that was using oversized CFL bulbs. Dim light intensities were all less than 6 lx with most farms operating at less than 3 lx. Where IN lights were used, energy cost savings for converting to CC or CFL systems were estimated. Depending on the farm, changing existing IN bulbs to CC or CFL bulbs may save 8,000 - 12,000 kWh/house/year. The payback period for conversion is affected by number of light fixtures, size of bulbs, lighting program, dimming system, range of illuminance, and electric power rates. Various estimates of payback periods generally fell in the range of 6 mo to 2 years. Estimates of payback periods did not include installing any additional fixtures that might be needed to maintain or increase the existing light intensity levels.

Key Words: light intensity, broilers, energy

1014 Evaluation of the effect of supplementing complex trace minerals on the development of claw lesions in stall-housed sows. S. S. Anil*[1], L. Anil[2], J. Deen[1], S. K. Baidoo[2], M. E. Wilson[3], and T. L. Ward[3], [1]*Veterinary Population Medicine, University of Minnesota*, *St Paul,* [2]*Southern Research and Outreach Center, University of Minnesota*, *Waseca,* [3]*Zinpro Corporation*, *Eden Prairie, MN*.

Claw lesions are very common in pigs and are reported to be associated with lameness. Trace minerals such as Cu, Zn and Mn are critical in the keratinization process and thus may affect the generation and development of lesions. Both the quantity and form (organic or inorganic) determine the bioavailability of the trace minerals. The objective of the present study involving 129 sows (mixed parities) was to evaluate the effect of supplementing complex trace minerals on the development of lesions in different claw areas (side wall, heel, sole, heel-sole junction, white line and overgrown dew claw and toe) of stall-housed gestating sows. The sows were allocated randomly to 2 groups and fed either a control diet (inorganic sulfate minerals, ITM; n = 66; Zn 125 ppm, Mn, 40 ppm and Cu, 15 ppm) or a diet containing complex trace minerals (CTM; n = 63) as a partial substitution of inorganic minerals (Zn, 50 ppm, Mn, 20 ppm and Cu at 10 ppm) fed at isolevels of total trace mineral supplementation. The lesions in different claw areas of these sows were scored by a trained person in 2 consecutive parities at mid-gestation, using a mechanical chute designed for the purpose. The total score for each claw area was obtained by adding the scores for that area in different claws. The proportions of sows showing either similar scores or lower scores in the second claw lesion examination in the sows fed CTM or ITM were compared using 2-sample proportion test (SAS v. 9.1). A higher ($P < 0.05$) proportion of sows fed CTM (95 vs. 82%) had a decrease in the severity or no change in severity of heel-sole junction lesion score. The proportions of sows with similar or lower scores for total lateral claw lesions, long toes, heel lesions, white line lesions and vertical side wall lesions were higher in the sows fed CTM, though not statistically significant ($P > 0.05$). These data suggest a protective effect of complex trace minerals on claw lesions in stall-housed sows.

Key Words: claw lesions, stall housing system, trace minerals

1015 Correlation between production traits and sexual behavior in white-faced yearling rams. V. A. Uthlaut*, G. E. Moss, R. H. Stobart, B. A. Larson, and B. M. Alexander, *University of Wyoming*, *Laramie*.

Of the 196,000 rams in the US, approximately 23% are expected to be non-performers. This results in an annual loss of $13.5 million to

US sheep producers. The objective of this study was to determine the discriminating value of production traits so that measures of production may be used as indicators of reproductive performance. White faced rams consigned to the Wyoming ram test in 2008 (n = 33) and 2009 (n = 41) were tested for expression of sexual behavior while being evaluated for production performance. At the time of behavior testing, rams were 10 mo to 1 yr of age. In 2009, rams were fed using the Grow-Safe feeding system and feeding behavior was correlated to sexual behavior. Sexual performance was evaluated by exposing individual rams to 2 ewes in estrus for 30 min for a maximum of 3 times. Sexual behavior was categorized as: anticipatory (ano-genital sniffs, Flehmen response, fore-leg kicks and nudges) and consummatory (mount attempts, mounts and ejaculations) behavior. Rams exhibiting consummatory behavior were not re-tested. Rams were classified low (LP; n = 18), intermediate (IP; n = 23) or mounting (M; n = 33) according to the level of sexual behaviors exhibited. Rams classified as LP and IP exhibited total anticipatory behaviors ≤9 (mean = 4.8 ± 2.7) or ≥10 (mean = 23.7 ± 10.7), respectively, but did not exhibit mounting behavior. M rams mounted a ewe at least once (anticipatory mean = 43.5 ± 24.7; consummatory mean = 9.5 ± 7.0). For production traits, each ram was assigned an index ratio based on body weight gain and adjusted for wool characteristics. Data were analyzed using GLM and CORR procedures of SAS. Sexual behavior classification did not influence ($P \geq 0.5$) index ratio, feed consumed per day, or number of feed intake episodes. Although anticipatory and consummatory behaviors (r = 0.48; $P < 0.05$) and test index ratio and feed consumption (r = 0.50; $P < 0.05$) were highly correlated, sexual behaviors were not significantly correlated with the index ratio (r = 0.08; $P = 0.5$). Measures of production performance do not appear to be reliable predictors of sexual behavior in yearling rams.
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1016 Optimal livestock gross margin for dairy insurance contract design. M. Valvekar, V. E. Cabrera*, and B. W. Gould, *University of Wisconsin*, *Madison*.

Volatility in milk and feed prices are a major source of dairy farm risk. Since August 2008 a new federally reinsured insurance program referred to as Livestock Gross Margin Insurance for Dairy Cattle (LGM-Dairy) has been available to many US dairy farmers to help manage the variability in dairy income over feed costs. In the design of the desired insurance contract, the dairy farmer has to decide on the percentage of monthly milk production to be covered by this insurance contract. The objective of this paper was to develop an algorithm and a user friendly software system to identify the optimal LGM-Dairy contract for a risk neutral dairy farmer in terms of monthly coverage at the lowest premium such that a target guaranteed income over feed cost (TGIOFC) is obtained. We optimize our nonlinear programming model via the use of a generalized reduced gradient method. The premium solver platform, V5.0 (Frontline systems, Incline Village, Nevada) within the Excel software system was used for optimization. The analysis was done for a representative 120 herd size dairy farm producing 8,873 kg milk per cow per yr. Wisconsin statistical data indicated that similar sized dairy farms require an income over feed cost (IOFC) of at least $110 per Mg milk to be profitable during the coverage period. Using these data for the July 2009 insurance contract to ensure $110 per Mg milk, the least premium cost contract was found to have a premium of $1.22 per Mg milk produced insuring approximately 52% of the annual production with variable monthly production covered over the September 2009 to June 2010 period. This premium represented 1.10% of the desired TGIOFC. An alternative non-optimal strategy, defined as a contract insuring the same proportion of milk as the optimal (52%), but with constant percentage coverage each month of the insurance contract was analyzed. The premium for non-optimal strategy was found to be almost twice the level obtained under the optimal solution representing 1.9% of TGIOFC.

Key Words: risk management, price risk, revenue insurance

1017 Do hyphenated techniques permit the speciation of metal glycinate complexes? C. Ionescu*[1], V. Vacchina[2], R. Lobinski[3], S. Oguey[1], and D. Bravo[1], [1]*Pancosma*, *Geneva, Switzerland*, [2]*UT2A*, *Pau, France*, [3]*CNRS*, *Pau, France*.

Trace elements inclusion as feed additives is based on their metal content. This is mainly due to the unavailability of analytical methods differentiating trace element sources. The objective was to develop a method allowing specific determination of Zn, Cu, Mn and Fe glycinate complexes (BT) from sulfate (SU), citrate (CI) or histidinate (HI), preserving BT molecular integrity. A mixture of the 4 BT standards was used to optimize the analytical conditions. Five couplings were tested: size exclusion liquid chromatography with coupled to inductively coupled plasma spectrometry (SE HPLC-ICP-MS); hydrophilic interaction liquid chromatography (HILIC) with ICP-MS; Zwiterionic (ZIC)-HILIC with ICP-MS and capillary electrophoresis (CE) coupled either with electrospray mass spectrometry (ESI MS/MS) or ICP-MS. The SE HLPC-ICP-MS, HILIC-ICP-MS or ZIC-HILIC-ICP-MS coupling did not permit separation of BT from SU. Coupling of CE with ICP-MS gave the best results. All BT electropherograms contained a single peak. The 4 BT injected simultaneously were separated suggesting an efficient electrophoretic separation. The ICP-MS signal specificity was proven comparing experimental vs. theoretic trace elements isotopic ratios and peak absence in the blank. BT Cu was well separated from SU, CI and HI. BT Zn was well separated from SU and HI but not from CI. BT Mn was well separated from SU but there was an overlapping with CI and HI. BT Fe was well separated from SU or CI but not from HI. However, CI and HI were reconstructed complexes and not standards. BT molecular integrity was checked using CE ESI-MS(/MS) coupling. BT polymers were destroyed explaining the single peak in CE-ICP-MS electropherograms. BT sulfate ligand was lost but metal-glycine link was preserved. These results make capillary electrophoresis a promising tool for the quantification of BT. Providing validation of the method, the coupling CE-ICP-MS may allow the quantitative speciation of BT in feedstuffs.

Key Words: traceability, glycine complex, chelate

1018 Determination of metal glycinate in premixes using capillary electrophoresis coupled with an inductively coupled plasma mass spectrometry detector (CE-ICP-MS). C. Ionescu*[1], V. Vacchina[2], S. Oguey[2], R. Lobinski[3], and D. Bravo[1], [1]*Pancosma*, *Geneva, Switzerland*, [2]*UT2A*, *Pau, France*, [3]*CNRS*, *Pau, France*.

Previous results have shown that capillary electrophoresis coupled to inductively coupled plasma mass spectrometry (CE-ICP-MS) was a promising tool for metal glycinate (BT) speciation. The objective was to validate this method and to use it to determine BT concentration in mixes. The analytical conditions developed included an electrolyte made of 20 m*M* ammonium acetate (pH 7.4), a voltage of 30 kV and a hydrodynamic injection of 1 s. Specificity of the method was previously discussed. The analytical figures of merit of the approach were then determined. The calibration curve, made of 6 points, was linear ($R^2 > 0.995$). The repeatability (n = 10 for concentrations in the middle range of the calibration curve) was below 12%. In the absence of Certified Reference Material, accuracy was evaluated by analyzing quality control samples in the lower, medium and upper range of the calibration curve

(n = 3). It was generally below 15%. Detection limits, calculated as 3 times the STD of the blank plus the blank, were between 0.05 and 0.2 μg metal.mL^{-1} depending on the BT due to the specific sensitivity of ICP MS. The coupling CE-ICP-MS was then used to quantify BT in four kinds of premixes based on either minerals (as sulfates), choline chloride, amino-acids or acid salts. The BT concentrations in premix were set as follows: BT Zn 8.9 mg/g, BT Cu 6.4 mg/g and BT Mn 18.7 mg/g. The electropherograms of the 4 premixes containing Cu, Zn and Mn BT were made of one peak absent from the corresponding control premix and matching the migration time of a BT standard. Concentrations in the premixes ranged from 8.8 - 9.1 mg/g for BT Zn, 6.3 - 6.6 mg/g for BT Cu and from 18.4 - 18.9 mg/g for BT Mn. These results show that BT can be analyzed and quantified in premixes, giving some new opportunities to the feed producers to introduce BT with precision in their diets and progress on the effective dose of these products.

Key Words: traceability, glycinate complexes, chelates

1019 Determining the optimal age for recording the retinal vascular pattern image of lambs. M. A. Rojas-Olivares[1], G. Caja*[1], S. Carné[1], A. A. K. Salama[1], N. Adell[2], and P. Puig[1], [1]*Universitat Autònoma de Barcelona*, *Bellaterra, Barcelona, Spain*, [2]*Universitat de Girona*, *Girona, Spain*.

A total of 143 newborn lambs of Ripollesa breed were used for assessing the optimal age at which the vascular pattern of the retina can be used as reference for identification and traceability. Retinal images (RI) from both eyes were recorded in duplicate using an OptiReader camera (Optibrand, Fort Collins, CO) at d 1, 8, 30, 90, 180 and 360 of age. Digital images (n = 2,544) were treated with the Optibrand Data Management Software (v. 4.1.3) and intra- and inter-age comparisons of pairs of RI were made using Optibrand's matching score (MS). A MS <70 was used as exclusion criterion (0.989 sensitivity, probability of a correct match; and, 0.995 specificity, probability of a correct non-match). Three Spanish commercial categories of harvesting lambs were used for evaluating RI as a tool for tracing live lambs: "lechal" milk-fed lambs (1-mo, 12 kg BW), "recental" fattened light lambs (3-mo, 25 kg BW) and "ovino mayor" fattened heavy lambs (6-mo, 35 kg BW). Values of MS did not show normal distribution as raw data or after different transformations, and were treated with a model based on the one-inflated bivariate β distribution by using the R computing software (www.r-project.org). Using likelihood ratio test to compare data, intra-age RI analysis showed that MS increased from d 1 to 180 (81 to 96, respectively). Percentage of RI with MS >70 increased from d 1 to 90 (76 to 100%) and steadied thereafter. No images before d 30 were satisfactory to be used as a reference. Inter-age RI for 1-mo "lechal" lambs showed that the 8-d RI tended to show a better traceability than those taken at 1-d of age (91.4 vs. 83.7%, respectively; $P = 0.070$). For 3-mo "recental" lambs, RI taken at 30-d of age traced better than RI taken at 8-d of age (99.2 vs. 89.8%, respectively; $P < 0.05$). Finally, for "ovino mayor" 6-mo lambs, the RI taken at 90-d of age showed the best traceability (99.2%) which was higher than those taken at 8-d (81.4%; $P < 0.05$), but did not differ from those taken at 30-d of age (94.8%; $P > 0.05$). In conclusion, retinal imaging was an accurate tool for auditing the identity and traceability of live lambs of different commercial categories.

Key Words: retinal image, identification, traceability

1020 Predicting probability of pregnancy using all activity signals prior to pregnancy diagnosis. A. H. Sanders*, A. De Vries, and J. Block, *University of Florida*, *Gainesville*.

Increased physical activity can signal estrus in dairy cattle. Activity in the milking interval before AI can indicate an improved probability of pregnancy. This study considered the addition of activity data collected between AI and pregnancy to the prediction of pregnancy probability. Data were 632 breeding records from the University of Florida research herd, and activity recorded at twice daily milkings as avg. steps/hr since last milking by S.A.E. Afikim pedometers. The percent deviation of each activity record from the previous 10d rolling average of the same (a.m. or p.m.) milking session was calculated. Using a threshold of 84.2%, deviations were re-coded as binary signals of increased activity. All inseminations were timed AI (TAI) following Ovsynch. All were in late morning by one inseminator. At 32d after TAI, pregnancy (P32) was determined by ultrasound. Overall, 45% of cows were pregnant. Logistic regression was used to evaluate the effect of 4 signal profiles on probability for P32. Signal profiles were no signal (NONE, n = 228), signal only on morning of AI (TAI, n = 98); no signal on morning of AI, but at least one signal before pregnancy diagnosis (POSTAI, n = 234); and signal on morning of TAI, and at least one other signal before pregnancy diagnosis (BOTH, n = 70). The lowest P32 was for POSTAI (18.4%; CI = 13.9–23.9), and the highest (80.6%; CI = 71.6–87.3) was for TAI. An additional later signal (BOTH) significantly reduced P32 compared with TAI (OR = 0.05.). A signal after AI (POSTAI+BOTH) significantly reduced P32 compared with cases with no later signal (NONE+TAI) irrespective of signal before TAI (OR = 0.13). First post-AI signals averaged 17d after TAI, with median = 19d and mode = 21d. Activity signals can provide information about probability of pregnancy before pregnancy diagnosis by ultrasound or palpation. Further study is needed to determine the potential value of this information, if used to initiate early intervention in cows predicted to be not pregnant.

Key Words: activity, pregnancy, pedometer

1021 Development of a model for heat stress response in primiparous sows during critical stages of reproduction. E. A. Coate*, M. C. Lucy, P. A. Eichen, and D. E. Spiers, *University of Missouri-Columbia*, *Columbia*.

Heat stress has detrimental effects on physiological status of sows that is compounded near farrowing and during lactation. A study was designed to identify superior determinants of heat response that encompasses these periods. Setup included primiparous sows (n = 15) housed in the Brody Environmental Center (University of Missouri) beginning the last 3 weeks of gestation through post-weaning period. Specific analysis periods were:1) several days before parturition, 2 and 3) 2 periods during mid-lactation, and 3) early postweaning. All animals were exposed to the same daily ambient temperature (Ta) cycle of 23.8–30.9°C. Daily measurements at 0800, 1200, 1600 and 2000 included rectal temperature (Tre) and respiration rate (RR). Skin temperature was recorded for ear, tail, rump, and shoulder sites using infrared thermography (Raytek, Santa Cruz, CA). Third order polynomial regression models were used to examine curvilinear Tre and RR relationships to Ta and skin temperatures across all periods. The range of correlation between Tre and RR to Ta was extremely low and not always significant ($P < 0.05$) at 0.03–0.14 and 0.09–0.31, respectively. In contrast, the combined relationship ranges for rump and shoulder temperatures were 0.15–0.42 (Tre) and 0.19–0.36 (RR). Although nearly all skin temperature relationships were significant at $P < 0.05$, there was a reduction in values from Periods 1 and 2 to Periods 3 and 4. Curvilinear relationships of Tre to skin temperatures exhibited a shift from Period 1 (preparturition) to Periods 2, 3, and 4, as characterized by a more than a 1°C shift in both skin and rectal temperatures. Similar comparisons for RR showed again the 1°C increase in skin temperature relative to RR. However,

there was no reliable shift in RR across periods. Skin temperature is possibly superior to ambient temperature in predicting thermal status because the pig utilizes shifts in its microenvironment (i.e., lying on the floor vs standing) without changing its general environment.

Key Words: pig, reproduction, heat stress

PSA Emerging Issues Symposium: Social Sustainability of Egg Production

1022 The egg industry—Market context and sustainability issues. J. A. Mench*, D. A. Sumner, and J. T. Rosen-Molina, *University of California*, *Davis*.

The egg industry is being pressured from many directions to change its production practices, particularly to address concerns about hen welfare in conventional cage systems. Responding to similar pressures, in 1999 the European Union banned conventional laying cages starting in 2012. This now impending European ban has led to the development of several alternative housing systems. These include non-cage systems like aviaries, and modified (enriched or furnished) cages that include perches, areas in which the hens can forage and dust bathe, and nests. Understanding the European experience is valuable as the United States considers alternatives. In the United States the proportion of eggs produced in alternative systems is small (less than 5 percent of output) but growing, at least in part due to market and political incentives for systems that provide hens with more behavioral freedom than conventional cages. Animal welfare, however, is only one element of a sustainable production system. Other elements include those related to public values, the environment, economics, worker health, and food safety and quality. Eggs are a primary source of animal protein globally, and the United States is the third largest producer of eggs in the world, behind China and the European Union. The national table egg flock comprises about 280 million hens housed in all regions, but with approximately 60% of eggs produced in the 10 leading states. Adopting new housing systems will have substantial effects on costs and other aspects of egg production on both a regional and national scale, with potential negative impacts that need to be carefully considered. This paper discusses the US egg industry in the context of legislation and standards related to hen housing systems. It also addresses initiatives by retailers, non-governmental organizations, and private certification organizations to shape production practices in the egg industry, and how those initiatives might affect various aspects of the sustainability of egg production.

Key Words: sustainability, egg production, housing systems

1023 Economic and market issues on the sustainability of egg production in the united states: analysis of alternative production systems. D. A. Sumner*[1], H. R. Gow[2], D. R. Hayes[3], W. A. Matthews[1], F. B. Norwood[4], J. T. Rosen-Molina[1], and W. N. Thurman[5], [1]*University of California*, *Davis,* [2]*Michigan State University*, *East Lansing,* [3]*Iowa State University*, *Ames,* [4]*Oklahoma State University*, *Stillwater,* [5]*North Carolina State University*, *Raleigh*.

Conventional cage housing evolved as a cost-effective egg production system. Imposing housing alternatives raises marginal production costs and requires sizable capital investment. Farm-level cost increases of about 40% per dozen for shifts from conventional cages to relatively low-cost barn housing are consistent with California data. Data on costs per dozen associated with such alternatives as furnished cages are not readily available for the United States and European data are difficult to extrapolate to the US industry structure. Even if mandated by government or major buyers, a shift to alternative housing systems would likely occur with lead-times of at least 5 years (consistent with the recent California schedule) and therefore egg producers and input suppliers would have considerable time to build new facilities and plan new systems. A small share of US consumers now pay high retail premiums for eggs from hens housed in alternative systems. Data from consumer experiments indicate that some consumers who do not now buy specialty eggs would be willing to pay significant premiums. However, current data does not allow easy extrapolation to understand the willingness to pay for such eggs by the vast majority of conventional egg consumers. US egg consumption tends to be relatively unresponsive to price changes, with farm level price increases of 40% likely to reduce consumption by less than 10%. This combination of parameters suggest that, unless low-cost imports grew rapidly, imposed changes to higher-cost hen housing systems would raise US egg prices considerably, while reducing egg consumption only marginally. Eggs are a low-cost source of animal protein and low-income consumers would be hardest hit. But, since egg expenditures are a very small share of the consumer budget, the real-income loss per consumer would be small in percentage terms. Finally, the high egg prices implied by alternative hen housing systems raise complex issues about linking policy costs to policy beneficiaries.

Key Words: egg economics, layer housing costs, economics of animal welfare

1024 The impact of different housing systems on egg safety and quality. P. S. Holt*[1], R. H. Davies[2], J. Dewulf[3], R. K. Gast[1], J. K. Huwe[4], D. R. Jones[1], D. Waltman[5], and K. R. Willian[6], [1]*USDA/ARS Egg Safety and Quality Research Unit*, *Athens, GA,* [2]*Veterinary Laboratory Agencies*, *Weybridge, United Kingdom*, [3]*Veterinary Epidemiology, Ghent University*, *Ghent, Belgium*, [4]*USDA/ARS Animal Metabolism Research Unit*, *Fargo, ND,* [5]*Georgia Poultry Laboratory*, *Oakwood,* [6]*Chemistry Department, Tuskegee University*, *Tuskegee, AL*.

A move from conventional cages to either an enriched cage or a noncage system may affect the safety and/or quality of the eggs laid by hens raised in this new environment. The safety of the eggs may be altered either microbiologically through contamination of internal contents with *Salmonella enterica* serovar Enteritidis (*S. enteritidis*) and/or other pathogens, or chemically due to contamination of internal contents with dioxins, pesticides, or heavy metals. Quality may be affected through changes in the integrity of the shell, yolk, or albumen along with changes in function, composition or nutrition. Season, hen breed, flock age, and flock disease/vaccination status also interact to affect egg safety and quality and must be taken into account. An understanding of these different effects is prudent before any large scale move to an alternative housing system is undertaken.

Key Words: egg safety, egg quality, alternative housing

1025 Environmental impacts and sustainability of egg production systems. H. Xin*[1], R. S. Gates[2], A. R. Green[2], F. M. Mitloehner[3], P. A. Moore Jr.[4], and C. M. Wathes[5], [1]*Iowa State University*, *Ames*, [2]*University of Illinois*, *Urbana-Champaign*, [3]*University of California*, *Davis*, [4]*USDA-ARS*, *Fayetteville, AR*, [5]*University of London*, *United Kingdom*.

As an integral part of a systemic assessment toward "*Social Sustainability of Egg Production*," we reviewed the current state of knowledge about environmental impacts of different egg production systems, and identified knowledge gaps requiring further research. Highlights of the current knowledge include: 1) High-rise (HR) cage houses generally have lower air quality and emit more ammonia than manure-belt (MB) cage houses; 2) Manure removal frequency in MB houses greatly impacts ammonia emissions; 3) Emissions from manure storage are largely affected by storage conditions including ventilation rate, manure

moisture content, air temperature, and stacking profile; 4) More baseline data on air emissions from (6) HR and (2) MB houses are being collected in US; 5) Non-cage (NC) houses generally have reduced air quality (ammonia and dust levels) than cage houses; 6) NC houses tend to be colder during cold weather due to lower stocking density than caged houses; 7) NC houses are more energy intensive in winter; 8) Hens in NC houses are less efficient in resource (feed, energy and land) utilization, leading to greater carbon footprint; 9) Excessive application of hen manure to cropland can lead to nutrient runoff to water bodies; 10) Hen manure on open range may be subject to runoff during rainfall, although quantitative data are lacking; 11) Mitigation technologies exist to reduce generation and emission of noxious gases and dust, however work is needed to evaluate their economic feasibility and optimize design; and 12) Dietary modification shows promise for emissions mitigation. The identified knowledge gaps and research needs include: 1) Indoor air quality, barn emissions, thermal conditions and energy use for alternative hen housing systems (1-story floor, aviary, and enriched cage systems) along with conventional housing systems under US production conditions; 2) Environmental footprint for different egg production systems in US through life cycle assessment; 3) Process-based models for predicting air emissions and their fate; and 4) Further exploration of practical means to mitigate air emissions from different production systems.

Key Words: hen-housing system, environmental footprint, emissions mitigation

1026 Values and public acceptability dimensions of sustainable egg production. P. B. Thompson*[1], M. Appleby[5], L. Busch[1,2], L. Kalof[1], M. Miele[3], B. Norwood[6], and E. Pajor[4], [1]*Michigan State University*, *East Lansing,* [2]*Lancaster University*, *Lancaster, UK*, [3]*Cardiff University*, *Cardiff, Wales, UK*, [4]*Calgary University*, *Calgary, AL, Canada*, [5]*World Society for the Protection of Animals*, *London, UK*, [6]*Oklahoma State University*, *Stillwater*.

A variety of standards regimens have emerged as key arenas where conflicting values and visions for sustainability in egg production are negotiated and action for reform is pursued. These include: Federal regulatory standards for food safety and environmental impact; State, local and Federal standards for air and water quality; Private standards for animal welfare and other variables set by producer groups and retailers. This paper reviews what is known about public attitudes and preferences with respect to standards for egg production and identifies key gaps in knowledge about what the public thinks. What people do as "consumers" (when they spend their money) is not always a good predictor of what they will do as "citizens" (how they will vote, how they will express their views, and what financial or other support they will lend to various forms of social activism). Inconsistent indicators of "what people want," or what they would find acceptable are thus common. Several measures indicate that political support for environmental quality and animal welfare has been growing steadily in the US public, but food safety rates very high as an area of concern in studies that ask respondents to comparatively rank concerns or expectations from the food system. Beyond economic indicators of consumer choice, we have few data that permit judgments about the relative importance or preferred trade-offs that might be made among the various dimensions of sustainable egg production. We have limited ability to forecast scenarios for mobilization of public opinion in support of or in response to specific policy initiatives or patterns of change in production methods. We do not know how subsets of the public would interpret results from scientific studies on environmental, animal welfare, food safety, health or economic dimensions of egg production. We have very limited data on public attitudes to support standards development that would be intended to improve public confidence in the sustainability of egg production.

Key Words: standards, public opinion, politics

1027 Hen welfare in different housing systems. D. C. Lay Jr.*[1], R. M. Fulton[2], P. Y. Hester[3], D. M. Karcher[2], J. B. Kjaer[4], J. A. Mench[5], B. A. Mullens[6], R. C. Newberry[7], C. J. Nicol[8], N. P. O'Sullivan[9], and R. E. Porter[10], [1]*USDA-Agricultural Research Service, Livestock Behavior Research Unit*, *West Lafayette, IN*, [2]*Michigan State University*, *East Lansing*, [3]*Purdue University*, *West Lafayette, IN*, [4]*Fed. Agri. Res. Centre*, *Celle, Germany*, [5]*University of California*, *Davis*, [6]*University of California*, *Riverside*, [7]*Washington State University*, *Pullman*, [8]*University of Bristol*, *United Kingdom*, [9]*Hy-Line International*, *Des Moines, IA*, [10]*University of Minnesota*, *St. Paul*.

Egg production systems have become subject to heightened levels of scrutiny due to animal welfare concerns. Multiple factors such as disease, skeletal and foot health, pest and parasite load, behavior, stress, affective states, nutrition, and genetics influence the level of welfare laying hens experience. Although the need to evaluate the influence these factors is recognized, research into these areas is still in the early stages. We compare conventional cages, furnished cages, non-cage systems, and outdoor systems. Attributes of each system are shown to impact welfare and those systems which have similar attributes are impacted similarly. For instance, environments, such as non-cage and outdoor systems, in which hens are exposed to litter and dirt provide a greater opportunity for disease and parasites. The more complex the environment the more difficult it is to clean, and the larger the group size the more easily disease and parasites are able to spread. Environments, such as conventional cages, which limit movement, can lead to osteoporosis; but environments which have increased complexity, such as non-cage systems, expose hens to an increase incidence of bone fractures. More space allows for hens to perform a greater repertoire of behaviors, although some deleterious behaviors such as cannibalism and crowding, which results in smothering, can occur. Less is understood about the stress which each system imposes on the hen, but it appears that each system has its unique challenges. Selective breeding for desired traits such as improved bone strength and decreased feather pecking and cannibalism may help to improve the welfare of laying hens. It appears that no single housing system is ideal from a hen welfare perspective. Although environmental complexity increases behavioral opportunities, it also introduces difficulties in terms of disease and pest control. In addition, environmental complexity creates opportunities for the hens to express behaviors that are actually detrimental to their welfare. As a result, any attempt to evaluate the sustainability of a switch to an alternative housing system requires careful consideration of the merits and shortcomings of each housing system.

Key Words: poultry, welfare, housing

1028 Valuing stakeholder input in setting research priorities for sustainable egg production. J. C. Swanson*, *Michigan State University*, *East Lansing*.

The importance of stakeholder input in setting future goals for sustainable animal production systems should not be overlooked by the agricultural animal industries. Stakeholders play an integral role in setting the course for an array of factors affecting producers, from influencing consumer preferences to setting public policy. The Social Sustainability of Egg Production Project included a stakeholder workshop to consider and integrate diverse values into the project white papers, which frame the issues and research priorities for the future of sustainable egg produc-

tion. Representatives from the environmental, food safety, food retail, consumer, animal welfare, veterinary, general farm and egg production sectors participated, along with members of the project coordination team, in a 1.5 d workshop to explore and construct a vision for socially sustainable egg production. This presentation will present information about how this vision can be integrated into the science while taking account of the realms of social, political, environment, technology, culture and economics.

Key Words: egg production, sustainable, stakeholder

1029 Characterization of physical factors affecting ruminal lipolytic activity *in vitro*. H. D. Edwards*[1], M. D. Hardin[1], R. K. Miller[1], N. A. Krueger[2], R. C. Anderson[2], and D. J. Nisbet[2], [1]*Texas A&M University, College Station,* [2]*USDA/ARS, Southern Plains Agriculture Research Center, Food and Feed Safety Research Unit, College Station, TX.*

Hydrolysis of dietary lipids to free fatty acids (FFA) is a prerequisite for ruminal biohydrogenation, a bacterial mediated process that rapidly and extensively saturates unsaturated FFA thus limiting the absorption and ultimate assimilation of these healthy nutrients into ruminant produced foods. To learn how to better enrich, isolate and study lipolytic bacteria from the rumen, we investigated the effects of various physical treatments on ruminal lipase activity of ruminal microbes (in 1 mL freshly collected ruminal fluid) during cultivation in 9 mL anaerobic salts medium containing 10% clarified ruminal fluid and 1% olive oil. We found that mean ± SD (n = 3) rates of FFA production (μmol mL^{-1} h^{-1}) were enhanced ($P < 0.05$) more than 20-fold when ruminal populations were incubated (48 h) in the presence of glass beads (0.22 ± 0.10 versus 0.01 ± 0.01 for cultures incubated with or without glass beads, respectively). Rates of lipolysis, however, were unaffected ($P > 0.05$) whether cultures were incubated with or without added H_2 (50% in CO_2). In a subsequent experiment, we found that rates of FFA accumulation by mixed populations of rumen bacteria incubated with glass beads as described above were more rapid ($P < 0.05$) when cultures were incubated horizontally than when incubated upright (0.62 ± 0.06 versus 0.31 ± 0.16 μmol mL^{-1} h^{-1}, respectively). When fluid fractions (10% vol/vol) from these initial cultures were transferred and incubated similarly in fresh culture medium, rates of FFA accumulation decreased by more than 24% compared with rates measured during the initial culture series. Conversely, when bead fractions were transferred to a subsequent culture series, rates of FFA accumulation increased more than 83% from those measured in the initial series. Results indicate that inclusion of glass beads to culture media provides an effective solid support matrix to promote both interfacial activation of lipase activity and colonization by lipase producing bacteria.

Key Words: rumen, lipolysis, food quality

1030 Potential for water intake to predict dry matter intake in finishing beef steers. M. H. Ramos*[1], M. S. Kerley[1], M. Brankovic[2], J. Gillespie[2], and C. Huisma[2], [1]*University of Missouri, Columbia,* [2]*GrowSafe, Airdrie, CA.*

Potential to predict individual dry matter intake (DMI) with accuracy would have production, selection and research application. Present equations cannot explain more than approximately two-thirds of variation of DMI. Correlation between DMI and water intake is known to be positive and relatively strong. The objective of this research was to determine the correlation between water intake and DMI by feedlot cattle. Cattle (n = 164 and metabolic body weight = 100 kg) were fed for 120 d a diet containing 59% barley, 10% brewer's grains, 8% DDGs, 19% silage and 4% supplement. Diet had a CP value of 15% and NEg of 1.36 Mcal/Kg. Water intake and DMI were both individually measured using GrowSafe intake system and GrowSafe Beef in pen weighing system. The equation used was: dmi = 36.1674 + 2.1624waterintake −0.2072waterbodycomposition −17.6386adg −2.1292waterintakeadjuster (R2 = 0.84; CV = 3.59; RootMSE = 0.42). Regression was done using PROC REG (SAS) with DMI as a dependent variable and wati, watcomp, adg and watdelta as independent variables. The PROC REG was used with backward and forward selection with a $P = 0.15$ used to identify parameters to stay in the model. Also PROC REG was used to identify the lowest AIC "an information criteria" and all variables were used. The equation developed had an R2 = 0.84 compared with actual DMI. Intake equation using effective energy equation had a R2 = 0.40 and NRC (1996) had a R2 = 0.44, with NRC equation underpredicting DMI. Water intake was correlated to DMI and improved accuracy of DMI prediction.

Key Words: DMI, water, intake

1031 Effect of calving season and finishing system on performance of beef steers in western Canada. H. C. Block[1], A. D. Iwaasa[2], L. C. Thompson[3], H. A. Lardner*[3], and S. L. Scott[1], [1]*Agriculture and Agri-Food Canada, Brandon Research Centre, Brandon, MB, Canada,* [2]*Agriculture and Agri-Food Canada, Semiarid Prairie Agricultural Research Centre, Swift Current, SK, Canada,* [3]*Western Beef Development Centre, Lanigan, SK, Canada.*

Steers (n = 124) from a 3-site Canadian study of effects of calving season [CS; early (EC; March) vs. late (LC; June)] on cow-calf production were allocated to 2 finishing systems [FS; rapid (RF) vs. slow (SF)]; with 2 pens of 13–17 steers per treatment. Effects of CS, FS, and their interaction on performance and carcass characteristics were evaluated. The RF was an 84-d backgrounding period followed by a high-barley grain finishing diet. The SF used more forage with longer backgrounding, pasture in June and July, and swath-grazing in August and September, followed by a high-grain finishing diet. The endpoint was 8 mm ultrasound backfat or 750 kg bodyweight (BW). Data were analyzed as a 2 × 2 factorial. The initial BW of EC steers was 18.2 kg heavier ($P < 0.01$). There were CS × FS interactions ($P \leq 0.01$) for time on feed, age at slaughter, DMI, ADG, total gain (TG), and final BW. Compared with ECRF, LCRF steers were on feed 21% longer, were 18% older at slaughter, consumed 38% more total DM, and had 19% higher ADG, 48% higher TG, and 19% heavier final BW (all $P \leq 0.05$). The ECSF steers were on feed 117% longer, were 60% older at slaughter, consumed 202% more total DM, and had 17% lower ADG, 83% higher TG, and 39% heavier final BW (all $P \leq 0.05$). The LCSF steers were on feed 81% longer, were 46% older at slaughter, consumed 160% more total DM, and had 8% lower ADG, 67% higher TG, and 29% heavier final BW (all $P \leq 0.05$). Feed efficiency (G:F) was 65% better for RF steers ($P < 0.01$) and 5% better for LC steers ($P < 0.01$). Yield grade was unaffected ($P = 0.23$ to 0.77). There was a reduction ($P = 0.04$) in AA quality grades with SF. The expected effect of the high-forage SF on slowing growth and increasing total DM, age, and final BW, and lowering G:F, was amplified for EC and attenuated for LC steers, indicating CS impacts selection of optimal FS.

Key Words: beef steers, calving season, finishing system

1032 Effects of a bacterial inoculant on fermentation of barley or corn silage and on the growth performance of steers fed the ensiled crop. W. Addah*[1,2], J. Baah[2], P. Groenewegen[3], E. K. Okine[1], and T. A. McAllister[2], [1]*University of Alberta, Edmonton, AB, Canada,* [2]*Agriculture and Agri-Food Canada Research Centre, Lethbridge, AB, Canada,* [3]*Alltech Canada, Inc., Calgary, AB, Canada.*

Barley and corn silages are principal components of backgrounding diets in North America. Responses of these forages to inoculants designed to enhance the ensiling process may differ, owing to differences in forage composition. Whole-crop barley (*Hordeum vulgare*) and corn (*Zea mays*)

were inoculated with a mixture of *Lactobacillus plantarum*, *Enterococcus faecium* and *Pediococcus acidilactici* to assess their impact on silage fermentation and growth performance of feedlot steers. Barley (B; 45% DM) and corn (C; 35% DM) forages were swathed, chopped (0.95 mm) and sprayed with water (control: CB, CC) or inoculant (inoculated: IB, IC) at a rate of 1.0×10^5 cfu/g DM. The forages were ensiled in laboratory-scale silos for fermentation analysis and in large silage bags that were opened after 63 (C) or 77 d (B). The bagged silages were used in backgrounding diets fed to steers (n = 25) for 84 d. Data were analyzed by the mixed procedure of SAS for main effects of inoculation, silage type, and their interaction. Terminal pH was lower ($P < 0.001$) in corn than in barley silage, and in inoculated silages compared with controls. Water soluble carbohydrate, propionic and acetic acid contents were lower in IB than in CB (38.2 vs. 60.2, 2.03 vs. 2.50, and 10.1 vs. 14.1 g/kg DM, respectively; $P \leq 0.037$) and lactic acid was higher (85.7 vs. 52.7 g/kg DM; $P = 0.001$), but these variables did not differ between IC and CC. Despite corn silage having lower pH, more acetic acid and more lactic acid-producing bacteria compared with barley silage ($P \leq 0.036$), its NH_3-N content was higher ($P = 0.001$). Yeasts were detected (4.44 $\log_{10}$ cfu/g DM) in corn silage but not in barley (<1 $\log_{10}$ cfu/g DM). Inoculation did not affect ($P \geq 0.236$) DMI or growth performance of steers, but steers fed barley silage had greater DMI ($P = 0.038$), ADG ($P = 0.002$) and feed conversion efficiency ($P < 0.001$) than those fed corn silage. In this study inoculant improved fermentation of barley, but not corn, during ensiling, but had no impact on animal performance during backgrounding.

Key Words: barley, corn, silage inoculant

1033 Interactions between animal age and media fatty acids on subcutaneous and intramuscular adipose tissue explants from Angus steers. D. T. Silvey*[1], G. Go[1], L. A. Gilmore[1], S. B. Smith[1], B. J. Johnson[3], and M. Doumit[2], [1]*Intercollegiate Faculty of Nutrition, Texas A&M University*, *College Station,* [2]*University of Idaho*, *Moscow,* [3]*Department of Food and Animal Science, Texas Tech University*, *Lubbock*.

Pasture feeding depresses adipose tissue development in beef cattle. Therefore, we hypothesized that specific fatty acids would differentially depress lipogenesis in explants of bovine subcutaneous (s.c.) and intramuscular adipose (i.m.) tissues. Angus steers were harvested at 12, 14, and 16 mo of age and i.m. and s.c. adipose tissue explants from the 5-8th thoracic rib region were dissected and cultured in media. In both depots, two concentrations (0 μ*M* and 40 μ*M*) of five fatty acids, stearic acid (18:0), oleic acid (18:1 n-9), *trans*-vaccenic acid (18:1 *trans*-11), conjugated linoleic acid (CLA, 18:2 *trans*-10, *cis*-12), and alpha-linolenic acid (18:3 n-3) were added to the media. After 48 h of culture, lipogenesis using [U-^{14}C]glucose and [1-^{14}C]acetate was measured. Lipogenesis from glucose decreased between 12 and 16 mo of age in s.c. adipose tissue (from 8.9 to 4.0 nmol per 2 h per 100 mg; $P = 0.001$) and i.m. adipose tissue (from 4.4 to 2.7 nmol per 2 h 100 mg; $P = 0.08$). Lipogenesis from acetate did not change over time in s.c. adipose (approximately 56 nmol per 2 h 100 mg; $P = 0.23$), but increased over time in i.m. adipose tissue (from from 11.3 to 17.1 nmol per 2 h 100 mg; $P = 0.02$). *Trans*-vaccenic acid increased lipid synthesis from glucose 81% ($P = 0.05$), CLA, 18:2 *trans*-10, *cis*-12 61% ($P = 0.02$), and α-linolenic acid 84% ($P = 0.02$) in s.c. adipose tissue. Stearic acid decreased lipid synthesis from glucose by 61% ($P = 0.03$) in i.m. adipose tissue. In s.c. adipose tissue only, stearic acid increased lipogenesis from acetate by 250% ($P = 0.03$). We conclude that fatty acids differentially affect lipid synthesis in i.m. and s.c. adipose tissues, which may account for the affects of pasture and grain feeding on adiposity.

Supported in part by grants from the National Cattlemen's Beef Association and the Angus Foundation.

Key Words: CLA, beef, adipose

1034 Characterization of feed efficiency traits and relationships with serum metabolites, cortisol and IGF-I in growing Brangus heifers. R. R. Gomez*, G. E. Carstens, T. H. Welsh Jr., P. A. Lancaster, L. J. Slay, and W. K. Krueger, *Texas A&M University*, *College Station*.

Physiological indicator traits that are biologically associated with residual feed intake (RFI) may be useful indicator traits. The objective of this study was to examine the relationships between RFI, and temperament and serum metabolites and hormones in growing heifers. A 4 yr study (n = 114–119 heifers/yr) was conducted with Brangus heifers (Initial BW = 273 ± 28 kg) that were weaned for 26 ± 9 d before being adapted to a high roughage diet (ME = 2.0 Mcal/kg DM) diet. Individual DMI were measured using Calan gate feeders and BW measured at 7-d intervals during the 70-d studies. RFI was calculated as the residual from the linear regression of DMI on mid-test $BW^{0.75}$ and ADG. On d 0 of the studies, blood samples were collected and exit velocity (EV; rate of distance traveled on exiting a chute) measured. Serum samples were assayed for complete blood counts (WBC, RBC, hemoglobin, Hb), metabolites (glucose, albumin, creatine, blood urea nitrogen, BUN; β-hydroxybutyrate, BHB) and hormones (cortisol, insulin-like growth hormone I, IGF-I). Across all heifers, RFI was positively correlated with DMI (0.67) and F:G (0.52), but not with ADG or initial BW. Heifers with low RFI (<0.5 SD from mean RFI) consumed 14% less DMI and had 11% lower F:G than heifers with high RFI (>0.50 SD from mean RFI). EV was positively correlated ($P < 0.05$) with cortisol (0.24) and negatively correlated ($P < 0.05$) with DMI (−0.15), but was not correlated with RFI or F:G. RFI was weakly correlated ($P < 0.05$) multiple serum parameters including WBC (0.18), Hb (−0.11), total protein (−0.12), albumin (−0.10), creatinine (−0.13) and β-hydroxybutyrate (0.14). These same serum parameters, with the exception of Hb (0.16, −0.26), were not significantly correlated with F:G or ADG. Serum cortisol and IGF-I were not correlated with either RFI or F:G. These results suggest that the serum metabolites and hormones evaluated in this study have limited utility as indicator traits for RFI in growing heifers.

Key Words: feed efficiency, cortisol, beta-hydroxybutyrate

1035 Effects of source and level of dietary roughage and ractopamine (Optaflexx) supplementation on growth performance, carcass traits, and beef quality. D. Glanc*, K. Swanson, C. Campbell, and I. Mandell, *University of Guelph*, *Guelph, Ontario, Canada*.

A high moisture corn/SBM based finishing ration was used to examine the effects of roughage source (corn silage, alfalfa hay), level of dietary roughage (8, 16, 24%), and ractopamine supplementation (none, Optaflexx) on growth performance, carcass traits, and beef quality for finishing 108 steers and 24 heifers (initial BW = 308 kg). Cattle were allocated by gender to 12 management regimen subclasses. Optaflexx was fed over the last 28 d on feed with cattle marketed after a common time on feed. Growth performance data were recorded (ADG, feed intake for individual cattle, and feed efficiency). Carcass measurements were recorded at a commercial packing plant with a primal rib and semitendinosus (ST) muscle from each animal processed at the University of Guelph Meat Laboratory for carcass and meat quality evaluations. Tenderness was determined using shear force assessment of product aged 7, 14, and 21 d. Treatment did not influence ($P > 0.37$) ADG with gains ranging from 1.73 to 1.79 kg/d across all main effects. While hot carcass weights (HCW) were not affected ($P > 0.49$) by roughage

source or use of Optaflexx, HCW were greater ($P < 0.01$) feeding the 8 vs. 16 and 24% roughage diets. Body composition was determined via rib dissection with no differences ($P > 0.11$) in % lean, fat, and bone across source and level of dietary roughage and use of Optaflexx. Source and level of dietary roughage and inclusion of Optaflexx did not affect color ($P > 0.41$) or shear force ($P > 0.20$) values for longissimus (LM) and ST steaks. However, hay diets tended to increase pH ($P > 0.01$) in LM steaks, but had no effect ($P > 0.41$) on ST steaks. Inclusion of up to 24% roughage in finishing diets may not negatively impact gains, carcass characteristics or beef quality; however, feeding 8% roughage in the diet increased HCW. Source of dietary roughage and supplementation of Optaflexx over the last 28 d on feed had minimal effects on gains, body composition, and meat quality.

Key Words: ractopamine, roughage level, shear force

1036 Natural and conventional diet and management effects on steer feedlot performance, carcass traits and economics [1]. M. M. Thompson*[1], C. S. Schauer[1], V. L. Anderson[2], B. R. Ilse[2], R. J. Maddock[3], and K. K. Karges[4], [1]*Hettinger Research Extension Center*, *North Dakota State University, Hettinger,* [2]*Carrington Research Extension Center, North Dakota State University*, *Carrington,* [3]*Department of Animal Sciences*, *North Dakota State University, Fargo,* [4]*Poet Nutrition, Inc.*, *Sioux Falls, SD*.

Seventy-six naturally raised Angus-cross steers were used to determine the effects of natural (NAT) vs. conventional (CON) diet and management strategies on feedlot performance, carcass traits and economics. Animals were stratified by BW and allotted to one of 12 pens (6 pens/treatment). Grow-finish diets were formulated to provide 1.14 Mcals NE_g/kg, 13% CP (DM basis; growing) and 1.43 Mcals NE_g/kg, 12.9% CP (DM basis; finishing) respectively. The NAT supplement contained active yeast and the CON supplement contained monensin. Two estrogenic implants (Ralgro, Component ES) were utilized in sequence in CON steers. Data were analyzed as a completely randomized design (PROC MIXED, SAS) with pen serving as experimental unit. Initial BW (BW = 248 ± 1.5 kg) was not different ($P = 0.31$) between treatments. Feed intake during the background phase was greater for NAT ($P = 0.02$); however, CON had greater DMI during finishing ($P = 0.001$). Conventional steers had greater ADG and heavier BW during the grow-finish periods ($P \leq 0.02$). Conventional animals had lower feed costs ($P = 0.005$) and gained more efficiently ($P \leq 0.02$) than NAT steers. Although 12th rib fat and yield grades were similar across treatments ($P \geq 0.39$), other carcass traits measured differed ($P \leq 0.04$). Conventional steers had $42.88 greater carcass value and $0.23/kg lower breakevens ($P \leq 0.02$) vs. NAT steers. Despite a $72.65 difference in pen closeouts, feeding losses were similar across treatment ($P = 0.13$). These data suggest that cattle managed with NAT production practices require higher market prices for equal returns to feeding to compensate for slower growth rates and greater cost of gain.

Key Words: conventional, natural, steer

1037 Effect of calving season and wintering system on cow performance. W. A. Griffin*[1], T. J. Klopfenstein[1], D. C. Adams[2], G. E. Erickson[1], L. A. Stalker[2], J. A. Musgrave[2], and R. N. Funston[2], [1]*University of Nebraska*, *Lincoln,* [2]*University of Nebraska West Central Research and Extension Center*, *North Platte*.

A 4-year study using two hundred seventeen cows/year (5/8 Red Angus, 3/8 Continental) was conducted to evaluate effects of calving season and wintering system on cow performance. Cows were assigned to one of 5 treatments: 1) spring calving cows (SP) wintered on native range, 2) SP wintered on cornstalks, 3) summer calving cows (SU) wintered on native range, 4) SU wintered on cornstalks, and 5) fall calving cows (FA) wintered on cornstalks. Calves were weaned at 221, 298, and 247 d of age for SP, SU, and FA, respectively. Cow BW and BCS were recorded 3 times during production: 21 d pre-calving, 50 d post calving (pre-breeding), and weaning. Data were analyzed as a completely randomized design and binomial measurements were analyzed using proc freq. Wintering system did not affect calf weaning BW ($P = 0.72$), cow BW ($P = 0.57$), cow BCS ($P = 0.61$) or rebreeding rates ($P = 0.86$). Across calving season, pre-breeding BW was lowest for SP (480 kg), intermediate for SU (570 kg), and greatest for FA (589 kg; $P < 0.01$). At weaning BW was lower for SP compared with SU ($P = 0.03$) and FA ($P = 0.14$) which were similar ($P = 0.64$). At pre-calving BW was greatest for FA (629 kg; $P < 0.01$), intermediate for SU (569 kg), and lowest for SP (533 kg; $P < 0.01$). Cow BCS in the different calving seasons followed the same pattern as BW. Rebreeding performance was numerically lower for FA (90.2%; $P = 0.22$) compared with SP and SU (93.2 vs. 94.3%). Calf ADG from birth to weaning was greatest for SP and lowest for SU ($P < 0.01$). However, calf BW at weaning was greatest for SU (254 kg; $P < 0.01$) compared with SP (238 kg) and FA (234 kg) due to differences in weaning age. In the current study, wintering system did not affect cow performance. Calving season significantly affected cow BW, BCS, and influenced rebreeding performance. In addition wintering system effected calf BW and ADG.

Key Words: calving season, cow-calf systems, wintering system

1038 Eating pattern of Holstein bulls and steers fed high-concentrate rations using a computerized concentrate feeder. M. Devant*[1], S. Marti[1], and A. Bach[2,1], [1]*Department of Ruminant Production, IRTA*, *Barcelona, Spain*, [2]*ICREA*, *Barcelona, Spain*.

A total of 132 animals (initial BW = 220 ± 22 kg and age = 172 ± 0.4 d) were used to study the effect of castration on eating pattern. Animals were randomly allocated in 6 pens with 2 pens for each treatment: 44 intact bulls, 44 steers castrated at 3 mo of age (CAS3), and 44 bulls castrated at 8 mo of age during the study (CAS8). The study finished at 285 d of life. Each pen had one computerized concentrate feeder (GEA WestfaliaSurge, Germany), one straw feeder, and one drinker. Concentrate and straw were offered ad libitum. Animals were weighed every 14 d and concentrate eating pattern was averaged for each 14-d period. The statistical model included initial BW as a covariate, treatment, period, and the interaction between treatment and period, as fixed effects, and animal as a random effect. Overall, average BW was 305 ± 58.3 kg, ADG 1.4 ± 0.53 g/d, feed efficiency 22 ± 9.1%, daily intake 6.3 ± 1.01 kg/d, daily feeder visits 6.3 ± 1.29 /d, meal size 1.1 ± 0.25 kg, meal duration 10.2 ± 2.20 min, inter-meal time 244.8 ± 55.38 min, and eating rate 112 ± 16.9 g/ min. Daily intake, meal size, and eating rate increased ($P < 0.001$) with age. The CAS8 steers grew and ate less concentrate ($P < 0.001$) the first 2 wk following castration than bulls or CAS3 steers. Meal size (1.3 ± 0.05 kg) and meal duration (12.4 ± 0.47 min) were greater ($P < 0.001$) in bulls during these 2 wk than in CAS3 steers (1.0 ± 0.05 kg and 9.7 ± 0.46 min, respectively) and CAS8 steers (0.8 ± 0.05 kg and 7.8 ± 0.47 min, respectively). In contrast, bulls visited the feeders less frequently (5.3 ± 0.34 /d) during these 2 wk than CAS3 steers (6.7 ± 0.34 /d) and CAS8 steers (7.7 ± 0.34 /d). Daily intake increases with age mainly through an increase in meal size and eating rate in combination with a slight increase in the number of daily feeder visits rather than an increase in meal duration. Surgical castration at 8 mo of age reduces daily intake, meal size and duration, and increases the number of daily feeder visits.

Key Words: beef, monitoring, eating pattern

1039 Formation of trans-18:1 and CLA isomers in rumen and digesta of bulls fed different polyunsaturated fatty acid diets. D. Dannenberger*[1], K. Nuernberg[1], X. Shen[2], G. Nuernberg[1], and R. Zhao[2], [1]*Leibniz Institute for Farm Animal Biology*, *Dummerstorf, Germany*, [2]*Nanjing Agricultural University*, *Nanjing, P.R. China*.

The understanding of mechanisms underlying the biosynthesis of individual trans-18:1 and CLA isomers in the rumen of cattle are important because the ruminal outflow affects the availability of bioactive fatty acids for incorporation into milk and muscle. The aim of the study was to investigate the formation of rumen and digesta trans C18:1 and CLA isomers for final deposition in tissue lipids of bulls by feeding different polyunsaturated fatty acids (PUFA). Twenty-five German Simmental bulls were divided into 3 groups in the experiment and fed diets high in n-3 and n-6 PUFA. The diet affected the biosynthesis of individual trans-18:1 and CLA isomers of the bulls. The isomer t-11c-13 CLA was detected as the most abundant isomer in the rumen of n-3 rich diet-fed bulls compared with n-6 rich diet-fed bulls. However, the main isomer in muscle lipids c-9,t-11 CLA was synthesized to a low extent in the rumen of n-3 fatty acid rich-fed bulls compared with higher concentrations of this isomer in the rumen of n-6 fatty acid rich-fed bulls. The second most abundant isomer in muscle lipids t-7,c-9 CLA was not detected in the rumen samples of bulls fed all 3 diets, however abundantly t-7,c-9 CLA was identified in the duodenum. The sum of trans 18:1 fatty acids in the rumen was not affected by the diet, however there was an obvious variation for some individual trans fatty acids. The concentration of trans-10–18:1 was significantly higher in the rumen of n-3 fatty acid rich-fed bulls compared with n-6 fatty acid rich-fed bulls. The results indicated that biosynthesis of trans C18:1 fatty acids and CLA isomers in rumen and duodenal digesta gives the opportunity of regulation the postruminal deposition of bioactive fatty acids in tissue lipids.

Key Words: rumen, digesta, CLA

Ruminant Nutrition: Beef: Forages and Grazing

1040 Effects of self-fed byproducts on animal performance, carcass traits and fatty acid profiles of pasture reared finishing cattle. D. D. Kiesling*, D. G. Morrical, D. R. Strohbehn, M. S. Honeyman, D. W. Busby, D. Maxwell, and J. S. Sellers, *Iowa State University*, *Ames*.

The objective of this study was to evaluate self-fed byproducts on pasture reared finishing cattle. Major effects studied were animal performance, carcass traits and fatty acid (FA) profile with specific emphasis on conjugated linoleic acid (cis-9, trans-11–18:2; CLA). Eighty-two crossbred yearling steers were utilized in a 2 × 2 factorial design with implanted and non-implanted cattle fed either Diet 1: corn/dried distillers grain with solubles (DDGS) or Diet 2: soyhulls/DDGS. Self-feeders were available to cattle that continually grazed cool-season grasses at 5.6 animals/ha. Ribeye facings were extracted for lipid content and esterified for FA analysis by gas chromatography. Data presented is from the first year of this 2 year trial, which second year data has yet to be analyzed. Average daily gains (ADG) over the entire trial of cattle fed Diet 1 were greater (1.59 kg/d vs. 1.52 kg/d, $P = 0.09$) compared with cattle fed Diet 2. Diets did not affect dressing percentage, yield grade or quality grade. As expected, implanted cattle gained faster (1.66 kg/d vs. 1.46 kg/d, $P < 0.0001$) than non-implanted cattle. No differences were observed among implant treatments relative to marbling scores (1031.0 vs. 1016.0, non-implanted vs. implanted, respectively, $P = 0.29$). However, percentage of cattle grading low choice or better was higher in non-implanted cattle (77.5% vs. 47.6%, $P = 0.005$). Cattle fed Diet 2 did have greater CLA levels (0.66 g/100g FA vs. 0.44 g/100g FA, $P < 0.0001$). However, supplementation of byproducts does lead to reduced levels of CLA when compared with grass-finished cattle. Neither diet nor implant treatments had an effect on total lipid, total saturated fatty acid (SFA), polyunsaturated fatty acid (PUFA) or monounsaturated fatty acid (MUFA). In conclusion, pasture reared cattle perform comparably to feedlot cattle in the yard and on the rail when supplemented with byproducts. As well, greater CLA levels can be achieved especially when fed a low starch diet such as soyhulls.

Key Words: beef cattle, by-products, fatty acid profile

1041 Diets containing thirty percent wheat straw or orchard grass hay fed at either ad libitum or restricted intake prepartum have modest effects on postpartum performance. N. B. Litherland*, M. L. Raeth-Knight, and J. G. Linn, *University of Minnesota*, *St Paul*.

The objectives of this study were to investigate the effects of forage type (wheat straw vs. orchard grass hay) and DM amount fed (ad libitum vs. 30% DMI restriction) prepartum on postpartum performance. A 2 × 2 factorial design with 10 cows per treatment was used to determine the effects of forage type in a TMR (wheat straw (WS) vs. orchardgrass hay (GH)) and amount fed (ad libitum (A) vs. 30% intake restriction (R) in DM based on NRC, 2001. Treatments included WS TMR A (WSA); GH TMR A (GHA); WS TMR R (WSR); GH TMR R (GHR). The WS TMR (DM basis) contained 30% WS, 21% corn silage, 10% alfalfa hay, 18% ground corn, 17% soybean meal, and 4% molasses (14.8% CP, 1.5 NE_L Mcal/kg, 37% NDF). The GH TMR contained 30% GH, 46% corn silage, 10% alfalfa hay, 10% soybean meal, and 4% molasses (15% CP, 1.5 NE_L Mcal/kg, 40% NDF). Cows received one lactation diet after calving (CP 17.8%, NE_L 1.6 Mcal/kg, NDF 26%). Cows were housed in a tie-stall barn, fed once daily prepartum and fed and milked twice daily postpartum. Thirty 6 cows were used in the final analysis using the Mixed procedure in SAS. As designed, dry matter intake as a percent of body weight was higher ($P < 0.05$) in WSA and GHA vs.WSR and GHR prepartum, but there was no difference postpartum. Fat corrected milk yield tended to be higher ($P = 0.10$) from GHR cows. Postpartum energy balance was less negative ($P = 0.04$) for GHA for wk 1 to 4. Milk fat production tended ($P < 0.08$) to be higher for GHR cows. Liver total lipids, body weight, body condition score, milk fat:protein, and fecal dry matter, did not differ among treatments. Feeding behavior was observed by 24 h video surveillance and 10 min video scans for 5 d pre- and postpartum. Cows fed WSA or WSR tended ($P < 0.06$) to have more eating bouts on d 2 and 4 postpartum than cows fed GHA or GHR. Results indicate that forage type and amount of DM fed have modest effects on performance and behavior of cows in tie stall barns if diets are formulated to meet NRC, 2001 requirements.

Key Words: restricted intake, ad libitum intake, transition cow

1042 In situ digestibility of grass hay after heifer diets were abruptly switched from 35 or 70% concentrate to 100% forage. L. A. Voigt*[1], R. L. Endecott[1], R. C. Waterman[2], and J. A. Paterson[1], [1]*Montana State University*, *Bozeman,* [2]*USDA-ARS*, *Miles City, MT*.

Twelve ruminally-cannulated Hereford-cross heifers (non-pregnant, 2-yr-old, 508 ± 2 kg) were randomly assigned to 3 individually-fed, pre-experiment diets (4 heifers/diet). Diets were: 1) all forage, (CONTROL); 2) 35% concentrate, (35%), and 3) 70% concentrate (70%). Heifers were fed the diets for ~100 d before the start of the trial. Pre-experiment diets consisted of grass-alfalfa hay (11.8% CP) and corn (9.8% CP), with soybean meal-urea supplement added to make the diets isonitrogenous at 13% CP. On d 0, diets were abruptly switched to grass hay (6.2% CP, fed at 2% BW). In situ digestibility runs were conducted starting on d −8 and ran continuously (d 1, 4, 7, 10, 13, 16, 19, 22) after the diet switch. Duplicate sample bags filled with 5 g of grass hay and a blank bag were incubated for 0, 24, 48, and 96 h. Pre-experiment diet × in situ run interactions occurred ($P \leq 0.04$) for OM and NDF digestibility. Organic matter digestibility of grass hay before the diet switch (d −8) was lower ($P \leq 0.10$) for 70% than for 35% or CONTROL; 48-h: 68.5, 66.7, and 53.0 ± 2.3%; 96-h: 76.3, 75.2, and 61.6 ± 1.0% for CONTROL, 35%, and 70%, respectively. A comparable pattern was observed for NDF digestibility; 48-h: 67.7, 65.6, and 48.8 ± 2.8%; 96-h: 77.0, 75.9, and 58.9 ± 1.1% for CONTROL, 35%, and 70%, respectively. In contrast, after the diet switch (d 1), OM digestibility of grass hay was higher for 70% than for 35% or CONTROL ($P \leq 0.10$; 48-h: 66.5, 66.0, and 69.0 ± 1.7%; 96-h: 75.9, 76.1, and 77.6 ± 0.7% for CONTROL, 35%, and 70%, respectively). Digestibility of NDF was likewise higher for 70% than 35% or CONTROL; 48-h: 65.5, 64.4, and 67.8 ± 2.2%; 96-h: 76.2, 76.3, and 78.1 ± 0.8% for CONTROL, 35%, and 70%, respectively. Organic matter and NDF digestibilities in subsequent in situ runs were similar ($P > 0.10$), regardless of pre-experiment diet. Rate of digestion was not influenced by pre-experiment diet ($P = 0.74$; avg 4.3 ± 0.002%/h). Forage digestibility was depressed when heifers were fed a high-concentrate diet; however, this effect disappeared within 48 h of feeding an all-forage diet.

Key Words: forage digestibility, diet switch, beef cattle

1043 Evaluation of annual ryegrass (*Lolium multiflorum*) in two fall grazing systems on forage quality and beef heifer performance. J. M. Kelzer*[1], R. S. Walker[2], S. L. Bird[3], and R. D. Mathison[3], [1]*University of Minnesota*, *St. Paul*, [2]*Extension Regional Center, University of*

Minnesota, *Andover*, [3]*North Central Research and Outreach Center, University of Minnesota*, *Grand Rapids*.

Effects of fall grazing stockpiled and windrowed annual ryegrass on forage quality and beef heifer performance were evaluated. One renovated, 2-ha pasture was seeded with annual ryegrass (*Lolium multiflorum*) in late June and treated with herbicide in August for weed control. In late September, stockpiled forage from one-half of the pasture was cut into single windrows while the other half was left standing. Weaned Angus beef heifers (n = 48) averaging 186 ± 7 kg initial BW were randomly assigned to 1 of 2 grazing treatments (3 replications per treatment; 8 heifers per replication): 1) stockpiled annual ryegrass (STO), and 2) windrowed annual ryegrass (WIN). Forage samples were collected to determine change in forage quality over time and weekly DM loss following grazing. Heifers were weighed at trial initiation, weekly, and at trial completion to measure animal performance. Percent forage DM at trial completion was 41.8 ± 2.8 and 38.4 ± 7.5% for STO and WIN, respectively. Final concentration of CP was greater ($P < 0.01$) for STO compared with WIN (13.6 vs. 11.4 ± 0.5%). Final concentrations of NDF (56.0 vs. 66.5 ± 0.5%) and ADF (36.5 vs. 42.3 ± 0.5%) were lower ($P < 0.01$), while TDN (60.4 vs. 55.9 ± 0.5%) and relative feed value (100.7 vs. 78.4 ± 1.3) remained greater ($P < 0.01$) for STO compared with WIN over time. Forage DM loss was estimated at 6.3 ± 4.0% and 2.5 ± 1.0% for STO and WIN. Heifers on STO grazed 5 d longer ($P < 0.01$) than WIN (45 vs. 40 d). Although final BW (206 vs. 201 ± 8 kg) and ADG (0.43 vs. 0.37 ± 0.04 kg) were similar for STO and WIN, overall BW gain was greater ($P < 0.05$) for STO (19.2 vs. 14.9 ± 1.5 kg). Results suggest grazing stockpiled and windrowed annual ryegrass may be viable systems to extend fall grazing; however, forage maturity can reduce forage quality to levels that may limit beef heifer performance.

Key Words: beef cattle, grazing system, annual ryegrass

1044 Effects of pen cleaning frequency and feeding high distillers grains and wheat straw on nutrient mass balance and performance of feedlot steers. A. R. Rich*, G. E. Erickson, T. J. Klopfenstein, M. K. Luebbe, and W. A. Griffin, *University of Nebraska*, *Lincoln*.

A summer experiment compared feeding wet distillers grains plus solubles (WDGS) with wheat straw to corn on steer performance, manure N, and N loss. Crossbred steer calves (365 ± 5kg) were stratified by BW, and assigned randomly to 16 pens (8 steers/pen) and fed for 145 d from May to October. Four treatments were tested as a 2 × 2 factorial with factors being diet and pen cleaning frequency (monthly or at the end of the feeding period). Diets consisted of 85% corn, 5% molasses, and 5% wheat straw (CON) or 70% WDGS and 25% wheat straw (BYP). Both diets contained 5% supplement. Nitrogen excretion was determined by difference between N intake and N retention. Total N lost was calculated by subtracting manure and runoff N from excreted N. Runoff was drained, quantified, and analyzed from retention ponds when rainfall occurred. No interactions ($P > 0.25$) between diet and cleaning frequency were observed for performance. Steers fed CON had greater DMI, ADG, HCW, marbling, and fat depth ($P < 0.02$) compared with BYP. Due to decreased ADG, steers fed BYP were fed an additional 14 d for performance, but mass balance data are for 145 d only. Cleaning frequency had no impact ($P > 0.35$) on cattle performance. Feeding BYP increased ($P < 0.01$) N intake and N excretion compared with CON due to differences in CP between diets (23.5 vs 11.6%), and was not impacted by cleaning frequency. Runoff N was not impacted ($P > 0.10$) by diet or pen cleaning treatments. Amount of DM, OM, and N removed in manure was almost doubled ($P < 0.01$) by feeding BYP compared with CON. Likewise, cleaning pens monthly almost doubled ($P < 0.01$) DM, OM, and N removed in manure. Despite increases in manure N, N losses were greater ($P < 0.01$) for BYP compared with CON. However, cleaning pens monthly decreased ($P < 0.01$) N losses by 8.4 kg and % N lost from 72.5 to 49.4% compared with cleaning once at the end. Feeding 70% WDGS with 25% wheat straw decreases ADG and G:F and increased N losses.

Key Words: cleaning frequency, nitrogen, wet distillers grains plus solubles

1045 Restricting intake of replacement heifers by limiting hay access time. W. J. Sexten* and D. K. Davis, *University of Missouri*, *Columbia*.

Spring-born replacement beef heifers are often developed using hay offered ad libitum with limited supplementation from weaning until breeding. The objective of this experiment was to evaluate restricted hay access time on replacement heifer performance and hay intake. Spring-born Red Angus crossbred heifers were randomly assigned to 8 h (8H) or 24 h (24H) access to hay in year 1 (YR1) (n = 52) and year 2 (YR2) (n = 64). Three pens per treatment were used in YR1 with a 107 d development period beginning 19 December 2007. During YR2 4 pens per treatment were used during the 93 d development period initiated 7 January 2009. Development periods concluded 4 April 2008 and 10 April 2009. Each pen was offered one large round bale of hay in a bale feeder. As hay was consumed another bale was offered in a second feeder. As the second bale was consumed the first feeder was moved and a third bale added. This rotational system was used throughout development. Hay not consumed was considered wasted. 8H access was restricted using polywire around hay feeding area. Heifers were fed 2.0 kg/animal per d of supplemental DM consisting of 93.7% distillers dried grains with solubles, 4.1% limestone and 2.2% mineral. Hay was 10.4% CP, 39.3% ADF and 60.3% NDF in YR1 and 10.4% CP, 41.3% ADF and 60.6% NDF in YR2. Data were analyzed as a randomized complete block design using the mixed procedure of SAS. Initial and final heifer weight was greater ($P < 0.02$) in YR1 than YR2 with no differences due to access time. Access time and year tended ($P = 0.09$) to interact for development ADG. In YR1 24H had greater ($P < 0.05$) ADG than 8H while in YR2 no differences ($P > 0.10$) were observed due to access time. Yearling pelvic area and reproductive tract score were not different ($P > 0.10$) due to access time or year. Total hay DMI was greater ($P < 0.01$) in YR1. Total hay DMI and daily hay DMI were reduced ($P < 0.01$) by 10.9% due to 8H. Prebreeding weight, yearling pelvic area and reproductive tract score were not influenced by restricting hay access time however development ADG was reduced in YR1. Restricting hay access time can reduce hay DMI of developing replacement heifers.

Key Words: beef heifer, hay, restricted intake

1046 Effect of stocking rate on nutrient quality of cornstalk residue. J. A. Gigax*, C. D. Buckner, L. A. Stalker, T. J. Klopfenstein, and S. J. van Donk, *University of Nebraska*, *Lincoln*.

A grazing trial compared the effect of stocking rate on corn residue removal and nutrient quality over a 65 d period. Treatments included no removal (control), light grazing (0.4 animal unit months/ha), and heavy grazing (0.8 animal unit months/ha), that were applied to 6 6.6 ha paddocks (2 replications) on a 53 ha center pivot irrigated field of corn residue from mid-December to mid-February. Residue samples were collected before and after grazing at 10 locations within each paddock using a 1/2 m^2 quadrat. After collection samples were sorted by plant part (leaf, stem, husk, cob, and grain), and analyzed for DM, OM, CP, and in vitro organic matter disappearance (IVOMD). No 3 or 2-way

interactions were observed for amount of residue OM (kg/ha; $P \geq 0.61$), but amount of residue was affected by plant part and time collected ($P \leq 0.02$). Of residue remaining before grazing, stems make up the greatest proportion (42.1%) followed by leaves (33.8%), cobs (14.1%), and husks (9.9%). Little removal of stems (2% of original amount) was observed. Cobs and leaves were moderately removed from the light stocking rate (40.1% and 34.4%, respectively) and heavy stocking rate (28.5% and 20.7%, respectively) compared with control (19.2% and 0.1%, respectively). Proportionally, most husks were removed from the heavy stocking rate treatment (87.8%), moderately for light stocking rate treatment (53.1%), and least for control treatment (32.2%). Husks (57.9%) and leaves (53.7%) had greater IVOMD than cobs (48.2%) and stems (49.0%; $P < 0.01$) and IVOMD decreased over collection time ($P = 0.03$). Leaves (5.4%) and husks (4.2%) had the greatest CP content compared with cobs (3.9%) and stems (3.0%; $P < 0.01$). Cattle grazing corn residue removed primarily husk, leaf, and to a lesser extent, cobs. Husk and leaf have greater IVOMD and CP than cob or stem.

Key Words: corn residue, grazing, cattle

1047 Ruminal pressure and pH dynamics of bloated steers grazing winter wheat forage. W. E. Pinchak*[1], D. W. Pitta[1], D. P. Malinowski[1], J. D. Fulford[1], T. A. Wickersham[2], and J. Coverdale[2], [1]*Texas AgriLife Research*, *Vernon,* [2]*Texas A&M University*, *College Station*.

We undertook an experiment to quantify ruminal pressure (mbar), pH and temperature to phenotypic timing and duration of frothy bloat in rumen cannulated steers grazing wheat pasture during the bloat prone period in North Texas through use of an inter-reticulo/rumen biotelemetry bolus system (Kahne Ltd, N .Z.). Environmental conditions (temperature, UV radiation, solar radiation, humidity, dew point wind speed and direction and precipitation) were measured via a recording weather station (WatchDog 2770, Spectrum Technologies, Inc., Plainsville, IL, USA) to determine their relationships to timing, frequency, severity and duration of bloat. Bloat (bloat score 1) was observed in 3 of 12 cannulated Angus cross steers (mean BWT 235 kg) of common ancestry and provenance by 7 February 2010. Analyses of ruminal biotelemetry data quantified cumulative increases in intraruminal pressure from about 1200 h on 8 Feb through most of 9 Feb. Pre-bloat intraruminal pressures of the 3 bloat prone steers on 4 Feb exhibited rapid cyclicity at 5 min sampling intervals throughout the 24 h period. In contrast, from 7 through 9 Feb, the cyclicity decreased, distinct plateaus at peak pressures up to 120 min and decreased amplitude among 5 min sampling periods were found. Peak sustain pressure occurred from evening of 8 Feb throughout 8 Feb. Unlike reports for frothy/foamy bloat in feedlot cattle there was not a concomitant decrease in ruminal pH. The opposite was observed where pH increased during the peak bloat on 9 Feb in all 3 steers. This bloat event was preceded by 3 d of cloudy conditions, high humidity (>60%) and temperatures above freezing. Peak bloat on 9 Feb was accompanied by a cold front, below freezing temperatures and frost. We suggest these preliminary results reinforce our frothy bloat research model where rapid changes in environmental conditions are primary catalysts to bloat onset and duration. Interestingly, finding an increase in pH with increasing ruminal pressure would suggest possible accumulation of ruminal ammonia and reinforces the long suggested role of soluble proteins in wheat pasture frothy bloat.

Key Words: ruminal pressure, pH, biotelemetry, environment

1048 Rumen bacterial diversity dynamics associated with changing from bermudagrass hay to grazed winter wheat diets. D. W. Pitta*[1], W. E. Pinchak[1], S. E. Dowd[2,4], J. Osterstock[3], V. Gontcharova[2], E. Youn[4,5], K. Dorton[6], I. Yoon[6], B. R. Min[1], J. D. Fulford[1], T. A. Wickersham[7], and D. P. Malinowski[1], [1]*1Texas AgriLife Research*, *Vernon,* [2]*Research and Testing Laboratory*, *Lubbock, TX,*[3]*Texas AgriLife Research*, *Amarillo,* [4]*Medical Biofilm Research Institute*, *Lubbock, TX,* [5]*Texas Tech University*, *Lubbock,* [6]*Diamond V Mills*, *Cedar Rapids, IA,* [7]*Texas A&M University*, *College Station*.

Bacterial populations in the rumen adapt to a wide range of changing dietary composition, nutrient density, and environmental conditions. The objective of this study was to explore the distinct bacterial niches associated with the fiber and liquid fractions of rumen contents in animals transitioned from bermudagrass hay diet to a grazed wheat diet. Briefly the experiment involved sampling of fiber and liquid rumen fractions and whole rumen contents of 14 (Angus × Hereford) ruminally cannulated steers sequentially fed bermudagrass hay (*Cynodon dactylon*; 34 d) and grazing wheat forage (28 d) to characterize and elucidate changes in bacterial diversity utilizing 16S bTEFAP pyrosequencing technique. Bermudagrass hay was a conserved C4 perennial grass with a lower protein (11%) and higher fiber (67%) content when compared with grazed winter wheat (*Triticum aestivum*), a C3 annual grass with higher protein (20%) and a large (66%) soluble fraction. Significant differences in the OTU estimates (Chao1, Ace, and Rarefaction) were detected between fractions of both diets, with bermudagrass hay supporting greater diversity than wheat forage. Sequences were compared with a 16S database using BLASTn and assigned sequences to respective genera and genera-like units based on the similarity value to known sequences in the database. Predominant genera were *Prevotella* (up to 33%) and *Rikenella-like* (up to 28%) genera on the bermudagrass diet and Prevotella (up to 56%) genus on the wheat diet irrespective of the fractions. Principle component analyses accounted for over 95% of variation in 16S estimated bacterial community composition in all 3 fractions and clearly differentiated communities associated with each diet. In summary, bermudagrass hay diets clustered more clearly and were more diversified than wheat diets.

Key Words: bermudagrass hay, wheat, bTEFAP pyrosequencing

1049 Fermentable fiber levels in diets for natural beef cattle markets. M. J. Baker*, D. E. Hogue, M. L. Thonney, and D. J. Ketchen, *Cornell University*, *Ithaca, NY*.

Eligibility requirements for "natural" beef often state that antibiotics, including ionophores, cannot be fed. To reduce the incidence of acidosis in diets without an ionophore, feeders often increase the NDF concentration, which lowers intake of digestible nutrients with a resulting increase in cost of gain. However, if the NDF has high potential fermentability (pfNDF), then feed intake may increase and compensate for the lack of an ionophore. The purpose of this experiment was to evaluate the interaction between monensin and levels of pfNDF on growth and feed efficiency of yearling steers. Crossbred steers (n = 32, BW = 485 kg) were blocked by weight with 2 large and 2 small steers assigned to each of 2 slatted floor pens per diet (Table 1) and fed for 87 d. Diets contained 70% whole shelled corn, 0 or 10% soy hulls, and a high NDF pellet formulated to meet protein, mineral and vitamin requirements. One steer died of causes unrelated to the experiment and carcass data for 2 others were not obtained. There were no significant interactions or main effects for growth or feed intake responses (Table 1). Cattle fed the 20% pfNDF diet had a higher ($P < 0.10$, 5.8, 5.2 ± 0.185) quality grades than cattle fed the 15% pfNDF. There was an interaction between monensin and pfNDF in carcass fat deposition ($P < 0.05$). Adding monensin to 15% pfNDF diets increased backfat, worsened yield grade, and tended ($P = 0.13$) to increase marbling, with little effect of monensin for 20% pfNDF diets. Diets with 20% pfNDF without monensin supported growth and

carcass characteristics similar to higher energy diets with monensin. This provides an opportunity to sell to "natural" cattle markets while avoiding the typical reductions in performance that occur when no ionophore is included in the diet.

Table 1. Effect of pfNDF and ionophore on growth and carcass traits of steers

Monensin:	0	0	+	+	
pfNDF:	15%	20%	15%	20%	SE
n (steers)	8	8	7	8	
Initial wt., kg	483	489	481	488	17
Final wt., kg	590	604	605	607	19
ADG, kg	1.22	1.32	1.41	1.36	0.11
HCW, kg	363	359	371	370	13
n (pens)	2	2	2	2	
gain/DMI	0.123	0.128	0.141	0.139	0.011
n (carcasses)[1]	8	7	7	7	
Marbling (500 = low Choice)	562	619	631	617	21
Quality grade (5 = low Choice)	5.1	5.8	5.5	5.7	0.3
Back fat, cm	1.2	1.7	1.3	1.2	0.1
REA, cm^2	85	85	85	98	2
Yield grade	3.1	3.7	3.4	3.0	0.2

[1]Adjusted to average carcass weight of 366 kg.

Key Words: beef, fermentable NDF, Natural diets

1050 Chemical composition and in situ digestion kinetics of fodder tree leaves. J. I. Sultan*[1], U. B. Cheema[1], A. Javaid[1], and M. Yaqoob[2], [1]*Institute of Animal Nutrition and Feed Technology, University of Agriculture, Faisalabad, Pakistan*, [2]*Department of Livestock Management, University of Agriculture, Faisalabad, Pakistan*.

This study evaluated the nutritional status of *Morus alba*, *Acacia nilotica*, *Syzygium cumuni* and *Ziziphus jujuba* tree leaves for use as supplement in ruminant animal feed. Chemical analyses revealed that DM ranged from 25% to 47% in *Morus alba* and *Syzygium cumunii*, organic matter was higher (94%) in *Syzygium cumuni* and *Ziziphus jujuba*. *Morus alba* had higher (23%) CP, whereas, NDF was greater in *Ziziphus jujuba* (32%). The ADF was higher in *Syzygium cumuni* (23%), while, acid detergent lignin was greater (7%) in *Morus alba* and *Syzygium cumuni*. Hemicellulose (15%) and ash content (10%) were higher in *Ziziphus jujuba* and *Morus alba*, respectively. Metabolizable energy was higher (10.5 MJ/kg) in *Morus alba* than the other species. Among minerals Ca and K was highest in *Acacia nilotica*, P in *Morus alba*, and Mg and Na in *Ziziphus jujuba*. In situ DM digestibility was higher (90.2%) for *Morus alba*, DM lag time was shorter (0.63 h) for *Acacia nilotica*, and rate of DM disappearance was lowest (5.34% per h) for *Syzygium cumuni*. Extent of DM digestion (98.26%) and NDF digestibility (84.10%) were higher for *Morus alba*. Shorter NDF lag time (0.71 h) and higher rate of NDF disappearance were evident for *Acacia nilotica*, but extent of NDF digestion was higher (96.80%) for *Morus alba*. Based on chemical composition and in situ digestion kinetics, *Morus alba* leaves proved the best supplement followed by *Acacia nilotica*, *Ziziphus jujuba* and *Syzygium cumuni* for the feed and optimum production of ruminants.

Key Words: Tree species; chemical composition, digestion, digestibility kinetics

1051 Productivity of lactating dairy cows as impacted by feeding lysine in a ruminally protected form. P. H. Robinson*[1], S. Juchem[1], and I. Shinzato[2], [1]*University of California*, *Davis,* [2]*Ajinomoto Co. Inc.*, *Tokyo, Japan*.

Increased milk production requires high intakes of crude protein in the diet, and/or improved supply and ratios of amino acids delivered to the duodenum to meet animal needs for milk and milk component synthesis. Our objective was to estimate the rumen escape potential of a ruminally protected Lys product (RPL) and to determine effects of feeding this product on feed intake and digestibility, as well as milk production and composition, of high producing dairy cows. The experiment was designed as a double (early and mid-lactation dairy cows) 2 × 2 factorial with 28 d experimental periods. All cows were fed the same total mixed ration (TMR), calculated to be first limiting in Lys, with treatment pens receiving 17 kg/pen/d of RPL (to deliver 38 g of Lys/cow/d) mixed into the TMR. Evaluation of the RPL suggested that this feeding level delivered between 18 and 22 g/cow/d of intestinally absorbable Lys. Control cows were fed the RPL without Lys (i.e., the fat matrix) at the same level as the fat matrix was fed in the RPL. Feeding the RPL did not influence dry matter (DM) intake in early lactation cows (26.3 kg/cow/d), but output of milk (48.0 vs. 50.0 kg/cow/d), as well as milk fat, true protein and lactose, and energy, were higher ($P < 0.05$) in lysine supplemented cows. In addition, the extent of body condition score (BCS) loss was lower ($P < 0.05$) with Lys supplementation (−0.069 vs. −0.0.035 units/28 d). In mid lactation cows, DM intake was also not influenced, and only milk fat and energy outputs increased ($P < 0.05$) with RPL feeding. BCS change was not influenced. Plasma Lys levels in cows of both parities were not impacted by RPL feeding, suggesting that Lys needs may not have been met at this level of supplementation. The contrast to an earlier study by our group, wherein milk fat synthesis was suppressed with Lys supplementation at an estimated 9 to 10 g/cow/d at the intestinal absorptive site in similar cows fed a very similar TMR, supports the hypothesis advanced in that study that body protein turnover is the first priority in early lactation cows followed by milk component synthesis.

Key Words: lysine, rumen protection, lactation

1052 The application of reliable wireless sensor provides better understanding of the rumen environment. J. Laporte-Uribe*, F. Brooks, M. Steer, P. Fernley, and M. Eivers, *Kahne Limited*, *Level 1, 64 Cook street, Auckland*.

During the last few years several techniques have evolved to obtain real-time information of the rumen environment. Kahne Limited has developed a wireless rumen bolus that does not required fistulated animals. Information such as pH, temperature, pressure is acquired telemetrically and in real-time. An experiment was designed to measure the reliability of the current sensors over time. Four fistulated and dry dairy cattle were placed in a 4 × 4 Latin-square design. Animals were fed fresh grass (ryegrass/clover) and in free range conditions, no attempt was made to manipulate the diet or the daily management practices. Measurement of pH, temperature and pressure were taken continuously for 7 d period, after which the probes were randomly changed. The sensors were calibrated at the beginning of the each run and at the end of the run, the drifting of probes was estimated by immersing the sensors in a battery of standard buffers solutions. Results were tabulated in a paired-*t*-test to observed differences between recordings. A linear mixed model (REML) was fitted to the results to evaluate the variance associated to the measurement of rumen variables; each single component of variability was taken into account and included in the model, date of sampling, time within date, animals effect, sensors and interactions of these factors. The drift of the pH electrodes at the end of each run (7 d) was minimal, less than 0.04 points of pH. The accuracy of temperature (0.20 oC) and pressure (1.50 mbar) sensors remained unchanged during the period of investigation. This experiment suggested that the Kahne sensors accounted for a very small amount of the variance associated to the recording of rumen environmental conditions, and supports the use of the wireless Kahne sensor technology as a reliable method to measure changes in the rumen environment.

Key Words: rumen pH, wireless sensor, continuous recording

1053 Top-dressing soybean meal in fresh cow, an end to the risks of dry matter intake decreases: Dry matter intake, milk production and nitrogen metabolism. M. Ghelich Khan*, H. Amanlou, and E. Mahjoubi, *Zanjan University*, *Zanjan, Iran*.

The objective of this study was to investigate the effects of high dietary crude protein (CP) levels on dry matter intake (DMI), milk production and nitrogen metabolism in fresh cows. As it has been proved in early lactation dairy cows there are negative energy and nitrogen balances. These shortages should be compensated for by adding a suitable feed stuff, since the produced colostrum contains high amounts of protein. Solvent-extracted soybean meal (SSBM) containing high energy and CP was selected for this purpose and the top-dressing method was employed to facilitate the task. Twenty-one Holstein fresh cows, free of clinically diagnosed transition disorders, were used in this experiment. The cows were randomly assigned to 1) basal diet (CP = 20.3%), 2) basal diet + 1 kg of top-dressing SSBM (CP = 21.8%) and 3) basal diet + 2 kg of top-dressing SSBM (CP = 24.4%). The cows were individually fed from immediately after parturition until wk 4 and were milked 6 times a day. DMI increased noticeably from treatment group 1 to 3 (17.53, 18.02 and 20.58 kg/d, respectively; $P < 0.05$). Average raw milk yields were 35.98, 36.87 and 42.27 kg/d, respectively, and tended to be significant ($P = 0.11$). Milk fat percentage decreased significantly (4.65, 4.51 and 3.86%, respectively; $P < 0.01$). 3.5% fat corrected milk yield increased while the treatments did not have noticeable differences (42.35, 42.52 and 45.24 kg/d, respectively). Milk protein and fat yields were not affected by treatments. Ruminal concentration of NH3-N and total VFA increased as dietary CP level increased but the differences in treatments were not significant. The treatments did not influence uric acid concentration, though a tendency was detected ($P < 0.15$). Urinary urea excretion increased by adding dietary CP causing noticeable differences in treatments (11.01, 16.01 and 19.72 mg/dl, respectively; $P < 0.01$). These results demonstrate that by adding top-dressing SSBM and using high levels of CP, DMI and milk production increase and at the same time ruminal condition and feces score stay in a desirable level.

Key Words: soybean meal (SSBM), top-dress, fresh cow

1054 Leucine had the highest regulatory effects on protein synthesis in bovine mammary epithelial cells when added to media deprived of other essential amino acids. N. A. Knoebel*[1], J. A. D. R. N. Appuhamy[1], J. Escobar[2], and M. D. Hanigan[1], [1]*Department of Dairy Science, Virginia Polytechnic Institute and State University*, *Blacksburg,* [2]*Department of Animal and Poultry Sciences, Virginia Polytechnic Institute and State University*, *Blacksburg*.

Protein synthesis responds to amino acid supply through several signaling proteins such as mammalian target of rapamycin (mTOR), ribosomal protein S6 (rpS6), eukaryotic initiation factor 4E binding protein 1 (4EBP1), and eukaryotic elongation factor 2 (eEF2). Increasing phosphorylation of mTOR, rpS6, and 4EBP1, and decreasing PS of eEF2 positively signal protein synthesis. Previous experiments in our laboratory showed that omission of Arg, Ile, Leu, Met, Thr, and Trp from media reduced casein synthesis rates in bovine mammary tissue slices. This study investigated the effects of the addition of essential amino acids (EAA) to media devoid of other EAA on phosphorylation state (PhS) of mTOR, rpS6, 4EBP1, and eEF2 in MAC-T cells to test the hypothesis that EAA can independently affect the PhS of key signaling proteins when media are deficient in other EAA. Cells were deprived of serum and EAA for 6 h and then cultured with media containing 3.5 m*M* all EAA (+EAA), no EAA (-EAA), Arg, Ile, Leu, Met, Thr, or Trp for 1 h. Cell lysates were analyzed by Western immunoblotting with antibodies against phosphorylated mTOR (Ser2448), rpS6 (Ser235/236), eEF2 (Thr56), and 4EBP1 (Thr37/46). The +EAA treatment significantly increased PhS of rpS6 by 1900% ($P < 0.0001$) and decreased PhS of eEF2 by 35% ($P = 0.016$) compared with that of -EAA. Addition of Leu alone significantly increased PhS of rpS6 by 785% ($P = 0.003$) and decreased PhS of eEF2 by 23% ($P = 0.033$) besides its association with 21% increase in mTOR PhS and 150% increase in 4EBP1 PhS. Addition of Ile and Met increased PhS of mTOR (25% each), 4EBP1 (138 and 127%), and rpS6 (273 and 134%) and decreased PhS of eEF2 (15 and 8%). Of the 6 EAA tested, Leu had the greatest signaling effects on PhS. Essential amino acids can independently affect PhS of key regulatory proteins regardless of the supply of other EAA.

Key Words: essential amino acids, protein synthesis, signaling proteins

1055 Hypophagic effects of propionate relative to acetate decrease as days in milk increase and plasma NEFA concentration decreases. S. E. Stebulis* and M. S. Allen, *Michigan State University*, *East Lansing*.

Thirty-one multiparous lactating dairy cows were used in a crossover experiment to evaluate factors related to responses to propionic acid infusion among cows. Cows between 3 and 40 DIM at the start of the experiment were blocked by calving date and randomly assigned to treatment sequence. Cows ranged from 23.4 to 49.5 kg/d milk yield, 513 to 760 kg body weight and 1.5 to 4.1 body condition score at the start of the experiment. Treatments were 1.0 *M* propionic acid (P) or 1.0 *M* acetic acid (A, control) adjusted to pH 6 with sodium hydroxide and infused intraruminally at 8.33 mmol/min from 6 h before feeding until 12 h after feeding. Feeding behavior was monitored for 12 h after feeding. The diet was formulated to contain 33.9% NDF and the primary starch source was coarsely ground corn. A preliminary period was used to measure factors potentially related to hypophagia from propionate. Propionate decreased dry matter intake (14.0 vs. 15.4 kg/12 h; $P < 0.001$) by decreasing meal size (2.18 vs. 2.63 kg; $P = 0.03$) and meal length (34.6 vs. 40.0 min; $P < 0.01$). Meal frequency and intermeal interval were not affected by treatment ($P > 0.20$). Propionate affected meal patterns following feeding; there was no difference in DMI in the first 6 h after feeding (9.1 kg, $P = 1.00$), but DMI was lower for P than A during the second 6 h after feeding (5.2 vs. 6.2 kg; $P < 0.01$). An interaction was detected between plasma NEFA concentration and treatment for DMI ($P = 0.09$); there was no difference in DMI for P vs. A at the lowest plasma NEFA concentration of 103 μEq/L (14.9 kg/12 h) but DMI was 1.8 kg greater for A compared with P at the highest plasma NEFA concentration of 1330 μEq/L (17.2 vs. 15.4 kg/12 h). There was a tendency for an interaction between treatment and DIM for DMI ($P = 0.11$) with a greater difference in DMI for P vs. A at 3 DIM (13.8 vs. 15.1 kg/12 h) than at 40 DIM (15.8 vs. 15.9 kg/12 h). Hypophagic effects of propionate relative to acetate decrease as DIM increase and plasma NEFA concentration decreases.

Key Words: propionic acid, feeding behavior, dry matter intake

1056 Effects of genetic improvements on efficiency of energy utilization in dairy cows. A. B. Strathe*[1], J. Dijkstra[2], J. France[3], and E. Kebreab[1], [1]*University of California*, *Davis*, [2]*Wageningen University*, *Wageningen, the Netherlands*, [3]*University of Guelph*, *Guelph, Ontario, Canada*.

In the last 3 decades, much progress in genetic improvements in milk production has taken place and numerous studies have been conducted on energy metabolism in dairy cows. This study investigated the effects of these improvements on key parameters of ME systems. These are net energy for maintenance (NE_M), efficiency of utilization of ME for milk production (k_l), growth (k_g) and efficiency of utilization of body stores for milk production (k_t). A large data set was collated by Kebreab et al. (2003) [J. Dairy Sci. 86:2904–2913] and further updated with data from the Netherlands. The data set contained a total of 701 individual cow observations from 38 calorimetry studies on Holstein-Friesian dairy cows. All energy related variables were selected for the study. Kebreab et al. (2003) estimated the 4 key parameters by deriving a function based on a linear relationship between milk energy and ME intake and correcting for tissue energy loss or gain. The function served as the basis of a full Bayesian hierarchical model where the between study variability in the 4 parameters was modeled by a multivariate normal distribution and the within study variability by a student t-distribution. The time trend was included as categorical variable with 3 levels differentiating the cows in experiments conducted before 1990, 1990–1995 and after 1995. In the analysis, an informative prior was introduced for the population parameter (NE_M ~N(0.45, 0.04)). The deviance information criterion (DIC) was used to compare models with varying complexity. There was a difference of 5 DIC units between the 2 models, favoring the simple model. Based on the data and an informative prior, the posterior distribution of NE_M, ME_M, k_l, k_g and k_t were estimated to be 0.34 (0.028) MJ/($kg^{0.75}$ BW d), 0.58 (0.034) MJ/($kg^{0.75}$ BW d), 0.58 (0.021), 0.89 (0.056), and 0.69 (0.047), respectively. The analysis does not support the hypothesis that genetic improvements in milk production from 1986 to 2007 have significantly altered key parameters. However, the ME_M value was higher than NRC recommendations (based on older data) and may reflect higher requirements in modern cattle.

Key Words: energy metabolism, lactation, meta-analysis

1057 Carbon dioxide, a greenhouse gas, is sequestered by dairy cattle. D. P. Casper*[1] and D. R. Mertens[2], [1]*Agri-King, Inc.*, *Fulton, IL,* [2]*USDA-ARS Dairy Forage Research Center*, *Madison, WI.*

The impact of dairy cattle on the environment is receiving considerable attention. Carbon dioxide (CO_2) is a greenhouse gas (GHG), which contributes to global warming in theory. When conducting whole body respiration calorimetry trials, CO_2 is measured to calculate the heat production of dairy cows. The objective of this study was to estimate the release of carbon (C) as CO_2 by dairy cattle when fed a wide range of diets. Data from 1,252 individual metabolism trials in the compiled Energy Metabolism Database by lactating dairy cows of different breeds and stages of lactation with milk >5 kg/d were used in the data analysis. Cows were fed diets that varied in forage types, grain sources, protein sources, and fat supplements. During the energy and nitrogen balance

trials, a 24 h composite of respired air was collected for 3 consecutive days and analyzed for CO_2, methane, and O_2 (adjusted to standard temperature and pressure). Data were analyzed using the means and linear regression procedures of SAS. Dry matter intake ranged from 3.9 to 29.4 kg/d with an average of 16.3 kg/d, while milk production ranged from 5.1 to 56.6 kg/d with an average of 23.0 kg/d. Carbon released as CO_2 ranged from 0.96 to 4.65 kg/d with an average of 2.82 kg/d. When related to milk yield only, the amount of CO_2 C kg released per kg of milk decreased curvilinearly with increasing milk yield: CO_2 g C/d = 0.369-.015*milk, (kg/d) + 0.00021*milk^2 (kg/d), R^2 = 0.76, SER = 0.03, $P < 0.01$. At a given level of milk production, improving feed efficiency by decreasing DMI will decrease the release of C as CO_2: CO_2 g C/d = 821.3 + 126.0*DMI, (kg/d) −1.18*milk, (kg/d), R^2 = 0.86, SER = 217.7, $P < 0.01$, while at a given DMI, improving milk yield will decrease the release of C as CO_2 by sequestering more C in the milk. The release of C as CO_2 by lactating dairy cows is dependent on the nutrient intake and the efficiency of conversion to milk. Dairy cows can sequester carbon in milk and reduce the effect of their CO_2 emissions on global warming.

Key Words: carbon dioxide, carbon sequestration, feed efficiency

1058 The variation in milk production by lactating dairy cows in a whole herd compared to groups within that herd. D. P. Casper*, K. E. Lanka, D. F. Jones, G. P. Gengelbach, D. H. Kleinschmit, and D. J. Schauff, *Agri-King, Inc.*, *Fulton, IL.*

The variation in milk production needs to be accounted for when formulating rations to meet the nutrient requirements of lactating dairy cows. The grouping strategy used on the dairy should allow for the development of rations that can closely match the nutrient requirements of each group. However, little information exists for factoring variation into ration formulation for single or multiple group TMR′s. The purpose of this study was to determine the variation in milk production by lactating dairy cows when expressed as the whole herd versus groups within that herd. Data for milk production and composition during the months of December 2009 and January 2010 were collected from 10 dairy herds based on monthly DHIA test. Cows producing less than 9.1 kg/cow/d were eliminated, which resulted in milk production and composition data from 7,178 cows (2,904 primiparous and 4,274 multiparous) in herds ranging from 59 to 3,533 lactating cows with 1 to 15 groups/herd. Overall, mean milk production was 34.4 kg and ranged from 9.1 to 73.1 kg/cow/d with a SD of 9.75 kg/cow/d and a CV of 28.4%. The difference in the CV and SD between the whole herd and groups within that herd were evaluated using the *t*-test procedure of SAS. The CV of milk production was significantly ($t < 0.01$) lower when cows were grouped compared with the whole herd CV, but this difference was small (3.03%). The SD of milk production was significantly ($t < 0.01$) lower when cows were grouped compared with the whole herd, but the difference was small (1.35 kg/cow/d). This study suggests that dairy farms are not grouping cows based on milk production; but, more likely, cows are being grouped based on reproductive status. Therefore, the variation in milk production within a group is approaching the variation across the entire herd. This variation in milk production has implications on ration formulation to meet the nutrient requirements of high producing dairy cows.

Key Words: milk variation, grouping strategy, lead feeding

1059 Reduced protein responses to sugar feeding may be due to microbial glycogen production. M. B. Hall*, *US Dairy Forage Research Center, USDA-ARS*, *Madison, WI.*

The goal of this in vitro study was to determine the influence of Isotrich spp. protozoa on the conversion of glucose (Glc) to glycogen (Glyc). In a 2 × 2 factorial, treatments were 1) ruminal inoculum mechanically processed to destroy Isotrich spp. (M+, verified microscopically) or not mechanically processed (M-), and 2) measurement of microbial Glyc accumulated by 3 h of fermentation with (L+; protozoa + bacteria) or without (L-; predominantly protozoa) lysis of the fermentation solids with 0.2 N NaOH for 15 min in a boiling water bath before Glyc analysis. Two 3 h in vitro fermentations were performed using Goering–Van Soest medium in batch culture vessels supplemented with 3 g Glc L^{-1}. Rumen inocula from 2 cannulated cows filtered through 4 layers of cheesecloth were combined, and maintained under CO_2 for all procedures. Fermentation vessel contents were transferred to centrifuge tubes using 0.9% NaCl, centrifuged twice at 13,000 × *g* for 45 min at 5°C, with pellet resuspended in 0.9% NaCl after the first centrifugation and supernatant decanted each time. Pellets were analyzed for Glyc using a Na acetate buffer, heat-stable α-amylase and measurement of released Glc. Values for samples at 3 h of fermentation were corrected for 0 h values representing α-glucan introduced with inocula. Microbial Glyc detected at 3 h of fermentation were 3.32 (4.69%), −1.42 (−2.01%), 6.45 (9.10%), and 3.65 (5.15%) mg (% of added Glc) for M-L-, M+L-, M-L+ and M+L+, respectively (SED = 0.50). M+ gave lower Glyc values than M- ($P < 0.01$), and L+ gave greater values than L- ($P < 0.01$); there was an interaction of L and M ($P = 0.02$). M+L- showed net utilization of α-glucan initially in the fermentation with no net Glyc production. Estimated bacterial Glyc was lower for M- (3.12 mg) than M+ (3.65 mg; $P < 0.01$). Although destruction of Glyc-accumulating protozoa decreased detected Glyc by ~40%, sequestration of Glc by bacteria accounted for 4–5% of dosed Glc, with Glyc synthesis also representing an energetic cost. Potential decreases in microbial growth related to Glyc could require changes in protein supplementation to maintain protein supply to the ruminant host.

Key Words: sugars, glycogen, rumen fermentation

1060 Liver transcriptomics in Holstein cows fed lipid supplements during the peripartal period. M. J. Khan*[1], E. Schmitt[1], M. A. Ballou[2], E. J. DePeters[3], S. L. Rodriguez-Zas[1], R. E. Everts[1], H. A. Lewin[1], J. K. Drackley[1], and J. J. Loor[1], [1]*University of Illinois*, *Urbana,* [2]*Texas Tech University*, *Lubbock,* [3]*University of California*, *Davis*.

Our objective was to determine the effects of saturated or marine oil supplementation on peripartal liver transcriptomics and relate these to blood metabolites and liver tissue composition. Treatments (n = 6/diet) were no supplemental lipid (control) or supplemental lipid from either Energy Booster (mainly 16:0 and 18:0) or fish oil. Treatment diets were fed from −21 d until 10 d relative to parturition. The doses of lipid used were 250 g/d prepartum or 1% of the previous day feed intake postpartum. Percutaneous liver biopsies were harvested at −10, 1, and 14 d relative to parturition. A 13,257 bovine oligonucleotide (70-mers) array was used for transcript profiling. Pre and postpartum feed intake, milk production, or body condition score were not affected by lipid supplementation. Blood NEFA ($P = 0.06$) and BHBA ($P < 0.05$) were lower postpartum in cows fed either lipid source but postpartal liver triacylglycerol did not differ in these cows (ca. 4% wet weight) relative to controls (4.5%). Initial ANOVA of data from d 1 postpartum comparing fish oil vs. control revealed 50 differentially expressed genes (DEG, $P < 0.01$) of which 13 were upregulated and 13 were downregulated by fish oil. Among downregulated genes were several metabolic enzymes including stearoyl-CoA desaturase (SCD), fatty acid binding protein 1 (FABP1), acyl-CoA synthase medium-chain 1 (ACSM1), and cAMP-dependent protein kinase type II-β regulatory chain (PRKAR2B).

In addition, genes associated with apoptosis/cellular stress (GADD45B) and cellular response to hypoxia (HIF1A) also were downregulated by fish oil. Preliminary results suggest that peripartal lipid supplementation affected blood metabolites and liver transcript profiles and did not hamper production or feed intake.

Key Words: transition cow, metabolism, gene expression

1061 Cattle differ in ability to adapt to small intestinal digestion of starch. H. A. Bissell[1] and M. B. Hall*[2], [1]*University of Wisconsin, Madison,* [2]*US Dairy Forage Research Center, USDA-ARS, Madison, WI.*

The objective of this study was to evaluate the impact of post-ruminal starch digestion on inflammatory response in dairy cattle. Six cull, nonpregnant, nonlactating, multiparous cannulated Holstein dairy cows (BW 804 ± 101 kg) were fed a high forage diet ad libitum starting 15 d before the infusion period. Cows were infused abomasally 12 h per day for 3 d with approximately 8 L d^{-1} of 0.9% saline solution (CTRL; 2 cows) or a 0.9% saline suspension of 4 kg of corn starch with 4 g xanthan gum (ST; 4 cows) using peristaltic pumps. Fecal samples, blood samples, and other measures were taken every 4 h (offset daily by 1 h). Data were analyzed as repeated measures with cow within treatment as a random variable. Fecal pH data showed 2 distinct responses to ST (ST1 and ST2). Fecal pH of all cows averaged 6.90 before infusion. During infusion days, fecal pH remained at 7.0 ± 0.25 for CTRL, but declined in ST cows to 5.1 (ST1) and 4.9 (ST2) by the end of d 2, and diverged to 5.3 (ST1) and 4.6 (ST2) by the end of d 3. The increase in fecal pH for ST1 cows during d 3 suggests an increase in small intestinal digestion of starch, whereas a continuing decline in fecal pH for ST2 cows suggests that they did not adapt similarly. Fecal pH differed among CTRL, ST1, and ST2 ($P < 0.01$). Blood values for haptoglobin decreased for CTRL and ST1 with day of infusion, but increased for ST2 with d 3 values of 12.3, 7.8, and 24.5 mg dL^{-1}, respectively ($P = 0.04$). Fibrinogen mg dL^{-1} tended to differ by treatment x infusion day, rising from 109 to 198, 143 to 188, and 221 to 250 between d 1 and 3 of infusion for CTRL, ST1, and ST2, respectively ($P = 0.11$). Neither ceruloplasmin ($P = 0.38$) nor α-acid glycoprotein ($P = 0.46$) differed by treatment. Hematocrit tended to be greater for CTRL than ST (32.9 v 29.1%; $P = 0.08$). Rectal temperature showed treatment x day effects with increases from d 1 to 3 of 38.5 to 38.7, 38.4 to 39.0, and 38.9 to 39.1°C for CTRL, ST1, and ST2, respectively ($P < 0.01$); CTRL tended to be less than ST ($P = 0.09$). Respiration rates did not differ ($P = 0.46$). The basis for differing cow responses to post-ruminal starch load requires further evaluation.

Key Words: starch, digestion, dairy cattle

1062 Physiological effects of season and parity on production and nutritional quality of milk in camel (*Camelus dromedarius*) under pastoral environment of Pakistan. S. Ahmad*[1], M. Yaqoob[1], M. Q. Biilal[1], G. Muhammad[1,2], M. Younas[1], and J. I. Sultan[1,3], [1]*University of Agriculture, Faisalabad-Pakistan*, *Department of Livestock Management*, [2]*University of Agriculture, Faisalabad-Pakistan*, *Department of Clinical And Medicine*, [3]*University of Agriculture, Faisalabad-Pakistan*, *Institute of Animal Nutrition And Feed Technology*.

Relatively little is known about the actual situation of milk production and quality in the Thal area of Pakistan, particularly when regarding seasonal variation in milk composition and with different parities. Therefore, this study was planned to evaluate the effect of season and parity on milk production and compositional quality of camels kept under pastoral environment of Pakistan. Based on purposive sampling method, 200 she-camels were selected in thal area (District Jhang) and their composite milk samples were collected. The research was carried out in 2 periods. The first period was the summer period covering May–June–July months and the second one was the winter period covering December–January–February months. The collected milk samples were analyzed through standard procedures to determine the percentages of milk fat, protein, lactose, acidity and solids not fat (SNF). Mean daily milk production and mean percentages of fat, protein, lactose, acidity and SNF were found to be 5.50 ± 0.18L and 3.40 ± 0.19%, 3.30 ± 0.11%, 4.67 ± 0.13%, 0.20 ± 0.01% and 9.56 ± 0.18%, respectively. Season of the year and parity imparted significant effect ($P < 0.05$) on daily milk production. The values for milk production (6.20 ± 0.20L), fat (3.98 ± 0.23%), protein (3.43 ± 0.16%), lactose (4.92 ± 0.21%) and SNF (9.14 ± 0.39%) were significantly higher ($P < 0.05$) during winter season compared with summer. In 3rd parity, significantly highest ($P < 0.05$) daily milk production (6.59 ± 0.30 L) and percentages of fat (4.00 ± 0.27%), protein (4.61 ± 0.41%), lactose (5.50 ± 0.36%) and SNF (11.33 ± 0.39%) was observed whereas she-camels in 6th parity produced significantly lower ($P < 0.01$) milk volume (2.90 ± 0.56 L) and percentages of fat (2.70 ± 0.30%), protein (1.69 ± 0.68%), lactose (3.79 ± 0.39%) and SNF (8.02 ± 0.48%). However, acidity of camel's milk was not influenced by season and parity. Efficient feeding strategies during scarcity periods and culling after 5th parity are imperative measures for getting maximum milk of high nutritive value from this novel animal.

Key Words: season, parity, Pakistan

Swine Species Symposium: Optimizing Swine Production for Lactating Sows and Young Pigs

1063 Nutritional management of sows during the perinatal period. S. W. Kim*, A. Saraiva, and Y. Zhao, *North Carolina State University*, *Raleigh*.

With improved genetic potentials, sows produce a larger number of fetuses than before and these fetuses possess genetic potentials to grow faster than before. Recent comparison shows that a porcine fetus is 40% heavier than 40 years ago. Thus the nutritional management of sows has been updated to reflect these genetic changes. Our recent study quantified nutritional needs for sows to support the growth of fetuses and mammary glands during gestation. Amino acid needs for fetal growth and mammary growth during late gestation (d 70 to farrowing) increased 19-folds and 24 folds, respectively, compared with those needs during early gestation (until d 70). Considering these increases, daily requirement of true ileal digestible Lys for a primiparous sows increases from 7 g (until d 70) to 15 g (d 70 to farrowing). Required qualities of proteins (i.e., amino acid ratios) also change with an advance of pregnancy as maternal, fetal, and mammary tissues have their unique amino acid compositions. Thus, sows can be under a severe catabolic status during late gestation if the feed does not provide sufficient amounts and qualities of proteins especially during late gestation. Under a several catabolic status, sows can have a limited nutrient supply for the growth of fetuses. Sows under a conventional feeding program had increased litter weight variations at farrowing (19%) compared with early gestation (3.0%). Our recent study also shows that sows under a conventional feeding program have a dramatic increase in a systemic oxidative stress during late gestation compared with early gestation when measured by plasma Î ± -tocopherol (56% decrease), plasma retinol (57% decrease), and DNA damage in white blood cells (125% increase) which were sustained until the early lactation period. Increased oxidative damages in sows negatively affect the growth and health of fetuses. We proposed that sow feeding during late gestation should reflect the changed needs for amino acids and antioxidants because a proper feeding during late gestation will eventually help producing uniform and healthy piglets.

Key Words: amino acids, oxidative stress, sows

1064 Proper nutrition to optimize performance for lactating sows and young pigs. V. J. Pearson*, *Land O'Lakes Purina Feed LLC*, *Shoreview, MN*.

Feeding the sow for maximum reproduction involves recognizing that the nutrient requirements are different during different stages of the sow's reproductive life. Lactation, though only 2 to 6 weeks, is a critical stage of this sow's reproductive life. Feed intake at this stage is affected by genotype, lactation length, parity distribution, mycotoxins, environmental temperature, formulation of lactation feed, water availability and disease levels. The key point to optimize a sow's performance is proper feed management during lactation. The objective of the feeding program for lactating sows is to ensure that the sow consumes sufficient feed on a daily basis to meet her nutrient requirements such as protein, amino acids, energy, trace minerals, vitamins and major minerals. The nutrient requirements needed by the sow depend on her weight, milk yield and composition along with the environment she is in especially temperature. Since most of the information we need to make the proper calculations to feed the sow are not known the sow is fed to appetite. The appetite of a lactating sow is lower the first week and increases by 3 weeks. So optimizing feed intake of the sow is extremely important. Sows should have access to high quality water at all times; temperature should be kept at 19–22°C. Water flow rate of 0.7 to 1 L per minute should be adequate. Sow data has demonstrated that approximately 20% of sows show a feed decrease for 2 to 3 d at the beginning of the second week. This caused a longer weaning-to-estrus interval, reduced farrowing rates and resulted in smaller subsequent litter size. Data has indicated even one day of the sow's consumption dropping below 1.8 kg will increase the chances of her being removed from the herd by 50%. Thus the sow should never be purposely deprived of feed. A feed allowance of 1.0% of the sows body weight plus 0.57 kg for each pig in the litter is a good guide to the minimum levels lactating sows should be daily fed.

Key Words: swine, lactation, nutrition

1065 Gene x environment interactions affecting litter phenotype in commercial sows. G. R. Foxcroft*, *University of Alberta*, *Edmonton, Alberta, Canada*.

Variation in litter growth performance after birth may be pre-programmed during embryonic and fetal development, yet may only express itself in the late grow-finish stages of production. Two particular hypotheses will be explored in the context of efficient pork production from contemporary sow populations: 1) Selection for increased litter size has resulted in indirect negative effects of intrauterine crowding on placental development in early pregnancy, leading to reprogramming of fetal development, less efficient post-natal growth performance, and adverse effects on carcass quality at slaughter. 2) Sow metabolic state at breeding can also affect the quality of litters born, acting through epigenetic mechanisms to affect early embryonic development. Effects of prenatal programming on postnatal health and survivability are also important, and are mediated through developmental limitations in immune, metabolic and gastrointestinal function in the early postnatal period. Negative pre-natal programming effects on post-natal performance are consistently seen in hyper-prolific sows that produce total numbers of pigs born that exceed uterine capacity for optimal birth weight. However, available evidence indicates that differences among litters is the major source of variance in pig birth weight in mature sow populations producing between 10 and 15 pigs per litter, with apparent repeatability of a low birth weight phenotype in this sow population. These developmental complications underlie the problems of managing low birth weight pigs through lactation and the nursery stage of production. Production strategies that might address variation in litter average birth weight and post-natal performance of litters include: 1) segregated management of litters based on birth weight phenotype, and 2) nutritional strategies in gestation and lactation and interventions in the farrowing house targeted at low birth weight phenotypes.

Key Words: sow, litter, phenotype

1066 Decision-making using swine records. J. Deen* and S. S. Anil, *University of Minnesota*, *St Paul*.

For sow herds, the objective function of decisions has historically been a simple maximization problem. Sow farms have been viewed as a mostly fixed cost enterprise with marginal production being viewed as having a very high profit margin. This was due to the fact that piglets were considered generic commodities after transfer from the sow herd. Though we see remnants of this attitude in record-keeping systems and pricing methodologies, we are seeing a greater emphasis on individual animal qualities. The major decisions at the individual pig level of

retention, treatment or euthanasia have focused in greater detail on its varied repercussions. For instance, culling a sow not only affects that sow, it also affects the quality of progeny and the utilization of building capacity; the treatment of a pig may not only have an effect on itself but also on surrounding pigs, especially when infectious pathogen transfer is a concern.

Record-keeping has not kept up with these potential considerations. Assumptions of normality and the independence of effects on outcomes need to be re-examined. Both atomistic and ecologic effects of decisions need to be considered. To measure these effects, individual animal characteristics and complementary observational analytic methods need to be utilized. Such measurement regimens and analytic processes are laborious and often complex and rely on proper sampling and disciplined approaches. However, when we do such analyses we are finding that the assumptions of normality and equality of effects across the distribution are often erroneous. In fact, most insults and interventions affect subpopulations that can be best described as compromised individuals. For instance, the likelihood of being weaned alive and greater than 5 kilograms in weight can range from 8% for the lightest 10th percentile at birth to 96% for the heaviest 10th percentile. Such ranges and responses suggest that individualized records and care are needed to optimize rearing conditions and decision-making.

Key Words: reproduction, records, swine

Teaching/Undergraduate and Graduate Education: Graduate and Undergraduate Teaching 2

1067 Engaging agriculture students in the publication process through popular press magazines. E. L. Walker*, *Missouri State University*, *Springfield*.

Traditional lecture based courses may not be the most effective in incorporating all the concepts of higher order thinking. Therefore, an alternative teaching method was created and incorporated into an upper division animal science feeds and feeding class which challenges students to obtain peer reviewed data and present it in a "popular press" type format. The objectives of this assignment were to: 1) incorporate Blooms Taxonomy into the teaching method of class and 2) to assist undergraduate students in their understanding of core concepts discussed in class and, 3) apply a basic understanding of animal based research into a production based setting. There are 3 phases of this assignment: 1) assignment of pods based upon student interest, 2) edit and selection of papers, 3) publication of paper. Students are placed into pods designated by the instructor based upon the students' general research interest. Within the pod, students are required to discuss their research interests and formally edit one another's papers. After completion of the editing process, the most well written paper is selected from within each pod. Each of these papers is then sent electronically to every student in the class for a second formal editing process. After each student reads and formally edits the top pod papers, the class must vote on a single paper they feel has the best chance to get published in a popular press journal. In each of the 3 phases, students are graded by the instructor. Extra points are given to the author of the winning pod paper, then to the pod that produces the paper voted by the class as the best overall paper, and then is given to the entire class if the paper is accepted for publication. If of superior quality, the second place paper is also submitted for publication for no class credit. This project has been conducted for 3 years and 5 papers authored and edited by students have been published in popular press journals across 3 states. Popular press magazines can be a critical link between the scientific, university, and agriculture communities.

Key Words: writing skills, Bloom's Taxonomy, popular press

1068 Teaching and experiencing entrepreneurialism in animal sciences. M. E. Benson*[1], A. B. Culham[2], and G. M. Hill[2], [1]*Washington State University*, *Pullman,* [2]*Michigan State University*, *East Lansing*.

A USDA Challenge Grant provided the opportunity for students in animal sciences to develop their entrepreneurial skills. In this project, students integrated information from technical disciplines with skills necessary for successful business development in an entrepreneurial arena. Three objectives were to: 1) design and implement a curriculum in which students learned techniques and procedures applicable to discovery and evaluation of marketing options and new product launches for animal agricultural enterprises; 2) develop a working laboratory where implementation of learned practices are applied to actual marketing of a product(s); and 3) communicate the results of this project to other students, industry professionals and other educators. The project was initiated at Michigan State University (MSU) where the students brainstormed ideas and completed development of business plans for their proposed ventures. Input from industry professionals on topics such as marketing strategies and risk assessment for niche markets further assisted the students in the development of their business plans. The course has also been added at Washington State University (WSU) and working laboratories have been established at both sites. At MSU, students added value to wool produced from the MSU flocks by creating Spartan blankets that were marketed through a variety of channels. Revenues generated are sufficient to make this a self-sustaining venture and currently new products are being evaluated. Resources from product sales have also supported student research and travel activities. At WSU, students are developing their own ideas and business plans as well as participating as a group in the process of creating, producing, and marketing woolen blankets. At both sites, this project has met with enthusiastic responses from students, livestock industry stakeholders and alumni. It has brought visibility to the department while offering students the opportunity to consider business opportunities and challenges that extend beyond traditional animal agricultural enterprises.

Key Words: entrepreneurialism, business skills

1069 The role of animals in societies of the world: When culture and roles clash. M. Russell*[1], H. Frigola[1], K. Kanne[2], and S. Damron[3], [1]*Purdue University*, *West Lafayette, IN,* [2]*Northwestern University*, *Evanston, IL,* [3]*Oklahoma State University*, *Stillwater*.

This course serves as a university-level freshmen honors course and is an introduction of the importance of animals in various cultures and societies of the world. Factors which influence the role of animals in society including physical and biological adaptations of animals and the role of traditions, culture, religions, language, politics, geography, climatic, and socio-economics are discussed. Learning objectives are to: broaden students′ understanding of the roles animals play in cultures around the world; critically analyze ethical and moral debates of animal use in society; and prepare students to interact with people who use animals in ways different from themselves. This course is co-taught with faculty in animal sciences and anthropology. Guest presenters include foreign graduate students and visiting faculty as well as Purdue faculty who share their experiences and specialty areas of expertise. Topics are presented with some lecture and facilitated discussion and many videos/DVDs as examples from many international cultures as well as the USA culture itself. Students develop writing assignments and lead class discussions in two major topics: A Use & Society topic which discusses how culture, geography, climatic, and socio-economics as well as the animals′ morphology/physiology affect the use of animals. The Current Issue assignment applies topics discussed in class to a specific issue or concern regarding a current controversy or animal topic use. This topic critically analyses ethical and moral dilemmas related to this chosen current issue as it affects animals, people, and the environment. We will share pedagogy and learning assessment methods in this innovative approach to assist under-classmen in understanding why certain species and breeds are best suited for our US industries and the other factors that determine the appropriate use of animals in our changing societies. This is important to broadening the world view of our students and help them to be more successful in dealing with professional and public policy dilemmas in the future.

Key Words: animal roles, cultural conflict

1070 Enhanced learning of lactation physiology by undergraduates conducting a class-based research project. R. L. Wrenn*, S. J. P. Lee, and R. C. Hovey, *University of California, Davis*.

The integration of materials from experiential research presents unique opportunities to enhance classroom learning by undergraduates in the animal sciences. The objective of an ongoing project at UC Davis is to

use a student/class-run project to teach junior and senior students the physiological basis of lactation and the fundamentals of dairy animal management. Animal science undergraduates (up to 165 students) enrolled in a required lactation course (ANS 124) were given the task of coordinating and conducting a class-based, quarter-long (10-wk) research project involving hormone-induced lactation. Nulligravid Holstein heifers (n = 8) were administered daily injections (sc.) of estradiol-17β (0.075 mg/kg) and progesterone (0.25 mg/kg) for 7 d, followed by a single dose of dexamethasone (15 mg) on d18 of the protocol. Students were responsible for all aspects of the project under the guidance of the faculty mentor. Each student performed morning and evening chores (at least one at each time per student) including hormone injections, blood sampling, weighing, data collection, milking, and basic husbandry practices. Mammary gland growth was monitored through daily udder measurements, including distance between the teats and individual teat length, and from photographs. Students analyzed blood samples for changes in the level of α-lactalbumin by ELISA to establish the onset of lactogenesis. Milking began on d 20 and continued for approximately 30 d. Changes in milk compostion were determined by SDS-PAGE. The project afforded numerous opportunities within the classroom for discussions about the physiological changes associated with mammary growth, anatomy, endocrinology, lactogenesis, and galactopoiesis. At the end of the study each student composed a redrafted research paper, with individual students preparing scientific abstracts for additional public audiences. In conclusion, a student-run project involving induced lactation provides an excellent opportunity for undergraduates to gain hands-on research and dairy management experience that also enhances classroom learning.

Key Words: lactation, experiential learning, induced lactation

1071 Frameworks for learning: a case study of approaches for building capacity for distance education. D. R. Mulvaney*[1,2], P. A. Curtis[3], and M. O. Kloepper[3,4], [1]*Coll. of Agr., Auburn Univ.*, *Auburn, AL,* [2]*Dept. Anim. Sci., Auburn Univ.*, *Auburn, AL,* [3]*Dept. Poult. Sci., Auburn Univ.*, *Auburn, AL,* [4]*IT Specialist, Auburn Univ.*, *Auburn, AL*.

Developing digital capacity among faculty is a necessary prerequisite to emerging distance education programs. Trends in higher education clearly substantiate future students learners are considered digital natives and many faculty are considered immigrants in a digital world. Informal approaches for faculty development have been initiated across the college of agriculture with goals of creating cultures enabling faculty to adapt to new technologies having relevance to teaching. Our objectives will be to share some of our experiences, both successes and failures, at creating opportunities for faculty to develop comfort and skill in using digital technologies with relevance to teaching and learning. Approaches designed with features of faculty learning communities have included creation of an Agricultural Instructional Media Academy, frameworks for learning seminars, Go-The-Distance Pit-Stop discussion sessions, Blackboard initiatives, technology simulations, hands-on workshops, one-on-one facilitation / mentoring and creation of a satellite technology units on the ag campus. Concurrent to these efforts have been changes in centralization of distance learning administration, policy, adoption of AG-IDEA initiatives, IT support and available technologies, and pockets of interest and energy, all which are collectively shaping change in the culture and capacity for distance education. In summary, rate of technological change seemingly out-paces the development of digital capacity of faculty and programs yet one-at-a-time change has had impact.

Key Words: distance education, digital learning, faculty development

1072 Trends in distance education and technologies in higher education: A call for adaptive leadership. D. R. Mulvaney*[1,2], P. A. Curtis[3], and M. O. Kloepper[3,4], [1]*Coll. Agr., Auburn Univ.*, *Auburn, AL,* [2]*Dept. Anim. Sci.*, *Auburn, AL,* [3]*Dept. Poult. Sci.*, *Auburn, AL,* [4]*IT Specialist*, *Auburn, AL*.

The emerging educational landscape is characterized by change. Distance education stands to be a key transformative factor for undergraduate education in agriculture. An adaptive challenge for educators and institutions is how to anticipate and prepare for a future they have not fully experienced. The objectives of this presentation are to provide a concise overview of the trends in higher education with an emphasis on distance education and reinforce challenges surfaced from the 2006 National Academy of Science Leadership Summit to Effect Change in Teaching and Learning. Robust availability of technologies conducive to just in time, mobile learning models, generational shifts characterized by learners from a digital culture, campus cultures and policies to accommodate distance consortia and alliances such as AG-IDEA, development of digital immigrant faculty plus challenges of dealing with new vistas for practicing scholarship are but a few components of the evolving future for higher education. Technologies around data visualization, information retrieval, creation of knowledge objects, gesture prompted technologies, gaming simulation and virtual reality software will allow for reinvention of teaching and learning environments. Because the challenges and trends around the emerging technologies will have significant impact on the teaching, there is a call for new pedagogical models and adaptive leadership among faculty and administrators.
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Key Words: distance education, trends in education, animal sciences

SYMPOSIA AND ORAL PRESENTATIONS

Animal Health: Probiotics, Performance and Antioxidants

1073 Thiamine status of feedlot cattle fed high concentrate diet. T. Karapinar*, M. Dabak, and O. Kizil, *University of Firat, Faculty of Veterinary Medicine*, *Elazig, Turkey*.

Thiamine deficiency causes a decrease in transketolase activity and an increase in thiamine pyrophosphate (TPP) effect on the erythrocytes. The objective of this experiment was to determine if ruminal acidosis alters erythrocytic transketolase enzyme activity as an indicator of thiamine level in feedlot cattle. A total of 65 feedlot cattle (1–2 years old) were fed either high concentrate diet (HCD, n = 50) or low concentrate diet (LCD, n = 15). The HCD group was fed a mixture of 75% cracked barley, 8% bran, 7% cotton seed meal and 10% straw for at least the last 3 mo, whereas the LCD group was fed a mixture of 30% cracked barley, 10% bran, 10% sugar beet pulp, 10% cotton seed meal and 40% straw. Rumen fluid samples of all cattle were obtained by rumenocentesis to determine ruminal pH. After ruminal samples were obtained, blood samples were collected from a jugular vein for erythrocytic transketolase enzyme activity using the Clausen's colorimetric method. Mean pH values of ruminal fluid samples in the HCD and LCD groups were 5.3 and 6.1, respectively. The mean TPP effect % in the HCD group (47.16 ± 3.17) was significantly higher than in the LCD group (19.53 ± 2.51) ($P < 0.01$). Ruminants with functional rumen are considered to have no specific dietary thiamine requirement due to extensive thiamine synthesis by rumen microbes. Thiamine deficiency in both chronic ruminal acidosis and acute ruminal lactic acidosis may occur because of inadequate synthesis of thiamine, bacterial production of thiaminase in the acidotic ruminal fluid. Furthermore, a decrease in ruminal pH may result in the release of bacterial thiaminases. The present study demonstrated that thiamine deficiency could occur in ruminants fed under intensive fattening regimens.

Key Words: polioencephalomalacia, transketolase, vitamin B1

1074 The effect of five herbal extracts on performance, carcass characteristics and immune system in broilers. M. Alempour[1], S. Rahimi*[1], M. A. Karimi Torshizi[1], and A. Rahimi[2], [1]*Tarbiat Modares University*, *Tehran, Iran*, [2]*Islamic Azad University*, *Tehran, Iran*.

The purpose of this study was to evaluate the effect of 5 herbal extracts and Virginiamycin antibiotic on growth performance, carcass characteristics and immune system in broilers. A total of 720 1-d-old broiler chicks (ROSS 308) were assigned to 9 treatments with 4 replicates of 20 birds per pen as follows: the basal diet, and basal diet supplemented with 15 ppm Virginiamycin, 1% aqueous extract of garden thyme (*Thymus vulgaris*), garlic (*Allium sativum*), thyme (*Thymus kotschyanus*), sage (*Salvia officinalis*), peppermint (*Mentha piperita*), a blend of garden thyme and peppermint and blend of thyme and sage. Performance and feed conversion were calculated at 14, 28 and 42 d of age. At end of the experiment 2 birds from each replicate (8 birds per treatment) were randomly selected to evaluate the carcass characteristics, relative weight of lymphoid organs and fat pad. Greatest and least body weight were belonged to virginiamycin and sage, ($P < 0.05$) respectively. Lowest and highest feed conversion ratio were related to virginiamycin and control groups ($P < 0.05$) respectively. There was no difference in carcass characteristics, fat pad and digestive organs weight. Relative weights of lymphoid organs (spleen and bursa of Fabricius) as 2 immune indices were unaffected by the treatments. According to results of this experiment, the herbal extracts did not show significant difference in performance and lymphoid organs weight in broilers.

Key Words: herbal extract, performance, immune system

1075 Comparison the effect of five herbal extracts and virginiamycin on serum lipids and immune system in broilers. M. Alempour[1], S. Rahimi[1], M. A. Karimi Torshizi[1], and A. Rahimi*[2], [1]*Tarbiat Modares University*, *Tehran, Tehran, Iran*, [2]*Islamic Azad University*, *Tehran, Tehran, Iran*.

The objective of this study was to investigate the effect of 5 herbal extracts and virginiamycin on blood metabolites in broilers. A total of 720 1-d-old (Ross 308) male broiler chicks were assigned to 9 treatments with 4 replicates of 20 birds per pen as follows: the basal diet (control) and basal diet supplemented with 15 ppm virginiamycin, 1% aqueous extract of garden thyme (*Thymus vulgaris*), garlic (*Allivum sativum*), common thyme (*Thymus kotschyanus*), common sage (*Salvia officinalis*), peppermint (*Mentha piperita*), a blend of garden thyme and peppermint and blend of common thyme and common sage with the same dose in drinking water as a completely randomized design.. At the end of the experiment 2 birds from each replicate were randomly selected to measure total cholesterol (TC), LDL cholesterol, triglycerides (TG) and HDL cholesterol levels. Garlic (*Allivum sativum*) significantly reduced the levels of TC, LDL, TG (97.89, 21.49 and 37.45 mg/dl respectively) and significantly increased the level of HDL (68.91 mg/dl) ($P < 0.05$). According to results of this experiment the herbal extracts could have beneficial effect on blood lipids in comparison with the control and antibiotic fed birds. Garlic was the most effective treatment in this trial.

Key Words: broiler, blood factors, herbal extract

1076 Characterization of a yeast autolysate in vitro and effect on piglet performance in vivo. A. Ganner*[1], S. Masching[2], M. Pelz[1], and G. Schatzmayr[1], [1]*Biomin Research Center*, *Tulln, Austria*, [2]*Biomin Holding GmbH*, *Herzogenburg, Austria*.

Dietary yeast derivatives have been proposed to improve piglet health by preventing infectious diseases, by modulating the immune system and by controlling pathogenic bacteria such as *E.coli* and *Salmonella*. Aim of the study was an in vitro characterization of a yeast autolysate and its effect on piglet performance. As an in vitro model the murine macrophage cell line J774A.1 was used. Cells were incubated for 48 hours with LPS of *E. coli* 0127:B8 and the autolysate. TNF-alpha, IL-12, TGF-beta and IL-10 were determined in the supernatant of the cultures with ELISA. Additionally the autolysate was examined for its capacity to bind *E. coli* F4 with a quantitative microplate-based assay by measuring the optical density as growth parameter of adhering bacteria. Subsequently, a feeding trial was conducted to evaluate the efficacy of the autolysate on performance

of weaning piglets in a 56 days study. 40 piglets were divided into 2 groups with 2 replicates: control group A, group B (0.1%). Statistical analyses were performed with t-test, SPSS 18. TGF-beta was enhanced up to 100% in comparison to the control (LPS of *E. coli*); no induction of IL-10. IL-12 was inhibited 60 to 80%; no effect on TNF-alpha could be observed. In the microbiological assay *E. coli* F4 adhered with 10^6 CFU/mg to the autolysate. In the course of the feeding trial a positive influence could be observed by the autolysate. Weight on day 56 (43.13 kg) and daily weight gain (dwg 604g) were improved in comparison to the control (40.92 kg weight day 56, P = 0.048; 505g dwg, $P = 0.025$). Feed consumption was increased ($P \geq 0.05$), FCR (kg/kg) of the trial group was 1.74, of the control 1.71 ($P \geq 0.05$). Pathogen binding and modulation of the immune system, as shown in vitro, might have been reasons for the increase in performance of piglets in the feeding trial. In vitro and in *vivo* results indicate that this particular yeast autolysate is a health and performance improving agent.

Key Words: yeast autolysate, cytokines, piglet performance

1077 Effect of several feed additives on growth performance and microbial load in Escherichia coli challenged broilers. A. R. Valipouri[1], S. Rahimi*[1], T. Zahraei Salehi[2], and A. Rahimi[3], [1]*Tarbiat Modares University*, *Tehran, Iran*, [2]*University of Tehran*, *Tehran, Iran*, [3]*Islamic Azad University*, *Tehran, Iran*.

The objective of this study was to compare the effects of different feed additives on performance and microbial load in *E. coli* challenged broiler chickens. A total of 528 d-old Ross 308 male broilers were used to study the effect of antibiotic, probiotic, prebiotic and organic acid on performance, cecal coliform load, immune system and internal organs weight. The birds were placed into 6 groups with 4 replicates and 22 birds per pen. Six dietary treatments include: 1) negative control as basal diet without any antibiotic growth promoter and coccidiostat (Ctl-); 2) Diet 1+ 0.9 g/kg of feed Primalac (Prim); 3) Diet 1+0.1 g/kg of feed Bactocell (Bact); 4) Diet 1+15ppm virginiamycin (VM); 5) Diet 1+2 g/kg of feed Fermacto (Ferm); and 6) Diet 1+2 g/kg of feed Formycin (OA). At d 7 all birds were orally gavaged with a 0.5 mL of 10^7 CFU of mixed culture of pathogenic *E. coli* (O2K12 and O78K80) verified for presence of genes including stx1, stx2, eaeA and hlyA. Eight birds from each group were killed for detection of challenged bacteria in liver, spleen and cecum content at d 14, 28 and 42. Overall weight gain ($P < 0.01$) and feed conversion ($P < 0.05$) were significantly improved in VM (2460.00 and 1.64) and Prim (2337.25 and 1.70) groups compared with control group (2280.50 and 1.82). The challenged serotypes were recovered only from Ctl- (46%) and VM (25%) fed groups. Feed supplementation with probiotic, prebiotic or organic acid, significantly decreased coliform population at all intervals in comparison with Ctl- and antibiotic treatments ($P < 0.05$). Feed additives supplementation had no influence on the internal organs weight at all intervals.

Key Words: alternative, antibiotic, *Escherichia coli*

1078 Improvement of microbial flora of broilers digestive system by medicinal plants supplementation. A. Niknam, S. Rahimi*, J. Azimi, K. Seifi, M. Hoseinzade, and M. Moradi Nejad, *Tarbiat Modares University, Tehran, Iran.*

The objective of this study was to compare the effects of dietary administration of medicinal plants, with antibiotics and probiotics on microbial flora of digestive tract in broilers. A total of 210, day old male broiler chicks (Arbor Acres Plus) were randomly allocated into 7 treatments. The treatments were as follow: control; dry peppermint (*Mentha piperita*); thyme (*Thymus vulgaris*); basil (*Ocimum basilicum*) leaves; or garlic (*Allium sativum*) bulb (15kg/ton feed); Virginiamycin (150g/ton feed); and Primalac (1kg/ton feed). At 42 d of experiment 9 birds from each treatment were randomly selected and sacrificed. Samples were collected from crop and ileocecal section of intestine and diluted in phosphate buffer saline (PBS). Then, samples were plated onto Mann Rogosa Sharpe (MRS), MacConkey and Plate-count agar to enumerate lactobacilli, coliforms and total aerobic bacteria, respectively. Crop contents of garlic and peppermint treatments contained the highest and lowest number of lactobacillus bacteria (5.88 vs. 3.68 Log10 cfu/g), respectively ($P < 0.05$). There was no significant difference in number of coliforms in crop. The maximum and minimum number of total aerobic bacteria observed for control and basil treatments (5.69 vs. 3.93 Log10 cfu/g), respectively ($P < 0.05$). Supplementation of diet with garlic increased number of lactobacillus bacteria in ileum (8.76 Log10 cfu/g) compared with other treatments ($P < 0.05$). Primalac increased both coliforms and total aerobic bacteria in ileum higher than other treatments ($P < 0.05$), while lowest number of these bacteria belongs to basil and control treatments (9.34 and 8.96 vs. 8.24 and 8.08 Log10 cfu/g), respectively. Microbial changes in crop and ileum of chicken demonstrate that administration of medicinal plants can increase number of lactobacillus and improve bacterial balance in gut.

Key Words: medicinal plants, digestive system, broilers

1079 Peripartal intravaginal probiotics lowered uterine infections and improved reproductive performance of Holstein dairy cows. B. N. Ametaj*[1], Q. Zebeli[1], S. Iqbal[1], M. Gänzle[1], Y. Wang[1], D. J. Ambrose[2], and S. M. Dunn[1], [1]*University of Alberta, Edmonton, Alberta, Canada*, [2]*Alberta Agriculture and Rural Development, Edmonton, Alberta, Canada*.

Uterine infections affect 1 in 2 dairy cows after parturition lowering their reproductive performance and increasing culling rates. The objective was to investigate the prophylactic effect of probiotic bacteria on postpartum metritis and the overall reproductive performance of dairy cows. Eighty pregnant multiparous and primiparous dairy cows 2 wk before the expected day of calving were assigned to one of 2 groups receiving: 1) 1 mL of carrier only (reconstituted skim milk), or 2) 1 mL of probiotic bacteria in reconstituted skim milk at 10^{10} to 10^{12} cfu/treatment. Intravaginal infusions were performed once during wk −2, −1, +1, +2, +3, and +4 relative to parturition with probiotic bacteria isolated from vaginal tracts of healthy cows, *Lactobacillus sakei* FUA 3089, *Pediococcus acidilactici* FUA 3140, and *P. acidilactici* FUA 3138. All cows were observed for reproductive performance and reproductive disease until next pregnancy. Probiotic treatment lowered the incidence of uterine infections in both multiparous (17 vs 48%; $P < 0.01$) and primiparous (16 vs 58%; $P < 0.03$) cows. The interval from calving to conception tended to be shorter (93 vs 145 d; $P < 0.10$) in treated cows, and pregnancy rate at first insemination in multiparous cows tended to be higher ($P < 0.10$). Both multiparous and primiparous cows receiving probiotics had lower incidence of purulent ($P < 0.008$ and $P < 0.02$) and foul-smelling ($P < 0.06$ and $P < 0.05$) discharges on +3 wk. Moreover, multiparous cows had lower rate of uterine horn fluctuations ($P < 0.05$), smaller cervix size on wk +3 ($P < 0.001$) and +5 ($P < 0.06$), and lower uterine horn asymmetry on wk +3 ($P < 0.01$) and +5 ($P < 0.01$). There was a tendency for probiotic treatment to reduce early calving ($P < 0.11$), the number of medications per cow ($P < 0.09$), and the number of cows in the clean-up program ($P < 0.06$). Further research is warranted to understand the beneficial effects of intravaginal probiotics on reproductive performance of dairy cows.

Key Words: dairy cow, probiotics, uterine infections

1080 Changes in ruminal-rectal temperature relationship associated with consumption of endophyte infected tall fescue. B. Scharf*, J. S. Johnson, H. L. Vellios, R. L. Weaber, and D. E. Spiers, *University of Missouri*, *Columbia*.

Little is known about changes in ruminal temperature after consumption of endopyte infected tall fescue. Twenty-four Angus steers (318 ± 8 Kg BW) were housed in the Brody Environmental Center (University of Missouri), and randomly assigned to a diet with either endophyte infected tall fescue seed (E+; 40µg ergovaline/kg/d) or endophyte free seed (E-; 0µg ergovaline/kg/d). Animals were housed for 7d at an ambient temperature (T_a) of 21°C (TN) before heat stress (HS), which consisted of daily cyclic T_a (26°C night: 36°C day) for 7d. A telemetric, temperature transmitter (SmartStock, Pawnee, OK) was placed into the rumen (T_{rum}) of each animal before the study. Rectal temperature (T_{re}) and respiration rate (RR) were measured 6 times daily. At TN, no differences were found in RR, T_{re}, or T_{rum} between E+ and E- animals ($P = 0.11$). T_{rum} - T_{re} difference was also not significant across treatments, with T_{rum} maintained ~1.1°C higher than T_{re}. Both groups increased RR during HS ($P < 0.001$), with E+ steers maintaining the higher rate (89.8 vs 76.7 ± 3.2bpm; $P < 0.01$). Similarly, T_{re} increased for both groups during HS ($P < 0.01$), with E+ animals showing the greatest increase (0.9 vs 0.6 ± 0.1°C; $P < 0.01$). T_{rum} also increased with HS. However, T_{re} showed a much greater rise than T_{rum} (1.0 vs 0.2 ± 0.2°C). T_{rum} - T_{re} difference decreased from TN to HS (1.1 vs 0.6 ± 0.1°C), with large differences between treatments. E+ steers showed a large increase in T_{re} but only a minimal change in T_{rum} during HS for a small T_{rum} - T_{re} difference (0.12 ± 0.1°C). E- animals showed a smaller increase in T_{re} and a similar increase in T_{rum} resulting in a significantly higher T_{rum} - T_{re} value (0.67 ± 0.1°C) than for E+ animals ($P < 0.05$). Consumption of endophyte infected tall fescue seed caused a considerable increase in rectal temperature. Unexpectedly, ruminal temperature showed only a minimal increase which is likely due to a decline in feed intake and an associated reduction in heat production.

Key Words: cattle, heat stress, transmitters

1081 Effect of dietary antioxidants and prepartum cooling on oxidative status and neutrophil function of periparturient Holstein cows during summer in Florida. D. Wang*, J. H. Shin, M. Garcia, J. E. P. Santos, and C. R. Staples, *University of Florida*, *Gainesville*.

The objective of this study was to evaluate the effect of supplementation with 0 or 250 mg of Agrado Plus per kg of dietary DM (Novus International; St. Louis, MO) on oxidative status and neutrophil function of periparturient Holstein cows managed under cooled (C; shade, fans, and sprinklers) or noncooled (NC; shade alone) conditions prepartum. Primiparous (n = 22) and multiparous (n = 13) pregnant Holstein cows were assigned randomly to one of 4 treatments arranged in a 2 × 2 factorial design at 35 d before calculated calving date. Upon calving, all cows were housed in a cooled free-stall barn and remained on assigned diets. Blood was collected at −15, 1, 8, 15, and 29 DIM for oxidative markers. Phagocytosis and oxidative burst of neutrophils were measured in whole blood collected at −15, 0, 7, and 14 DIM. Rectal temperature of cooled cows was lower prepartum (39.2 vs. 39.7C). Mean erythrocyte glutathione peroxidase activity (GPx) corrected for packed cell volume were increased for NC vs. C multiparous cows fed the control diet (8,854 vs. 12,247 nmol/min/mL) but feeding antioxidants reversed this pattern (10,720 vs. 8697 nmol/min/mL); GPx in primiparous cows was not affected by treatments (diet by cooling by parity interaction, $P < 0.05$). Mean plasma concentrations of thiobarbituric acid reactive substances were reduced in NC vs. C cows fed the control diet (1.73 vs. 2.33 nmol/mL) but were unchanged by cooling cows fed antioxidants (1.83 vs. 1.78 nmol/mL). Mean concentrations of superoxide dismutase activity in erythrocytes were not affected by treatments. Cooled cows had fewer lymphocytes (3455 vs. 5411/uL). Mean phagocytosis and mean florescence intensity by neutrophils was increased by cooling multiparous cows (77.5 vs. 72.0% and 37.3 vs. 33.8, respectively) but was decreased by cooling primiparous cows (74.3 vs. 81.0% and 55.4 vs. 68.7, respectively). Cooling prepartum and feeding antioxidants influenced oxidative status and neutrophil function.

Key Words: antioxidant, immunity

1082 Isolation, characterization and antioxidant activity of an exopolysaccharide produced by *Enterobacter cloacae* Z0206. M. L. Jin*[1], Y. M. Wang[1], Z. Q. Lu[1], M. Huang[1], C. L. Xu[2], and Y. Z. Wang[1], [1]*Zhejiang University*, *Hangzhou, China*, [2]*Northwestern Polytechnical University*, *Xi'An, China*.

A water-soluble extracellular polysaccharide (EPS-1) was isolated from the submerged culture broth of *Enterobacter cloacae* Z0206 through fermentation, ethanol precipitation, anion-exchange and gel-permeation chromatography. Its structural characteristics were investigated by chemical analysis, high performance liquid chromatography (HPLC) and Fourier transform infrared (FTIR) spectrophotometer. Bioactivity tests were carried out to investigate the antioxidant activity of EPS-1. 40 ICR (Institute of Cancer Research) male mice (18 ± 2 g) were randomly divided into 4 groups of 10 each. Three immunosuppressed groups were administered with EPS-1 (0, 200 and 400 mg/kg body weight (BW)) by gavage once daily, and cyclophosphamide (CP) was given intraperitoneally at 50 mg/kg BW on the 12th day. Control mice received the same volume of 0.9% normal saline. The experiment lasted for 14 d. Activities of antioxidant enzymes such as glutathione peroxidase (GSH-Px), catalase (CAT) and superoxide dismutase (SOD) in liver were studied. The results indicated that the average molecular weight of EPS-1 was about 23982 Da. It was hypothesized that EPS-1 belongs to the α-type heteropolysaccharide with pyran group, consisting of glucose, mannose and galactose with a molar ratio of 6.860: 1.180: 0.455. CP, as expected, showed suppressive effect on antioxidant status. Compared with CP-treated animals, activities of GSH-Px, CAT and SOD were increased by 22.38% ($P < 0.05$), 16.89% ($P < 0.05$) and 5.67% ($P > 0.05$) respectively, and recovered to the normal levels in animals treated with EPS-1 (400 mg/kg BW). It is suggested that EPS-1 produced by *Enterobacter cloacae* Z0206 could provide protection against CP-induced oxidative damage in mice, and it may act as a potent antioxidant agent.

Key Words: polysaccharide, *Enterobacter cloacae*, antioxidant

1083 Chinese medical plants and extracts moderating effects on antioxidant status of small intestinal mucous and IEC-6 cells under heat stress. K. J. Guo[1,3], X. Z. Song[2], G. L. Cheng[1,3], W. L. Luan[1], F. H. Liu*[1,3], and J. Q. Xu[4], [1]*Department of Animal Science and Technology, Beijing University of Agriculture*, *Beijing, China*, [2]*College of Animal Science and Technology, Jiangxi Agricultural University*, *Nanchang, 330045, P.R. China*, [3]*Beijing Key Laboratory of TCVM, CAU-BUA TCVM Teaching & Research Team*, *Beijing, China*, [4]*TCVM Laboratory, CAU-BUA TCVM Teaching & Research Team, College of Veterinary Medicine, China Agricultural University*, *Beijing, China*.

The aims of the study were to determine: 1. the effects of supplemental Chinese medicine additives on antioxidant status of intestinal mucous in piglets under heat stress; 2. the effects of active components of above studied medicine: *Herba Agastachis* essential oil and *Cortex Phellodendri* alkaloid on antioxidant status of IEC-6 cells after high-temperature treatment. In exp. 1, 16 35-d-old weaned Chinese experimental mini

piglets (6.50 ± 1.05kg) were randomly divided into 4 groups: Normal temperature control group, NTC; High temperature stress group, HTS; High temperature + 0.5% Chinese medicine additives group 1, CMA1 and High temperature + 0.5% Chinese medicine additives group 2, CMA2. NTC pigs were housed under the condition of 23°C and 60% humidity for 10days, while the other 3 groups were housed under the same conditions with NTC but treated with 40°C from 10:00 to 15:00 each day for 10 consecutive days. At the end of experiment, duodenum, jejunum, ileum samples of piglets were collected and SOD, GSH-PX activity, MDA contents of intestinal mucous were determined by kit. In exp. 2, IEC-6 cells were cultured under 37°C for 41 h as control and those under 37°C for 38 h and 41°C for last 3h as experimental group (EG). 200μg/mL, 100μg/mL, 50μg/mL essential oil or alkaloid were added into EG and the contents of SOD, GSH-PX activity, MDA were analyzed. The results showed: (1) Chinese medicine additives could significantly increase SOD ($P < 0.05$), GSH-PX ($P < 0.05$) activity and decrease MDA content ($P < 0.05$) in heat stressed piglets. (2) 200μg/mL essential oil and 100 μg/mL alkaloid significantly increased the levels of SOD ($P < 0.05$) and GSH-Px ($P < 0.05$) and decreased the content of MDA ($P < 0.05$) in IEC-6 cells treated by high temperature. In conclusion, Chinese medicine additives can play important role on improving the antioxidant status of intestinal mucous in piglets. *Cortex Phellodendri* alkaloid and *Herba Agastachis* essential oil are the main effective components.

Key Words: Chinese medical plants and extracts, heat stress, antioxidant function

1084 Immune responses and gene expression in red swamp crayfish (*Procambarus clarkii*), induced by selenium-enriched exopolysaccharide (Se-ECZ-EPS) from *Enterobacter cloacae* Z0206. X. X. Wang*, Z. Q. Lu, Y. F. Zhang, L. N. Zhu, Y. Ren, and Y. Z. Wang, *Feed Science Institute of Zhejiang University*, *Hangzhou city, Zhejiang province, China*.

Selenium-enriched exopolysaccharide (Se-ECZ-EPS), produced by *Enterobacter cloacae* Z0206, is an important polysaccharide but little information is available about the potential crustacean immune response to this compound. To investigate the modulation of immunity in crustaceans, we examined phenoloxidase activity (PO), respiratory bursts ability ($O2^{-1}$) and superoxide dismutase (SOD) levels, as well as expression profiles of several immune-related gene in red swamp crayfish (*Procambarus clarkii*) that were individually injected with Se-ECZ-EPS at 1 μg g^{-1}. The protection of crayfish against white spot syndrome virus (WSSV) by Se-ECZ-EPS was also investigated. During the experiment period, the water temperature was maintained at 22 ± 1°. Duncan's multiple comparison tests were used to compare significant differences among treatments. At 24, 48 and 72h post-injection, PO activities of crayfish in treatment groups were 0.26±0.03, 0.40±0.02 and 0.38±0.03 respectively, and significantly ($P < 0.05$) higher than those of control groups (0.16±0.03, 0.15±0.01 and 0.11±0.01). Respiratory burst levels were 0.74±0.05, 1.21±0.28 and 1.53±0.28 and SOD activities were 34.00±2.52, 43.60±3.41 and 42.00±5.76, respectively at 24, 48 and 72h post-injection, and were significantly($P < 0.05$) higher than those of their respective control groups; 0.61±0.04, 0.61±0.03 and 0.51±0.04 for respiratory burst, and 24.23±2.68, 24.91±2.46 and 24.97±2.98 for SOD activities. Among the examined genes, at 24h and 48h after Se-ECZ-EPS treatment, the mRNA expression of serine proteinase (9.94±1.86 and 2.97±0.69, respectively), HSP70 (9.38±1.91 and 12.96±1.02, respectively) and Mn-SOD (2.72±0.22 and 4.95±0.84, respectively) were significantly up-regulated ($P < 0.05$). No significant expression changes of proPO were observed from 24h to 72h. The survival rate of crayfish that received Se-ECZ-EPS was significantly higher than that of control group after 14 days (59.7% and 0%, respectively). It can be concluded that Se-ECZ-EPS is an efficient immunostimulant and can improve immunity of crayfish.

Key Words: immune responses, exopolysaccharide, *Procambarus clarkii*

1085 C-di-GMP signaling pathways are critical for acid resistance of *E. coli* O157:H7. M. J. Zhu*[1], B. L. Wang[1], W. Yue[1], V. K. Koseoglu[1], H. Wang[1], X. Fang[2], W. J. Means[1], R. J. McCormick[1], and M. Gomelsky[2], [1]*Department of Animal Science*, *Laramie, WY,* [2]*Department of Molecular Biology, University of Wyoming*, *Laramie*.

Surviving the acidic environment of gastrointestinal tract is important for *E. coli* O157:H7 pathogenesis. However, factors contributing to acid resistance remain poorly understood. The second messenger cyclic diguanosine monophosphate, c-di-GMP, affects various aspects of bacterial physiology. To test its role in acid resistance, strain O157:H7 and selected mutants in c-di-GMP metabolism were exposed to pH 3.5 for 15 min. Cell survival and mRNA levels (measured by qRT-PCR) of selected genes involved in c-di-GMP metabolism and acid resistance were analyzed. In the wild type, acid challenge resulted in increased mRNA levels of the newly identified c-di-GMP receptor gene, *ydiV* (7-fold) and the major c-di-GMP phosphodiesterase gene, *yhjH* (13-fold). Deletion of *ydiV* or *yhjH* impaired acid challenge survival by 600 and 35 fold, respectively. Consistent with this observation, expression of several genes responsible for acid resistance, *asr*, *dsbA* and *katP*, were decreased in the *ydiV* and *yhjH* mutants, compared with the wild type. Interestingly, overall expression profiles of the *ydiV* and *yhjH* null mutants were not identical. In the *ydiV* mutant, mRNA levels of *katG* were lower, whereas those of *gad*, *oxyR* and *cysB* were higher, compared with the *yhjH* mutant and wild type. Under neutral pH conditions, expression of all listed genes was not different among tested strains. In conclusion, in *E. coli* O157:H7, (i) acid stress strongly affects expression of genes involved in c-di-GMP metabolism; (ii) c-di-GMP signaling pathways are critically important for acid resistance, and (iii) c-di-GMP apparently affects acid resistance by several pathways.
NIH P20RR016474 INBRE; USDA AFRI 2009, Agricultural Experiment Station at University of Wyoming.

Key Words: *E. coli* O157: H7, c-di-GMP, acid resistance

1086 Monensin level, supplemental urea, and administration of ractopamine on fecal shedding of *Escherichia coli* O157:H7 in feedlot cattle. Z. D. Paddock*, C. E. Walker, J. S. Drouillard, D. G. Renter, and T. G. Nagaraja, *Kansas State University*, *Manhattan*.

Inclusion of distiller's grains (DG) in cattle diets has been shown to increase fecal shedding *E. coli* O157. Therefore, factors affecting ruminal fermentation of DG may impact fecal shedding of *E. coli* O157. The effect of feeding monensin at the new maximum limit 44 mg/kg of feed on fecal shedding of *E. coli* O157 in cattle has not been determined. The objectives of the study were to evaluate the effects of monensin level (33 or 44 mg/kg DM), supplemental urea (0, 0.35, or 0.70% of DM; administered with the final diet of the step-up program), and ractopamine (0 or 200 mg/steer daily; administered during the last 42 d of the finishing phase) in a steam-flaked corn-based diet containing 30% wet sorghum DG on fecal shedding of *E. coli* O157. Seven-hundred and 20 crossbred beef steers (initial BW 453 ± 23.1 kg), housed in 48 pens (15 steers/pen), were assigned to dietary treatments in a randomized complete block design with a 2 × 3 x 2 factorial treatment arrangement. Fresh pen floor fecal samples (10 per/pen) were collected every 2 wk for 14 wk and cultured for *E. coli* O157. Fecal prevalence data were analyzed with repeated measures negative binomial regression (PROC GENMOD) to examine effects and interactions of sampling day, urea, monensin, and ractopamine. Cumulative fecal prevalence of *E. coli* O157 was 7.6%, and ranged from 1.6 to 23.6%. Cattle fed monensin at 44 mg/kg had lower ($P = 0.05$) *E. coli* O157 prevalence than cattle fed 33 mg/kg (4.3 vs 6.8%). Supplemental urea that could potentially alter ruminal fermentation had no effect on fecal shedding of *E. coli* O157 ($P = 0.87$). The effect of ractopamine was not significant ($P = 0.89$), but the power to detect an effect was low due to low *E. coli* O157 prevalence in the final phase of the study. Additional research is needed to confirm the reduction in fecal shedding of *E. coli* O157 in cattle fed 44 mg/kg monensin and to assess the effect of ractopamine on fecal shedding of *E. coli* O157.

Key Words: *E. coli* O157:H7, distillers grains, monensin

1088 Effect of feeding rumen undegradable intake protein on gut *Campylobacter* concentrations in fed cattle. R. C. Anderson*[1], T. A. Wickersham[2], W. E. Pinchak[3], N. A. Krueger[1], T. R. Callaway[1], T. S. Edrington[1], R. B. Harvey[1], and D. J. Nisbet[1], [1]*USDA/ARS, Southern Plains Agricultural Research Center, Food and Feed Safety Research Unit*, *College Station, Texas,* [2]*Texas A&M University*, *College Station,* [3]*Texas AgriLife Research*, *Vernon*.

Campylobacter are a leading bacterial cause of human foodborne illness worldwide, causing more than 2 million infections in the United States alone. These bacteria readily colonize the gut of food animals, but because they lack 6-phosphofructokinase, they do not ferment sugars and thus must derive a substantial proportion of their energy from amino acid catabolism. To test our hypothesis that diets promoting amino acid flow to the lower gut may increase intestinal carriage of *Campylobacter*, 10 ruminally and duodenally cannulated Angus steers, averaging 431 kg, were adapted (n = 5/diet) to diets formulated to achieve 0 or 30% dried distiller′s grains with solubles (DDG; DM basis). Control steers were maintained on the basal diet containing cracked corn, supplemental fat and cottonseed meal. Steers receiving DDG were adapted via incremental increases (every 14 d) to treatment diet and remained on the 30% WDGS diet for 7 d. Duodenal and fecal samples collected before the start of each step up period (on d 0, 14 and 27) and at the end of the final period (d 33) were enumerated for *Campylobacter* spp. via viable cell count and $\log_{10}$ transformations of resultant bacterial colony forming units (CFU) were analyzed for effects of diet, period and their interaction by a repeated measures ANOVA. Fecal *Campylobacter* concentrations ranged from 1.6 to 3.0 $\log_{10}$ CFU/ml (SEM = 0.5) but did not differ ($P > 0.05$) due to diet, period or their interaction. Similarly, main effects of diet or period were not observed ($P > 0.05$) on duodenal *Campylobacter* counts but in this case a diet × period interaction was observed, due to higher recovery of duodenal *Campylobacter* from the WDGS-fed steers during the 2nd (3.1 $\log_{10}$ CFU/ml) than the 1st or 3rd periods (1.4 and 1.3 $\log_{10}$ CFU/ml, respectively). No other differences in duodenal *Campylobacter* concentrations were observed, with values ranging from 1.6 to 2.3 $\log_{10}$ CFU/ml (SEM = 0.5). These results do not support our hypothesis that diets high in rumen undegradable intake protein will increase proliferation of *Campylobacter* in the bovine gut.

Key Words: *Campylobacter*, distillers grains, pathogen

1089 Development of a broader spectrum phage cocktail to decrease *Salmonella* shedding in livestock. J. Zhang[1], B. L. Kraft[1], Y. Pan[2], S. K. Wall[1], A. C. Saez*[1], and P. D. Ebner[1], [1]*Purdue University*, *West Lafayette, IN*, [2]*Zhejiang University*, *Hangzhou, China*.

Salmonella shedding in many livestock species can increase significantly following transport and lairage. These increases in shedding can

amplify the amount of *Salmonella* that enters the processing facility and the likelihood of end product contamination. We previously produced an anti-*Salmonella* phage cocktail that reduced colonization in swine when the pigs were exposed to an environment heavily contaminated with *Salmonella* similar to what might be seen in a holding pen. The purpose of the current study was to increase the efficacy of the phage treatment by: 1) expanding its spectrum of activity; and 2) developing a more cost-effective microencapsulation technique. We collected samples from wastewater treatment facilities and isolated 20 distinct phages that were lytic against *Salmonella*. From this library we identified 10 phages that lysed *Salmonella enterica* Typhimurium, Enteriditis and Kentucky (3 serovars commonly associated with meat and poultry products). We characterized each phage by morphology and electron microscopy. The phages were microencapsulated using a sodium-alginate based method with or without poly-L-lysine which only reduced the cocktail titer by approximately one log (pre-microencapsulation: 10.4 $\log_{10}$ PFU/mL; post-microencapsulation with poly-L-lysine: 9.2 $\log_{10}$ PFU/mL; post-microencapsulation without poly-L-lysine: 8.9 $\log_{10}$ PFU/mL). Microencapsulated phages remained stable at both 4C and 22C with no appreciable drop in titer for up to 14 d (mean titer: 8.9 $\log_{10}$ PFU/mL). Taken together, these data indicate that multi-valent phage cocktails are easily produced and a cost-effective microencapsulation process adequately protects the phages over an extended period of time. Therefore, it may be possible to simultaneously treat large numbers of animals with phage therapy through feed or water.

Key Words: *Salmonella*, phage therapy, food safety

1090 Use of a biophotonic *E. coli* XEN-14 to determine time of contamination in the life cycle of the house fly, *Musca domestica* Linnaeus (Diptera: Muscidae). G. Schuster*[3], K. E. Moulton[1], P. R. Broadway[4], S. Willard[2], J. Behrends[4], and T. B. Schmidt[1], [1]*Department of Animal, Mississippi State University and Dairy Sciences*, *Mississippi State*, [2]*Department of Biochemistry, Mississippi State University*, *Mississippi State*, [3]*Agronomy, Texas A&M University-Kingsville*, *Kingsville*, [4]*Food Science, Nutrition, and Health Promotion, Mississippi State University*, *Mississippi State*.

Researchers have reported that the house fly (HF), *Musca domestica* Linnaeus (Diptera: Muscidae) is capable of carrying *E. coli* O157:H7, and thus serve as mechanical cross contamination vector. There is limited data identifying when during the life cycle that *E. coli* ingestion occurs. The objective of this trial was to utilize *E. coli* transformed with the XEN-14 gene cassette (BP-E.coli) to monitor the progression of *E. coli* contamination through the life cycle of the HF. HF larvae were incubated in 100-mL cup containing 50-g of sterile manure (72% moisture) inoculated with BP-E.coli at 1×10^4, 10^5, or 10^9 CFU for 24 or 48-h (larva), 7 d (pupae), and 10 d (fly). Post-incubation, larvae, pupae, and flies were imaged intact and macerated to determine uptake of BP-E.coli. After photonic imaging, larvae, pupae, and flies were serially diluted to quantify total CFU's of BP-E.coli ingested. Serial dilution of larvae exposed to BP-E.coli for 24 and 48-h revealed that 86% and 80% of larvae had ingested 3.1×10^5 and 1.9×10^6 CFU of BP-E.coli, respectively. There was no difference ($P > 0.05$) in terms of total CFU ingestion between the 2 incubation periods (24 vs. 48 h) or the inoculation concentration of BP-E.coli for larvae. Serial dilution of pupae 7-d post incubation revealed that 53% of pupae were positive for BP-E.coli (6.9×10^2 CFU), there was no difference ($P > 0.05$) in ingestion of BP-E.coli by pupae between the 3 inoculation concentrations. Serial dilution of adults 10 d post-incubation revealed that 13.8% of adults emerge from the pupae stage contaminated with 3.9×10^2 CFU of BP-E.coli, no difference ($P > 0.05$) in the BP-E.coli retained by the adult between the 3 concentrations. Results of this trial suggest that HF can ingest *E. coli* before pupating and emerging with high concentrations of *E. coli*.

Key Words: *E. coli*, house fly, biophotonic

1091 Effect of crust freezing on the survival of *Escherichia coli* and *Salmonella* Typhimurium in raw poultry products. B. D. Chaves*, I. Y. Han, and P. L. Dawson, *Clemson University*, *Clemson, SC*.

Escherichia coli and *Salmonella* spp. are ubiquitous to the poultry production environment and hence their transmission to poultry products is a concern. Industry has widely used freezing as a strategy to halt pathogen growth and more recently, crust freezing has been claimed to improve operations, quality, and even safety of poultry products. Purpose: To determine the effect of crust freezing and the presence of skin on the survival of *E. coli* and *S.* Typhimurium in raw poultry products. A completely randomized experiment was designed. Ampicillin-resistant *E. coli* JM 109 and nalidixic acid-resistant *S.* Typhimurium were used in the trials. A set of cultures was subjected to cold-shock stress by storage at 4 °C for 10 days. Commercial chicken breasts without skin and chicken thighs with skin were inoculated with each bacterium in separate experiments being either cold-shocked or non-cold-shocked prior to inoculation. Samples were crust frozen at −85 °C for 20 min or completely frozen at −85 °C for 60 min. *E. coli* and *S.* Typhimurium were recovered in duplicated plates of appropriate selective (Violet Red Bile Glucose Agar and BG Sulfa, respectively) and non-selective media (Tryptic Soy Agar) containing the corresponding antibiotic. ANOVA of the log reductions and injury extent values from three replicates were performed. No significant differences ($p>0.05$) were observed in the reduction of cold-shocked or non-cold-shocked bacteria on products that were crust- or completely frozen, with or without skin. Reductions tended to be greater for *S.* Typhimurium than for *E. coli*, although none of the final reductions were greater than the desired target (1 log). Bacterial cell injury was not significantly different ($p>0.05$) among any of the treatments. The treatments did not show practical significance for initial reduction of these pathogens thus freezing nor crust freezing should not be considered strategies for the reduction of these pathogens on poultry. However, additional studies are underway to compare crust freezing to refrigeration for inhibition of bacteria on raw poultry products.

Key Words: crust-freezing, poultry, pathogens

1092 Heating wash water for shell eggs...Is it necessary? S. L. Christian*[1], P. A. Curtis[1], L. K. Kerth[1], M. T. Musgrove[2], and K. E. Anderson[3], [1]*Auburn University*, *Auburn, AL*, [2]*UDSA-ARS*, *Athens, GA*, [3]*North Carolina State University*, *Raleigh*.

Current egg washing regulations state that wash water should be at 32.2°C or higher, shall be at least 6.7°C warmer than the internal temperature of eggs to be washed, and approved cleaning compounds should be used in the wash water (Voluntary Grading of Shell Eggs 7 CFR § 56.76 (f)). These regulations were made when eggs were immersed in water. Studies have shown that immersion washing leads to an increase in microbial load, not the temperature of the wash water. Also, previous research has proven that cool wash water temperatures utilized in an in-line operation did not add to the internal microbial content of the egg. Therefore, the objective of this research was to evaluate the effectiveness of using detergent formulated for cool water in a commercial in-line shell egg processing facility with a temperature of approximately 20°C versus an identical system utilizing a traditional detergent and temperatures. Samples were gathered during normal processing hours over the course of 3 consecutive days and for 3 separate weeks (9

replicates). Egg samples (15 eggs/treatment) were randomly selected from the collector belt before the eggs were washed from both lines and after they were washed but before they reached the packer belt. Eggs were also gathered at the beginning, middle and end of each shift over the course of 2 shifts; therefore, eggs were collected 6 times per day per line (12 treatments total). Water samples (50 mL) were collected from each wash tank at the same time egg samples were taken. Exterior egg shells, egg contents, and wash water samples were evaluated using Aerobic Count Plates and *Enterobacteriaceae* Petrifilms to determine the aerobic microorganisms and Enterobacteriaceae loads. A storage study was also performed in which the eggs were stored at 4°C for 0, 2, 6 and 10 weeks and the microbial load of the exterior egg shells and contents were determined. Cool water washing of shell eggs did prove to be a viable solution for processing shell eggs.

Key Words: shell eggs, cool water, *Enterobacteriaceae*

1093 Multiplication of *Salmonella* Enteritidis in egg yolks after inoculation outside, on, and inside vitelline membranes and storage at different temperatures. R. K. Gast*, R. Guraya, J. Guard, and P. S. Holt, *Egg Safety and Quality Research Unit, USDA-ARS*, *Athens, GA*.

Prompt refrigeration to restrict bacterial growth can reduce the risk of egg-borne transmission of *Salmonella* Enteritidis to consumers. A recently published federal rule for *S*. Enteritidis control requires eggs to be refrigerated within 36 after they are laid, but allows ambient temperature storage until this time. Although the nutrient-rich interior of the yolk is a relatively infrequent location for initial *S*. Enteritidis deposition in naturally contaminated eggs, migration across the vitelline membrane can result in rapid bacterial multiplication inside eggs stored at warm temperatures. The objective of the present study was to measure the multiplication of *S*. Enteritidis in egg yolks after introduction at 3 different locations and subsequent storage at a range of temperatures. Using an in vitro egg contamination model, approximately 100 cfu of a phage type 13a strain of *S*. Enteritidis were inoculated either inside yolks, onto the exterior surface of vitelline membranes, or into the adjacent albumen. After storage of samples from each inoculation group at 10°, 15°, 20°, and 25°C for 24 h, *S*. Enteritidis was enumerated in yolks. For all 3 inoculation locations, the final *S*. Enteritidis levels in yolks increased significantly with increasing storage temperatures. At all storage temperatures, significant differences in *S*. Enteritidis multiplication were observed between inoculation sites (yolk inoculation > vitelline membrane inoculation > albumen inoculation). At 25°C, final $\log_{10}$ *S*. Enteritidis concentrations of 7.76 cfu/ml (yolk inoculation), 2.01 cfu/ml (vitelline membrane inoculation) and 0.76 cfu/ml (albumen inoculation) were attained in yolks after storage. These results demonstrate that, even when the initial site of *S*. Enteritidis deposition is outside the egg yolk, substantial multiplication supported by yolk nutrients can occur during the first day of storage and the risk of bacterial growth increases at higher ambient storage temperatures. This reinforces the value of rapid refrigeration for protecting consumers from egg-transmitted illness.

Key Words: *Salmonella* Enteritidis, eggs, multiplication

91 Genome-wide analysis of cecal gene expression in *Salmonella*-challenged and probiotic-treated neonatal chicks. S. E. Higgins*[1], A. D. Wolfenden[2], G. I. Tellez[2], B. M. Hargis[2], and T. E. Porter[1], [1]*University of Maryland*, *College Park*, [2]*University of Arkansas*, *Fayetteville*.

Salmonella spp. often cause no clinical signs in infected poultry flocks, however, it is the most common food-borne pathogen in human infections. While some probiotics have been proven to be effective for improvement of health and to reduce enteric pathogens of poultry, the mechanisms of action of these beneficial microflora are not completely understood and have been postulated to involve elicitation of innate host defense mechanisms. Presently, we evaluated global gene expression in the cecae of neonatal chicks following *Salmonella* challenge and probiotic treatment to determine gene expression and potential gene networks involved in reduction of *Salmonella* by probiotic treatment. In this study, day-of-hatch chicks were challenged with *Salmonella enterica* ssp. Enteritidis (SE), and treated one h later with a poultry-derived, *Lactobacillus*-based probiotic culture (FloraMax-B11, B11). Twelve and 24h post-treatment, cecae were collected for *Salmonella* detection and RNA isolation. Cecal RNA samples were then analyzed using long oligonucleotide microarrays containing probes for 21,120 genes. At both 12 and 24h, SE was significantly reduced by 4 or 3 $\log_{10}$ respectively in the B11-treated chicks as compared with the challenged chicks ($P < 0.05$). Microarray analysis revealed gene expression differences among all treatment groups. At 12h, 170 genes were expressed at significantly different levels ($P < 0.05$), with a minimum difference in expression of 1.2 fold. At 24h, the number of differentially regulated genes with a minimum 1.2 fold change was 201. Pathway analysis revealed that at both time points, genes associated with the NFκB complex were significantly regulated, as well as genes involved in apoptosis, such as *growth arrest-specific 2* (*GAS2*) and *cysteine-rich, angiogenic inducer, 61* (*CYR61*). Probiotic-induced differential regulation of the genes *GAS2* and *CYR61* may result in increased apoptosis in the cecae of chicks. Because *Salmonella* is an intracellular pathogen, we suggest that increased apoptosis may be a mechanism by which B11 reduces *Salmonella* infection.

Key Words: *Salmonella*, probiotic, microarray

1094 Microbiological difference of eggs from traditional cage and free range production. D. R. Jones*[1], K. E. Anderson[2], and M. T. Musgrove[1], [1]*Egg Safety and Quality Research Unit, USDA-ARS*, *Athens, GA,* [2]*Department of Poultry Science, North Carolina State University*, *Raleigh*.

Eggs from alternative production systems are a growing market share in the US. Meeting consumer requests for greater diversity in retail egg options has resulted in some unique challenges such as understanding the food safety implications of eggs from alternative housing practices. A study was conducted to determine what, if any, differences exist between nest run cage and free range produced eggs. A flock of hatch mate brown egg layers were maintained in traditional caged and free range production with egg and environmental sampling every 6 wks from 20 to 79 wks of age. Aerobic, coliform, and yeast and mold populations were monitored. Traditional caged (TC) egg shells had the highest aerobic levels compared with free range nest box (FRNB) and free range floor eggs (FRF) (3.90, 3.55, and 3.48 log cfu/mL, respectively). FRNB and FRF egg shell coliform levels were greater than TC (1.64, 1.40, and 0.25 log cfu/mL, respectively). FRF egg shell yeast and mold levels were greatest (2.49 log cfu/mL). Range grass (RG) microbial levels were greatest for all populations monitored compared with cage swabs (CS) and nest box swabs (NBS). CS maintained the lowest levels of coliforms and yeast and molds throughout the study but had elevated levels of aerobic bacteria. Seasonal effects were also seen for all monitored populations with summer and fall having the highest levels. Understanding the differences in microbial populations present on traditional cage and free range produced eggs can lead to the development of effective cleaning procedures for free range eggs thus enhancing food safety.

Key Words: egg, cage, free range

Horse Species Symposium: Pathogenic and Reproductive Dysfunction in Horses

1095 Monitoring pathogen progression during uterine infection in the mare using biophotonic imaging technology and *lux*-modified bacteria. P. L. Ryan*, D. L. Christiansen, R. M. Hopper, F. K. Walters, K. Moulton, J. Curbelo, and S. T. Willard, *Mississippi State University*.

Premature birth is the leading cause of prenatal morbidity in humans with an incidence of 12.5% (Berhman, 2006). Moreover, 40% of premature births may be attributed to antenatal infection (Lettieri et al., 1993) of which *Escherichia coli* (*E. coli*) has been identified as the most common organism isolated from pregnant women (Lavanya and Jogalakshmi, 2002). In cattle, the rate of uterine infection has been estimated to be from 2.2 to 37.3% (Kelton et al., 1998) with *E. coli* being the most common isolated bacteria in cows with postpartum uterine infections. Similarly, placental infection due to opportunistic pathogens such as *Streptococcus equi* subspecies *zooepidemicus* and *E. coli* are common causes of abortion, still birth and premature delivery in horses (Giles et al., 1993). Moreover, pathogen progression during uterine infections and placentitis may involve invasion of endometrial and fetal tissues, including the brain, leading to increased pro-inflammatory cytokine expression resulting in onset of premature delivery and/or fetal neurological damage (LeBlanc et al., 2002). However, little is known about bacterial pathogenesis during uterine infections in the equid species. Recently, transgenically modified bacteria transformed with the pAK1-*lux* plasmid have been utilized to better understand pathogen progression in the late-term pregnant ewe and mare. A Peltier cooled slow scan CCD camera and a XR/MEGA-10Z bioluminescence imaging camera were employed in these studies to detect *lux*-expressing bacteria. This presentation will explore the use of biophotonic imaging technology and *lux*-modified bacteria to better understand pathogen progression and invasion during uterine infections in pregnant mares, and rate of pathogen clearance postpartum following therapy. The data will demonstrate that bioluminescence and real-time imaging provide a novel means of understanding pathogenesis of bacterial-induced placentitis and preterm birth in horses. Application of this novel imaging technology with *lux*-modified organisms may facilitate the development of more targeted therapeutic interventions.

Key Words: uterine infection, biophotonic imaging, mare

1096 Contagious equine metritis: An insidious threat to the US horse breeding industry. P. J. Timoney*, *Maxwell H. Gluck Equine Research Center*, *Lexington, KY*.

The objective of this presentation is to assess the significance of contagious equine metritis (CEM) as a threat to the economy of the US horse industry.

CEM has given rise to international concern since it was first recognized as a novel venereal disease of equids in 1977. Initial reports highlighted the dramatic clinical features of the disease and how readily transmissible it was. The etiologic agent was identified as a previously undescribed bacterium, *Taylorella equigenitalis*. International concerns over CEM centered on the ease with which this bacterium could be disseminated, the significance of *Taylorella equigenitalis* as a cause of short-term infertility in the mare and existence of the carrier state in the stallion and the mare. The first known outbreak of CEM in the USA was in Kentucky in 1978. The economic impact on the state′s TB industry was substantial. Prior to 2008, additional small-scale outbreaks occurred in Missouri in 1979, Kentucky in 1982 and Wisconsin in 2006, all traced to the importation of carrier animals. On each occasion, appropriate measures were taken to eliminate the infection, resulting in the US regaining its CEM-free status. With the exception of the 1978 occurrence in Kentucky, none of the subsequent outbreaks impacted significantly on the horse industry. That changed dramatically in 2008 after discovery of a culture positive QH stallion in Kentucky. Subsequent investigations turned up 22 carrier stallions and 5 carrier mares in 8 states. Shipment of infective semen and indirect venereal contact in stallion collection centers were major factors in the spread of *Taylorella equigenitalis*. Trace-back investigations of some 991 exposed and carrier stallions and mares in 48 states have failed to confirm the origin of this latest CEM event. Neither clinical evidence of CEM nor decreased pregnancy rates were reported in infected/exposed mares. In light of these findings, was the considerable expense incurred in investigating the latest CEM occurrence warranted? Only time will tell whether the disease has once again been eradicated from the US and if the cost of regaining CEM-free status was justified.

Key Words: CEM, impact, eradication

1097 Use of fluorescent *in situ* hybridization (fish) to identify endometritis pathogens in the mare. M. R. Petersen*, H. Lehn-Jensen, and A. M. Bojesen, *Faculty of Life Sciences*, *Copenhagen, Denmark*.

Presence of bacteria in the uterus as a cause of infertility was suggested more than 80 years ago. Nielsen, JM 2005 demonstrated that the diagnostic sensitivity and specificity by culture was improved when a endometrial biopsy was used compared with a swab. As *Streptococcus equi* ssp. *zooepidemicus* (*S. zoo*) was isolated more often using a biopsy compared with a swab, we decided to determine location of *S. zoo* within the endometrium. FISH can be used to demonstrate the spatial distribution of bacteria within infected tissue. Endometrial biopsies were analyzed from young non-infected research mares and from broodmares from which S. zoo had been isolated. Experimental infections in research mares with S. zoo were carried out and biopsies recovered at specific time points. Using FISH S. zoo could be localized in endometrial biopsies from mares positive for S. zoo. In the research mares large number of bacteria were localized at the luminal epithelia following inoculation, but no bacteria could be visualized at 96 h. In biopsies from chronically infected broodmares the bacterial localization was markedly different. In all of the biopsies from broodmares S. zoo was localized in distinct foci, either below the epithelial lining, within the endometrial crypts or deep in the stratum compactum, but never at the luminal epithelia as seen in the experimentally infected mares. Since this initial study we have performed FISH to visualize S.Zoo in biopsies from broodmares treated with antibiotics. Streptococci are in general sensitive to the antibiotics used for treatment of endometritis, but treatment failure of chronic cases have been described. Eventhough the mares were treated with antibiotics streptococci could still be visualized deep in the endometrium. Since the general perception has been that endometritis is a superficial infection, treatment has not been focused on bacteria localized deeper in the endometrium. We therefore suggest a treatment regimen for chronically infected mares utilizing antibiotics with a capacity to penetrate cell membranes allowing deep tissue penetration.

Key Words: endometritis, FISH, horse

1098 Chronic equine endometritis: What is missed with traditional diagnostics. M. M. LeBlanc*, *Rood and Riddle Equine Hospital, Lexington, KY*.

Endometritis, a major cause of mare infertility arising from failure to remove bacteria, spermatozoa and inflammatory exudate post-breeding, is often undiagnosed. Defects in genital anatomy, myometrial contractions, lymphatic drainage, mucociliary clearance, cervical function, angiosis (damage to arterioles) or inflamm-aging (increased levels of pro-inflammatory cytokines associated with aging) underlie susceptibility to endometritis. Diagnosis is made through detecting uterine fluid, vaginal discharge, abnormal inter-estrous intervals, inflammatory uterine cytology and positive uterine culture. However, these signs may be absent in gram-negative infections. Hypersecretion of an irritating, watery, neutrophilic exudate underlies classic, easy-to-detect streptococcal endometritis. In contrast, biofilm production, tenacious exudate, and focal infection may characterize chronic endometritis, commonly caused by gram-negative organisms, fungi and staphylococci. Clinical signs of chronic endometritis may include dry, splotchy vaginal mucosa, hyperechoic lines visualized ultrasonographically, or absence of intrauterine fluid during estrus only to appear after ovulation. Gram-negative uterine pathogens can be missed on culture swab while cytological specimens may only contain heavy debris and few, if any, neutrophils. Culture of uterine biopsy tissue, or small volume uterine lavage efflux are twice as sensitive as guarded swabs in detecting gram-negative organisms. Uterine biopsy, a technique that has lost favor in equine veterinary practice, may detect deep inflammatory and degenerative changes, such as angiosis, lymphatic lacunae or destructive fibrosis while endoscopy reveals focal lesions invisible on ultrasound. New treatments designed to improve pregnancy rates in mares with endometritis have been evaluated recently. These include lavage one hour before breeding, cloprostenol post breeding, cervical dilators, intrauterine chelators (tris-EDTA), mucolytics (DMSO, kerosene, n-acetyl-cysteine), corticosteroids (predisolone, dexamethasone) and immunomodulators (cell wall extracts of Mycobacterium phlei and Propionibacterium acnes).

Key Words: equine, endometritis, diagnostics

International Animal Agriculture 1

1099 Challenges for the Mexican animal industry. M. Huerta-Bravo*, R. Núñez-Domínguez, and R. Ramírez-Valverde, *Universidad Autónoma Chapingo*, *Chapingo, México*.

Livestock production challenges have worldwide impact due to globalized economies. The objective is to identify these challenges for the Mexican animal industry and to propose specific tasks for government, producers, and researchers to solve them. Statistical data and information about Mexican livestock was analyzed to identify challenges and define tasks. We must recognize that animals play an important and changing role for humankind since their domestication, and that they are providers of the most nutritive foods. Mexico faces a deficit in most animal products coupled with food consumption pattern favoring health problems such us iron and zinc deficiencies, obesity, and chronic-degenerative diseases. Population growth and income improvement will increase food deficit. Future animal production increases have several challenges: less agricultural land per capita, climate change, high economical and technological dependence on supplies for animal production, food security at risk due to poverty and low food sovereignty, conservation and sustainability of genetic diversity, use of arable land and grains to produce biogas, and low or less federal funds for animal production, research, and technological development. Government tasks include strategies to achieve food security and sovereignty, to provide healthier and nutritive foods from livestock, to increase efficiency of agricultural production systems, to convert animal wastes to products, to restore environment and to increase support for research and development. Producers should recognize that their well-being is a priority but depends on an efficient farm with animal welfare and minimum environmental impact. Researcher's tasks should focus on key elements that insure sustainability of production systems. Human values, faithful application of laws, and efficient administrators are key elements to achieve the well-being of our families.

Key Words: Mexico, animal industry, food security

1100 Effect of varying dietary energy levels during last trimester of pregnancy on the performance of Sahiwal heifers. M. Abdullah*, M. Fiaz, M. E. Babar, J. A. Bhatti, T. N. Pasha, and M. A. Jabbar, *University of Veterinary and Animal Sciences*, *Lahore, Pakistan*.

To study the effect of feeding diets with different energy levels during the last trimester of pregnancy on the performance of Sahiwal heifers, 5-6 mo pregnant Sahiwal heifers (n=16) were assigned to four dietary treatments having 4 heifers on each treatment. Iso-nitrogenous (CP=14.1%) diets having varying energy, viz; A=100% (Control), B=88%, C=112% and D=124% of NRC recommended levels for pregnant heifers were fed to the respective groups until calving. After calving, all heifers were fed a similar diet having CP and energy level as recommended by NRC for lactating animals. Data were analyzed using ANOVA. Pre-calving weight gain was higher ($P \leq 0.05$) in treatment C and D (486 ± 13 and 497 ± 05 g/d, respectively) as compared to A and B. Heifers fed control diet (A) also had greater ADG ($P \leq 0.05$) than those fed diet B (444 ± 07 vs. 397 ± 08 g/d, respectively). A similar trend was observed in feed efficiency. Body condition score at calving in heifers fed diet-D (3.87 ± 0.07) was greater ($P \leq 0.05$) than that of diets A (3.60 ± 0.09) and B (3.50 ± 0.04) whereas it was also greater ($P \leq 0.05$) in heifers fed diet C (3.75 ± 0.03) than that of diet B. Birth weight of calves born from heifers fed different experimental diets did not differ. Daily milk yield in heifers fed control diet was greater (5.87 ± 0.06 kg) than that of other diets, whereas, it was similar among diet C (4.68 ± 0.10 kg) and diet D (4.72 ± 0.14 kg) but lower in diet B (4.2 ± 0.07 kg) as compared to other experimental diets, whereas milk composition among animals fed different experimental diets did not differ ($P \leq 0.05$). The performance of heifers fed only ad libitum green fodder kept under farm management in terms of weight gain (300 ± 0.09 g/d), BCS (3.12 ± 0.12) and milk yield (2.56 ± 0.28 kg/d) was lower than that of those fed experimental diets. It is concluded that feeding extra energy during the last trimester of pregnancy improved weight gain and body condition score but first lactation yield was optimum in heifers fed a diet having an energy level as per recommendations of NRC.

Key Words: dietary energy, milk yield, Sahiwal heifers

1101 Development of the organic beef foodchain in the Mexican tropics—Eight years of experience. P. Fajersson*[1] and P. Parada[2], [1]*Colegio de Postgraduados, Campus Veracruz*, *Veracruz, Veracruz, Mexico*, [2]*Carnes La Rumorosa*, *Poza Rica, Veracruz, Mexico*.

The global organic market, recently a niche market, is currently the fastest growing segment of the mainstream market. Mexico has a law for organic production and also regulations based on the European norms adapted to local conditions. Despite a 25% growth rate of the domestic organic food market during 2009, the products are mainly sold within the captured market, due to inadequate information to consumers and lack of marketing. In the state of Veracruz, a pioneer effort to develop the organic beef food chain, based on a strategic alliance between academia, cattle ranchers and an organic certification agency started in 2002. It was incorporated into The Gulf of Mexico States Accord in order to extend the project regionally. Twenty producers began their organic certification in 2002, guided by the academics and the certification agent. Two producers had previously conditioned their ranches to organic production and in 2003 obtained the certification of their foodchains. Mexico lack political backing of organic agriculture, but even so organic beef producers have managed to achieve a 15% added value to their products. After eight years, technical difficulties and increasing costs of production and postharvest processing have been overcome and the quality of the organic beef is excellent .An upscale restaurant in Veracruz organized a gourmet dinner with 50 invited expert guests, who gave the beef highest marks. The beef is sold to organic markets and stores, some with restaurants, in seven states. Producers have been slow to conclude their certification, which has led to the loss of three important international market opportunities; upscale restaurants and hotels in Scandinavia, Hong Kong and participation in a 12 million dollar beef business in Florida. This due to inability to comply with the quantities required on time. Producers and university students are the principal participants in training courses organized. The state of Chiapas has earmarked ;130 000 dollars for an organic beef project, and in Campeche 130 producers are lined up to begin organic beef projects like the one in Veracruz. In conclusion, the impact of the project is growing steadily, but political endorsement and promotion are required to detonate the organic beef food chain in Mexico.

Key Words: organic beef, tropics, foodchain

1102 Wool comfort factor variation in Australian crossbred sheep. A. E. O. Malau-Aduli* and D. J. Deng Akuoch, *School of Agricultural Science/TIAR, University of Tasmania*, *Hobart, Tasmania 7001, Australia*.

Comfort factor (CF) is defined as the percentage of wool fibers with diameter less than 30 microns. Our objective was to investigate the effects of sire genetics, nutrition, level of supplementation and gender and their interactions on CF in crossbred sheep either grazing or supplemented with dietary protein. Correlations between CF and other wool traits were also investigated. Texel, Coopworth, White Suffolk, East-Friesian and Dorset sires were mated with 500 Merino ewes at a ratio of 1:100 in individual paddocks. Five hundred of the crossbreds were raised on pasture until weaning at 12 weeks of age. Forty of the weaners with initial BW range of 23-31 kg (average of 27 ± 3.2 kg) were fed with lupins or canola at 1 or 2% BW for 6 weeks in a 5 × 2 × 2 × 2 factorial experimental design. CF and other wool quality traits were commercially measured at the Australian Wool Testing Authority. Data were analyzed in SAS using MIXED models procedures with sire fitted as a random effect, whereas sire breed, nutrition, supplement, level of supplementation and gender and their interactions were fitted as fixed effects. We found that neither supplement ($P > 0.14$) nor level of supplementation ($P > 0.16$) influenced CF which did not differ between pasture-fed and supplemented sheep. However, highly significant effects of sire breed ($P < 0.01$), gender ($P < 0.01$) and interactions between sire breed × level of supplementation ($P < 0.01$), sire breed × gender ($P < 0.03$) and supplement × level of supplementation ($P < 0.01$) on CF were detected. White Suffolk crosses had the highest CF (90.1 ± 8.7%) and East-Friesian crosses the least (81.5±10.1%). Males fed canola at 1%BW had the highest CF (90.8 ± 7.0%), while females fed lupins at 1%BW had the least (81.1 ± 10.8). White Suffolk sired males ranked the highest (91.1 ± 10.5%) and East Friesian females the least (74.7 ± 7.9%). CF was significantly correlated with fiber diameter (−0.89), spinning fineness (−0.95) and wool curvature (0.33). Our findings provide useful information to sheep farmers in crossbreeding dual purpose sheep that will also deliver desirable wool comfort outcomes to the fabric industry.

Key Words: wool comfort factor, pasture-fed sheep, protein supplements

1103 Supplementation of Starbio probiotic and yeast on milk production and nutrient digestibility of lactating Holstein cows fed a ration containing cassava meal. E. Sulistyowati*, I. Badarina, and E. Soetrisno, *Animal Science Dept., College of Agriculture, University of Bengkulu (UNIB)*, *Bengkulu, Indonesia*.

The aim of this research was to evaluate the effects of Starbio probiotic and yeast on milk production and nutrient digestibility of lactating Holstein fed a ration containing cassava meal in a rural area farm in Bengkulu, Indonesia. There were eight lactating Holstein Cows which were assigned in a replicated Latin Square (2 × 4 × 4) to receive four treatments: basal diet of 65% field grass and 35% concentrate containing cassava meal, as control (SR0); basal diet + Starbio 1% of concentrate (SR1); basal diet + 20 g yeast (SR2); and basal diet + Starbio 1% of concentrate + 20 g yeast (SR3). The application was run for four 3-wk periods. Yeast supplementation (SR2) increased milk production ($P < 0.05$) for as much as 2.13 kg/d, equivalent to 24.85%. The highest milk fat content (4.10%) was found with the combination of these probiotics (SR3). Nutrient (dry matter, organic matter, crude protein, fiber, and ether extract) consumptions and nutrient digestibility were not different ($P > 0.05$) among treatments. However, digestibilities were relatively high, ranging from 80.93 to 85.55%. The most efficient ratio between dry matter intake and milk production was found in SR2 (1.64). In conclusion, yeast supplementation for as much as 20 g/d into a basal diet with 35% concentrate containing cassava meal resulted in the highest increase in milk production (2.13 kg/d) with slightly lower milk fat (4.05%), combined with the most efficient ratio of milk production and dry matter intake (1.64) in lactating Holstein cows.

Key Words: Starbio, yeast, milk production, nutrient digestibility, Holstein cows

1104 Effects of protease supplementation on growth performance of broilers fed corn-soy-DDGS based diets. F. Yan*[1], L. Garibay[2], J. Arce[2], C. Lopez-Coello[2], D. Camacho[1], M. Vazquez-Anon[1], M. Manangi[1], N. Odetallah[1], and S. Carter[1], [1]*Novus International Inc.*, *St. Charles, MO*, [2]*Universidad Michoacana de San Nicolas de Hidalgo*, *Morelia, Mich, Mexico*.

A floor pen study was conducted to determine the effects of a protease enzyme (CIBENZA DP100, Novus International Inc.) on growth performance of broilers fed corn-soy-DDGS based diets from 1 to 46 d of age. Four treatments in a 2 × 2 factorial arrangement were evaluated with 2 levels of CP (positive control and 7.5% reduction) with or without protease at 0.05%. The positive control diet was formulated with corn soybean meal and 14% DDGS to contain 22%, 21%, and 18.5% CP for starter (1–21 d), grower (22–35 d), and finisher (36–46 d) respectively, and the 7.5% reduction in CP along with the limiting amino acids Lys, Met, and Thr, were achieved primarily through decreasing amount of soybean meal and adjusting supplemental synthetic amino acids. A total of 1400 Ross male broilers were randomly distributed into 28 pens (50 birds per pen) at 1 d of age with 7 pens per treatment. Birds were weighed at 7, 14, 21, 28, 35, and 46 d; feed conversion ratio (FCR), feed intake, and mortality were also determined at each weigh day. Body weights were significantly reduced by lowing dietary CP at 14, 21, 28, 35 and 46 d ($P < 0.05$), and protease supplementation significantly increased body weights at 35 d ($P < 0.05$) regardless of dietary CP levels. A significant interaction was observed between dietary CP and protease for FCR at 14 and 21 d where protease improved FCR when it was added to the diet with the control CP level ($P < 0.05$), but not to the diet with the reduced CP level. At 35 and 46 d of age, protease significantly improved FCR by 5.2 and 4.3 points respectively ($P < 0.05$), irrespective of dietary CP level. Regardless of protease supplementation, reducing dietary CP level increased mortality. In summary, use of a protease in a corn-soy-DDGS based diets improved FCR of broilers throughout the trial, and the effect was independent of dietary CP levels at 35 and 46 d of age.

Key Words: protease enzyme, amino acids, broiler

1105 Effects of a novel phytase on phosphorus digestibility in corn-soybean meal diets fed to weanling and growing pigs. F. N. Almeida* and H. H. Stein, *University of Illinois*, *Urbana*.

Two experiments were conducted to evaluate the effects of a novel bacterial 6-phytase expressed in a strain of *Aspergillus oryzae* (Ronozyme HiPhos, DSM Nutritional Products, Parsippany, NJ) on the apparent total tract digestibility (ATTD) of P in corn-soybean meal diets fed to weanling and growing pigs. In Exp. 1, 6 diets were formulated. The positive control (PC) was a corn-soybean meal diet that contained dicalcium phosphate to bring the total concentration of P to 0.66%. A negative control (NC) diet (0.36% P) without dicalcium phosphate was also formulated. Four additional diets similar to the NC diet were formulated to contain microbial phytase at levels of 500, 1,000, 2,000, or 4,000 phytase units (FYT) per kg. The 48 weanling pigs (initial BW: 13.5 ± 2.45 kg) were placed in metabolism cages and randomly allotted to the 6 dietary treatments in a randomized complete block design. Feces were collected for 5 d. The total P output and the P concentration in feces were reduced (linear, quadratic, $P < 0.01$) as phytase was added to the NC diet. The ATTD of P was greater ($P < 0.01$) for the PC diet (60.5%) than for the NC diet (40.5%) and increased (linear, quadratic, $P < 0.01$) as phytase was added to the NC diet (40.5 vs. 61.6, 65.1, 68.7, and 68.0%). The breakpoint for the ATTD of P (68.4%) was reached at a phytase inclusion level of 1,016 FYT/kg. In Exp. 2, 6 diets were formulated as in Exp. 1. A total of 24 growing pigs (initial BW: 36.2 ± 4.0 kg) were randomly allotted to the 6 dietary treatments in a balanced 2 period changeover design. The total P output and P concentration in feces were reduced (linear, quadratic, $P < 0.01$) as phytase was added to the NC diet. The ATTD of P was greater ($P < 0.01$) for the PC diet (59.4%) than for the NC diet (39.8%) and increased (linear, quadratic, $P < 0.01$) as phytase was added to the NC diet (39.8 vs. 58.1, 65.4, 69.1, and 72.8%). The breakpoint for the ATTD of P (69.1%) was reached at a phytase inclusion level of 801 FYT/kg. Ronozyme HiPhos effectively improved the ATTD of P and reduced P excretion in both weanling and growing pigs.

Key Words: phosphorus, pigs, phytase

1106 Enzyme complex containing NSP-enzymes and phytase improves the growth performance and bone mineralization of piglets fed wheat and barley-based diet. A. Preynat*[1], J. M. Gomez[2], and G. Uzu[1], [1]*Adisseo France SAS*, *92160 Antony, France*, [2]*PRIMEX SAS*, *La Gare de Baud, BP21, F-56440 Languilic, France*.

The experiment was conducted to investigate the benefits of a multi-enzyme complex (Rovabio Max) containing carbohydrolases and phytase activities on the performance and bone mineralization of piglets. A total of 240 weaned 28 d-old piglets (Pietrain x Landrace x Large White) were allocated into 4 experimental treatments (10 replicates per treatment, 6 animals per pen) in a randomized complete block design. The animals were fed according to 2 phases: weaner (28–42d) and starter (43–70d) diets. Diets were formulated as follow: a positive control (PC) diet formulated to be adequate in nutrient and a negative control (NC) diet with a decrease in digestible phosphorus (−1.5 g/kg digP), total calcium (−1.0 g/kg Ca) and net energy (−70 kcal/kg). NC diet was supplemented or not with enzymes at 2 rate of incorporation (0.2 and 0.3 L/t). Bodyweight and feed intake were determined at 28, 42 and 70 d. One femur bone from 10 pigs per treatment was collected for ash content determination at 70 d. During the weaner period, feed to gain ratio of NC groups was degraded compared with PC group ($P < 0.01$). During the starter period, animals fed NC diet had the lowest performances (average daily feed intake (ADFI) and average daily gain (ADG); $P < 0.01$) than PC group. ADFI and ADG were significantly improved irrespective of the level of enzyme supplementation of the NC diets. On total period, ADFI (775, 731, 782 and 771 g/d for PC, NC, NC+0.2 and NC+0.3, respectively; $P < 0.05$), final body weight (31.3, 29.4, 31.3 and 31.1 kg; $P < 0.01$) and ADG (566, 518, 566, 561 g/d; $P < 0.01$) were comparable between NC+enzyme to those observed in the PC group. Moreover, the ash content was fully compensated by enzyme supplementation: 14.7, 11.2, 14.0 and 14.4 g/100g. These results confirm the efficiency of multi-enzyme complex to reduce the digP, Ca and energy specifications of wheat and barley-based diets without performance losses in piglets.

Key Words: NSP-enzymes, phytase, piglets

1107 Effect of dietary calcium concentration and microbial phytase addition on P utilization and growth performance in weaned pigs. A. Narcy[1], M. P. Letourneau Montminy*[2], E. Bouzouagh[1,4], N. Meme[1], M. Magnin[3], and J. Y. Dourmad[4], [1]*INRA UR83*, *Nouzilly, France*, [2]*Agriculture and Agri-Food Canada*, *Sherbrooke, Qc, Canada*,

[3]*BNA Nutrition Animale*, *Chateau-Gontier, France*, [4]*INRA UMR1079 Agrocampus*, *St-Gilles, France*.

The study was conducted to assess the effect of microbial phytase according to various dietary calcium (Ca) concentrations on growth performance, femur characteristics and phosphorus (P) digestive and metabolic utilization in piglets fed with low-P diets (available $P = 0.22\%$). After a 5-d adaptation period on a standard diet, 40 male piglets weaned at 28 d of age (initial BW = 8.7 ± 0.8 kg) were blocked by weight and allotted to one of the 6 dietary treatments in a 29-d experiment. A 3x2 factorial arrangement was used with maize-soybean meal diets formulated to contain combinations of 3 concentrations of Ca: 0.50, 0.75 and 1.00% with or without the addition of 1000 FTU/kg of Natuphos microbial phytase. Increasing dietary Ca concentration linearly reduced ($P < 0.05$) final BW (19.4, 19.1, 18.7kg) and BW gain (406, 396, 379 g/d) whereas feed intake was unaffected by the diet. Phytase significantly improved ($P < 0.001$) femur dry matter, ash weight and ash concentration (9.53, 20.1 and 9.71% respectively). P digestibility increased ($P < 0.001$) in diets supplemented with phytase (55.1 vs. 75.2%) whereas it decreased linearly ($P < 0.001$) when dietary Ca increased (67.4, 65.0, 63.1%). The lack of interaction between dietary Ca concentration and phytase addition indicate that Ca equally depressed P digestibility in diets supplemented or not with phytase. As a result, Ca did not modify the release of phytate-P by phytase. However, in piglets receiving diets with phytase, P urinary losses increased 13-fold when Ca was reduced from 1.0 to 0.5% (CaxPhytase, $P < 0.001$) while P retention was reduced by 8.3% (CaxPhytase, $P < 0.01$). These results suggest that although decreasing dietary Ca concentration can ameliorate P digestibility, it may also cause an imbalance between metabolic Ca and P that leads to extra P urinary losses and impairs P retention.

Key Words: calcium, phytase, piglet

1108 The role of sodium in the physiological response of growing broilers to phytate and phytase. A. J. Cowieson*[1], M. R. Bedford[1], P. H. Selle[3], and V. Ravindran[2], [1]*AB Vista*, *Marlborough, Wiltshire, UK*, [2]*Massey University*, *Palmerston North, New Zealand*, [3]*University of Sydney*, *Sydney, New South Wales, Australia*.

A total of 240 Ross 308 broilers were used to investigate the effect of sodium (0.15 or 0.25%), phytate-P (0 or 0.32%) and phytase (0 or 500FTU/kg; 2 × 2 × 2 factorial) on endogenous amino acid flow using the enzyme-hydrolyzed casein method. The ingestion of phytate increased endogenous amino acid flow (~30%; $P < 0.001$) compared with the phytate-free control diets. Phytase reduced endogenous amino acid flow only when fed in concert with phytate resulting in a significant phytate × phytase interaction. Instructively increasing dietary sodium concentration from 0.15% to 0.25% reduced ($P < 0.001$) endogenous amino acid flow by around 10%. This blunting of endogenous flow was particularly evident in diets which contained phytate, resulting in a significant sodium × phytate interaction for several amino acids including Thr and Ser. Further, high sodium concentrations muted the effect of phytase resulting in a significant sodium × phytase interaction for some amino acids. Three-way interactions were rare. The concentration of Asp, Thr, Ser and some other amino acids was increased in the endogenous protein in response to the ingestion of phytate. Both sodium and phytase essentially restored the composition of endogenous protein to that of the phytate-free control. Further, as both sodium and phytase had similar effects there were significant interactions between sodium and phytase for most amino acids, such that one was only effective in the absence of the other. These data confirm previous reports that phytate is a nutritional aggressor causing quantitative and qualitative changes in endogenous protein flow. However, this is the first report which has shown that dietary sodium concentrations play a role in the severity of this antinutritional effect and consequently may blunt the efficacy of exogenous phytase. The mechanism is obscure though it has been previously demonstrated that sodium can disrupt phytate:protein complexes, thus mitigating one of the mechanisms by which phytate exerts its antinutritional effect.

Key Words: phytate, phytase, sodium

1109 Effect of a thermo-tolerant xylanase on performance in broilers fed diets with different energy and amino acid densities. C. L. Wyatt*[1], T. J. Walsh[1], M. R. Bedford[1], A. J. Cowieson[1], and S. Davis[2], [1]*AB Vista*, *Chapel Hill, NC*, [2]*Colorado Quality Research Inc.*, *Wellington, CO*.

A total of 1632 Ross 708 male broilers were used to investigate the effect of feeding a thermo-tolerant xylanase (XYL; ECONASE XT) in pelleted diets with different energy and amino acid densities on performance and carcass yield to d49. All diets contained Quantum Phytase. This was a 2 by 2 by 2 factorial design with 2 energy (HiE; LoE −96 kcals/kg), 2 AA (HiAA; LoAA −15%) and 2 XYL levels (0 or 100g/mt) fed with 12 reps/trt containing 17 birds/pen. Significant main effects for dietary energy and XYL ($P < 0.10$) were found for FCR but not bwt gain. Significant interactions were found for AA by XYL, and E by AA by XYL ($P < 0.10$) for FCR. Birds fed HiE and HiAA diets containing XYL had 5 pts better FCR compared with birds fed the LoE and LoAA diets with XYL. There were no significant effects on bwt gain and mortality. Percent breast yield and % hot carcass were significantly improved with the HiAA diets compared with the LoAA diets but there was no effect of dietary E or XYL. There was an interaction between dietary E x AA for yield with birds fed HiAA and LoE diets having better % yield compared with birds fed the LoAA and LoE diets. The data would support previous findings from our holo-analysis that there are several key dietary factors impacting the response to feeding XYL in a corn based diet on FCR with a significant improvement in high density diets.

Key Words: xylanase, broilers, dietary energy

1110 Additions of glucanase, xylanase and phytase to low-energy low-lysine diets for broilers including canola meal and DDGS as alternative ingredients. S. Gómez*[1,2] and M. L. Angeles[1], [1]*INIFAP*, *Ajuchitlán, Colón, Qro, México*, [2]*FESC-UNAM*, *Ajuchitlán, Colón, Qro. México*.

An experiment was carried out to evaluate the productivity, ileal digestibility of nutrients and villi morphology of broilers fed diets based on sorghum and soybean meal (SSBM) including canola meal (CM) and DDGS and added with glucanase, xylanase and phytase enzymes. One hundred and 20 Ross B308 males, individually fed, from 35 to 49 d were assigned to 6 dietary treatments: 1) SSBM diet including 10% CM and 8% DDGS containing 3218 kcal of ME and 0.91% digestible Lys, 2) SSBM, 10% CM, 8% DDGS low-energy (2900 kcal of ME/kg) low-Lys (0.82%) diet, 3) As 2, added with 300 ppm glucanase (Ronozyme VP), 4) As 2) added with 300 ppm of xylanase (Ronozyme WX), 5) As 2) added with 150 ppm of glucanase and 150 ppm of xylanase, and 6) As 5) plus 150 ppm of phytase (Ronozyme-P (CT); Ca and available P were also adjusted in this diet. The daily weight gain was lower and feed conversion ratio was higher ($P < 0.05$) for broilers fed diet 2) with no added enzymes compared with broilers fed diet 1); these variables were partially recovered with added glucanase and xylanase and almost fully recovered when glucanase, xylanase and phytase were combined (Diet 6). The ileal digestibility of dry matter, ashes and nitrogen were lower ($P < 0.05$) for diet 2) compared with diet 1), and

were improved for glucanase, xylanase and glucanase-xylanase added diets. The greatest ashes digestibility was for the glucanase, xylanase and phytase added diet (6) and there was a trend for greater dry matter and nitrogen ileal digestibility in broilers fed the enzyme combination. The height, thickness and area of the villi were reduced in diet 2 ($P < 0.05$), but were totally recovered when the enzymes were combined. In the duodenum, maltase and sacarase specific activities were increased ($P < 0.05$) when enzymes were combined. In summary, the addition of glucanase, xylanase and phytase to low-energy, low-Lys diets including canola meal and DDGS improved the growth, nutrient digestibilities, villi morphology and endogenous enzymes activities in the duodenum of broiler chickens.

Key Words: broilers, enzymes, growth

1111 Allzyme SSF increased AME_n of the corn-soy diet and improved performance of boilers. T. Ao*, J. L. Pierce, B. Hoskins, M. Paul, A. J. Pescatore, A. H. Cantor, M. J. Ford, and W. D. King, *Alltech-University of Kentucky Nutrition Research Alliance*, *Lexington, KY*.

Allzyme SSF is a naturally fermented product with activities of multiple enzymes such as carbohydrase and phytase. A study was conducted to investigate the effect of supplementing Allzyme SSF on AME_n and retention of P and DM of the diets and growth performance of broiler chicks in a 21d period. Dietary treatments included: 1) corn-soy reference diet containing 3150 kcal ME_n /kg and 0.45% nonphytate P; 2) corn-soy low P and ME diet containing 3000 kcal ME_n /kg and 0.25% nonphytate P; 3) diet 2 + 200 g Allzyme SSF /MT diet; 4) diet 2 + 400 g Allzyme SSF /MT diet. A total of 192 1-d old chicks were randomly assigned to 4 dietary treatments with 8 replicate groups of 6 chicks per treatment. Chicks were housed in starter cages in an environmentally controlled room with an ad libitum access to feed and water. Celite (acid-insoluble ash) was used as an internal marker with an inclusion rate of 1% for the assay of AME_n and retention of P and DM on d 20 by using 24h fecal collection. Chicks fed the low P and ME diet had lower ($P < 0.01$) weight gain and higher ($P < 0.01$) feed to gain ratio compared with other treatment groups. Dietary supplementation of Allzyme SSF in low nutrient diet at both levels increased ($P < 0.01$) weight gain and decreased ($P < 0.01$) feed to gain ratio of chicks. AME_n of the low nutrient diet was increased ($P < 0.01$) by supplementing Allzyme SSF at both levels. The retention of P and DM was significantly increased by supplementing 400 g/MT Allzyme SSF. Data from this trial indicate that supplementation of Allzyme SSF in corn-soy diet can improve the performance of broiler chicks by increasing AME_n value and retention of P and DM of the diet.

Key Words: AME_n, broiler, Allzyme SSF

1112 Effects of multiple dietary manipulations on the mass balance of N and P during the swine finishing phase. T. Walraven*, S. Carter, J. Jarret, M. Bible, and H. Kim, *Oklahoma State University*, *Stillwater*.

Eighty-eight crossbred (D × (L × Y)) pigs (32 kg BW) were used to evaluate the effects of reducing dietary CP, Ca, and P with the addition of phytase on the mass balance of N and P during a 94-d finishing period. Pigs were stratified by sex, weight, ancestry, and randomly allotted to 1 of 2 dietary treatments. Pigs were housed in an environmentally controlled building with 4 identical rooms (22 pigs/room, 2 rooms/treatment). Dietary treatments consisted of a fortified corn-soybean meal diet and a Reduced Excretion (REx) diet. REx had a 3.0% unit reduction in CP with Lys, Thr, and Met added as needed and a reduction of available P of 0.10% with phytase inclusion. Also, in the REx diet, monocalcium phosphate replaced dicalcium phosphate and CaCl replaced 50% of $CaCO_3$. Diets were formulated to similar SID lysine. The estimation of mass balance, on a per pig basis, assumed that N and P entered the finisher via the feed and pigs, and exited via the slurry, exhaust air, and pigs. On d 0 and 94, 6 and 24 pigs (6/room), respectively, were ground to estimate initial and final body composition. Feed intake and composition were used to estimate N and P entering via feed. Slurry volume and composition, and NH_3-N emission were used to estimate N and P exiting via slurry and air. The amount of N and P entering via pigs was similar ($P > 0.10$). However, N (5.4 vs. 4.5 kg) and P (1.0 vs. 0.81 kg) in the feed were reduced ($P < 0.03$) for the REx diet. Thus, REx reduced total N (6.4 vs. 5.4 kg; $P < 0.08$) and P (1.2 vs. 0.98 kg; $P < 0.04$) entering by 15 and 20%, respectively. REx did not affect ($P > 0.10$) the amount of N and P exiting via the pigs. However, N (3.2 vs. 2.3 kg) and P (0.64 vs. 0.40 kg) exiting via slurry and NH_3-N (0.27 vs. 0.15 kg) in exhaust air were reduced ($P < 0.05$) for pigs fed REx. Thus, REx reduced total N and P exiting by 16 and 20%, respectfully. The proportion of N and P entering the finisher that exited via the pigs increased from 47 to 55% for N and 49 to 60% for P for pigs fed REx compared with those fed the control diet.

Key Words: pig, nutrient, mass balance

1113 Predicting variations in total and phytic phosphorus in raw materials of plant origin. C. Gady*[1], S. Virden[2], and P. A. Geraert[1], [1]*Adisseo SAS*, *Antony, France*, [2]*Adisseo USA Inc.*, *Alpharetta, GA*.

The assessment of phosphorus value of ingredients contributes to the optimization of phosphorus nutrition and reduction of phosphorus release into the environment. The main objectives of this study were to measure phytic phosphorus (phytic P) in relation to the total phosphorus (total P) in a range of ingredients and to investigate the prediction of those variations by near infrared spectroscopy (NIRS). A total of 227 samples mainly representing cereals, cereals by-products, oilseeds and oil meals were collected worldwide during one year. All samples were analyzed for their concentrations in total and phytic P using mineralization and enzymatic methods respectively. Additionally, using NIRS, these samples were also analyzed for their absorbances from 1100 to 2500 nm. For all the analyzed samples, prediction models were then calculated to determine correlation between absorbances to both total and phytic P, using mPLS regression. Due to the wide range of ingredients studied, results showed that phytic P content represents from 18% (cassava) to 83% (rice bran) of the total P content. There were also large variations intra-species in the ratio phytic P/total P (and corresponding concentrations in phytic P in % as fed) which ranged from 64 to 87% (0.14-0.30) in corns, from 64 to 80% (0.16-0.27) in wheats, from 66 to 95% (0.54-0.98) in rapeseed meals and from 59 to 69% (0.36-0.57%) in soybean meals. Prediction models developed using NIRS explained 93 and 92% of the variations measured in total and phytic P with standard error of 0.05 and 0.04%. When comparing nonphytic phosphorus calculated from chemistry vs. NIRS of samples external to database, we confirmed differences by 0.01, 0.02, 0.07 and 0.02% as fed for corn, wheat, rapeseed meals and soybean meals respectively. This study confirmed the need for better qualifying major ingredients for their nonphytic phosphorus contribution to feed formulation. With respect to the range measured among ingredients, the feasibility study using NIRS showed that the tool may contribute to better mastering those variations.

Key Words: total phosphorus, phytic phosphorus, near infrared reflectance spectroscopy

1114 A heat-tolerant β-mannanase: Its biochemical properties and effect on broiler growth performance. H. Y. Hsiao*, D. M. Anderson, L. Liu, and M. E. Jackson, *ChemGen Corp.*, *211 Perry Parkway, Gaithersburg, MD*.

β-Mannanase from *Bacillus lentus* has been shown to improve broiler growth performance and body weight uniformity as well as reduce circulating acute phase protein levels when fed a diet containing soybean meal. Due to its sensitivity to heat, the application of β-mannanase to pelleted feed is limited to spraying liquid enzyme post-pelleting; therefore, improved thermal tolerance would greatly expand its application. Recently, a heat-tolerant β-mannanase (HT) from *Bacillus lentus* is selected and its biochemical properties are described here. The heat tolerance of β-mannanase-HT in a dry formulation was evaluated at the feed mill of Kansas State University. β-Mannanase-HT is shown to have retained 95% and 90% activity when conditioned at 88°C (190°F) with 30 and 60 s of residence time, respectively. β-Mannanase-HT was also found to retain 60% of its activity after incubation under simulated conditions of the gizzard (pH 3.0, 40°C for 60 min with the presence of 2.8 mg/ml pepsin) and intestine (pH 6.7, 40°C for 120 min with the presence of 1.8 mg/ml pancreatin), consecutively. This result, along with the fact that the pH optimal of β-mannanase-HT is 6.5, suggests that β-mannanase-HT might remain active for a longer duration in a bird's digestive tract. A 42-d male broiler (Cobb × Cobb) trial was conducted to determine the dosage effect of β-mannanase-HT. The testing diet was a typical corn and soybean meal-based diet. Two thousand chicks were allocated in a randomized complete block design to five treatments, with 8 pens per treatment. The mortality and weight adjusted feed conversion (WAFC) of birds supplemented with β-mannanase–HT at four different levels of 22, 44, 66 and 88 MU/ton of feed were determined to be 1.784, 1.770, 1772 and 1.765, respectively; each of the enzyme groups was significantly better than the WAFC of the Control group at 1.927(linear, $P < 0.05$). It can be concluded that a newly developed form of β-mannanase is heat stable and efficacious in raising broilers.

Key Words: heat-tolerant, β-mannanase, broiler

Nonruminant Nutrition Symposium: Nutrient and Non-Nutrient Sensing and Signaling in the Gastrointestinal Tract

1115 Bitter taste receptors and gastrointestinal chemosensing. C. Sternini*[1], H. E. Raybould[2], L. M. Rinaman[3], and E. Rozegurt[1], [1]*UCLA, School of Medicine*, *Los Angeles, CA,* [2]*UC Davis, School of Veterinary Medicine*, *David, CA,* [3]*University of Pittsburgh*, *Pittsburgh, PA*.

Bitter taste has evolved as a warning signal against the ingestion of toxins, playing a crucial role in survival. The gastrointestinal (GI) lumen lining is exposed to nutrients and non-nutrients and might use the same mechanisms mediating oral taste signaling to detect harmful substances. This is supported by the discovery that signaling molecules transmitting bitter taste in the tongue are expressed in the GI mucosa, including the bitter taste receptors family, T2Rs, and the heterotrimeric G-protein subunits, α-gustducin (αGust) and α-transducin (αTrans). We identified transcripts for T2Rs, αGust and αTrans in the mammalian GI mucosa and in enteroendocrine STC-1 cell line, by RT-PCR. We showed that αGust and αTrans immunoreactivities (IR) are localized to set of enteroendocrine cells producing CCK, GLP1, PYY or ghrelin, peptides involve in food intake and GI function. T2R138-IR, the phenylthiocarbamide receptor, is also localized to GI epithelial cells. Intragastric administration of T2R agonists in rodents activates neurons in the brainstem via a vagal pathway. Selective T2R agonists inhibit food intake when administered intragastrically and induce conditioned flavor avoidance as measured with the 2-bottle choice paradigm, suggesting that GI T2Rs represent a second line of defense in the lumen. T2R agonists induce increase in intracellular calcium and CCK release in STC-1 cells and intraluminal T2R ligands significantly increased pCAMKII-IR, a marker of cell activation, in duodenal CCK cells and in the nodose ganglia. This suggests that T2R activation of enteroendocrine cells release CCK and activate vagal neurons. Overall, these findings support the concept that the GI mucosa lining is equipped with a chemosensory machinery for the detection of harmful substances, including food-borne toxins, drugs, and bacteria. We propose that activation of GI T2Rs by toxins induces a cascade of events triggering intracellular calcium increase and release of signaling molecules from enteroendocrine cells that in turn activate neuronal pathways responsible for initiating a protective response to guard the body from environmental hazards.

Key Words: enteroendocrine cells, vagal afferents

1116 T1R-mediated taste transduction mechanisms. S. C. Kinnamon*, *University of Colorado Denver*, *Aurora*.

Taste buds in the oral cavity are the chemosensory end organs that guard the entrance to the alimentary canal. Each taste bud comprises approximately 50–100 individual taste cells that detect the chemicals that elicit the sweet, salty, sour, bitter, and umami (glutamate) taste qualities. During the past decade, considerable progress has been made in identifying the receptors involved in the transduction of each taste quality. Ion channels are involved in the detection of salts and acids, while G protein coupled receptors (GPCRs) and second messengers mediate the transduction of bitter, sweet, and umami taste stimuli. Two classes of GPCRs have been identified, the T2R bitter receptors and the T1R receptors for sweet and umami stimuli. Three T1Rs have been identified, T1R1, T1R2, and T1R3. T1R3 combines with T1R1 (T1R1/T1R3) to bind glutamate and 5′-ribonucleotides, while T1R3 combines with T1R2 (T1R2/T1R3) to bind sugars, synthetic sweeteners, and sweet proteins. These receptors share similar downstream signaling effectors. The canonical transduction pathway involves Gβγ activation of PLCβ2, production of the second messengers IP3 and diacylglycerol, release of Ca^{2+} from intracellular stores, and Ca^{2+}-dependent activation of a monovalent-selective cation channel, TRPM5. These events lead to membrane depolarization and release of ATP as a transmitter to activate gustatory afferent nerve fibers. Genetic knockout of PLCβ2, IP3R3, and TRPM5 each severely compromises both sweet and umami taste responses, validating their central role in the transduction process. The Gα that mediates sweet and umami transduction is Gα-gustducin, which activates PDE to decrease intracellular cAMP. Although the exact role of cAMP in transduction is not clear, gustducin knockout mice have reduced responses to both sweet and umami stimuli. My lab has shown recently that α-gustducin knockout mice have elevated cAMP levels in taste buds, suggesting that gustducin is tonically active in the absence of taste stimuli. We suggest that α-gustducin tonically activates PDE to keep cAMP levels low and prevent chronic adaptation to taste stimuli.

Key Words: gustducin, T1R3, TRPM5

1117 Gut sensors for spices and odorants. T. Braun[1], P. Voland[2], L. Kunz[1], C. Prinz[2], and M. Gratzl*[1], [1]*Institute of Anatomy, Ludwig Maximilian University Munich*, *Munich, Germany*, [2]*II. Med. Dept., Technical University Munich*, *Munich, Germany*.

Enterochromaffin cells release serotonin in response to mechanical stimulation or in response to certain nutrients in the lumen of the intestine. The secreted serotonin then stimulates sensory components of the enteric nervous system, ultimately controlling gut peristalsis as well as water and chloride transport by enterocytes. Microarray gene chip data suggested that enterochromaffin cells might express olfactory G-protein-coupled receptors that are typically found in the nose. Laser capture-microdissected human intestinal enterochromaffin cells and a cell line derived from human enterochromaffin cells were found to express the same 4 olfactory receptor genes by RT-PCR: OR73, hOR17–7/11, OR1G1, and hOR17–210. Thymol, which binds to OR1G1, is a component of thyme spice. Thymol triggers a transient rise in intracellular calcium and a dose-dependent increase in serotonin release, whereas phenol does not. Other odorant ligands showed similar responses: eugenol and isoeugenol (binds OR73), methylsalicylate (receptor unknown), geraniol (binds hOR17–7/11 and OR1G1), bourgeonal (binds hOR17–7/11 and hOR17–4), and helional (binds hOR17–7/11 and hOR17–40) increased intracellular calcium, and stimulated serotonin release by exocytosis. Our study indicated that enterochromaffin cells express olfactory receptors that may be stimulated by odorant ligands in the intestinal lumen to release serotonin. The results suggest that luminal odorants may influence gut motility and secretion.

1118 Amino acid sensing in the gut epithelium. D. G. Burrin* and B. Stoll, *USDA Children's Nutrition Research Center, Department of Pediatrics, Baylor College of Medicine, Houston, TX.*

Amino acids are elemental substrates for cellular protein synthesis in the body. Amino acids are present in the diet and absorbed across the intestinal epithelium into the portal blood by a family of transport proteins that are specific for different structural properties of amino acids. Our previous work has shown that dietary amino acids are also extensively metabolized by the gut epithelium and in the case of glutamate, used as a major oxidative fuel. However, recent evidence shows that amino acids are more than just nutrients or metabolic substrates, but also functions as signaling molecules in intestinal physiology and cell metabolism. The recent discovery of novel proteins reveals the molecular mechanism of

how gut epithelial cells "taste" or recognize specific amino acids. One such group of proteins is the taste receptors, which is a small family of 3 G-protein-coupled receptors (T1R1, T1R2 and T1R3) that form heterodimeric complexes that bind glutamate and sugars. Another more well known group of proteins, the metabotropic glutamate receptors are also expressed throughout the gastrointestinal tract. Both the taste and metabotropic receptors are localized on epithelial, endocrine and neuronal cells and when activated stimulate signal processes that are involved in gastric emptying, secretion and insulin release. Dietary glutamate increases vagal afferent nerve activity in the brain and is blocked by cholinergic inhibitors suggesting that these processes are mediated via extrinsic nerve pathways. Arginine is an amino acid that is conditionally essential in the neonate and can be extensively metabolized in the intestine. Recent studies suggest that arginine specifically stimulates protein synthesis in intestinal epithelial cells via activation of mammalian target of rapamycin (mTOR) and downstream signaling targets, p70S6 kinase and 4EBP-1. The mechanism whereby arginine activates mTOR does not involve production of nitric oxide, a key signaling product of arginine metabolism. The presentation will discuss these 2 examples of amino acid sensing mechanisms in the gut and the implications for animal growth and development.

Key Words: glutamate, arginine, enteroendocrine cells

1119 Nutrient sensors expressed in gut enteroendocrine cells regulate nutrient-responsive secretion of satiety hormones. S. Shirazi-Beechey*, K. Daly, A. Moran, and J. Dyer, *University of Liverpool*, *Liverpool, UK*.

The gastrointestinal (GI) tract is a sensory organ that responds to signals arising in its lumen. Intestinal nutrient sensing plays an important role in controlling GI function including regulation of gastric emptying, gut motility and nutrient absorption. In addition, molecular events in the lumen of the GI tract induce satiety hormone release from enteroendocrine cells that lead to activation of systemic, hormonal and/or neural pathways involved in the regulation of food intake and appetite. I shall describe mechanisms by which the intestinal epithelium senses nutrients i.e., sugars and short chain fatty acids resulting in secretion of gut hormones that regulate nutrient absorption and food intake. We showed that the sweet taste receptor (T1r2 + T1r3) and its coupled G-protein, gustducin, are expressed in intestinal enteroendocrine cells and act as the intestinal glucose sensor. We then demonstrated that dietary sugars and artificial sweeteners increase expression of intestinal glucose absorptive capacity in wild type mice, but not in T1r3 or gustducin knockout mice. In addition it has been shown that these knockout mice have deficiencies in secretion of glucagon-like peptide 1 (GLP-1) and glucose-dependent insulinotropic peptide (GIP) in response to orally ingested carbohydrate, or when glucose was directly administrated into the intestinal lumen. Such data indicate that sweet taste receptor in intestinal enteroendocrine cell detects extracellular sugar and then responds with secretion of gut hormones. It is proposed that dietary fiber can increase GLP-1 release providing potential mechanisms for the stimulation of satiety and suppression of hunger. Dietary fiber is fermented in the large intestine to short chain fatty acids, acetate, propionate and butyrate. It has been shown that GPR41, and GPR43 may act as the SCFA sensor. Work in our laboratory has shown that these GPRs are expressed in the large intestinal endocrine cells. Furthermore exposure of L-type enteroendocrine cells to either SCFA or a compound known to specifically activate GPR43 results in secretion of GLP-1.

Key Words: nutrient sensing, intestine, GLP-1

1120 Effect of artificial sweeteners on the expression of swine intestinal Na^+/glucose co-transporter 1, SGLT1. A. Moran*[1], D. Batchelor[1], C. Ionescu[2], D. Bravo[2], and S. Shirazi-Beechey[1], [1]*University of Liverpool*, *Liverpool, UK*, [2]*Pancosma*, *Geneva, Switzerland*.

A shorter suckling period in piglets leads to several disorders including nutrient malabsorption, diarrhea, malnutrition and dehydration. We have shown that a low concentration of a combination of artificial sweeteners, saccharin and neohesperidin dihydrochalcone (Sucram) included in piglets' diets enhances the expression of intestinal SGLT1 and the gut capacity to absorb glucose. We determined previously that the sweet taste receptor comprised of T1R2+T1R3 is expressed in intestinal enteroendocrine cells and that dietary sugars and artificial sweeteners act in the intestine, on the sweet taste receptor, and its coupled G-protein gustducin, to elicit upregulation of SGLT1. Our studies in mouse intestine showed that only those artificial sweeteners that activated mouse lingual epithelium sweet taste receptor led to upregulation of intestinal SGLT1. Aim: to determine effects of sucralose, cyclamate, aspartame and acesulfame K (aceK) on intestinal SGLT1 expression. Five groups of 28 d old piglets (n = 8 per group) were weaned onto a commercial diet lacking any artificial sweeteners, with their drinking water containing either no sweetener, sucralose (2 mM), cyclamate (10 mM), aspartame (1 mM) or aceK (10 mM). All consumed the same amount of food and water. Subsequently, they were sacrificed by euthanasia under ethical permission. SGLT1 expression was assessed at levels of mRNA, protein and function. Results: there was a 2.73- ($P = 0.003$), 3- ($P < 0.0001$) and 2.8- ($P = 0.0005$) fold increase in SGLT1 expression in response to inclusion of sucralose, cyclamate and aspartame in the drinking water respectively compared with that in the control. AceK had no effect on SGLT1 expression. Results indicate that intestinal sweet taste perception in pig is different to some other species. These are due to sequential differences in amino acid residues of sensor proteins interacting with artificial sweeteners, the knowledge of which is essential for designing species-specific sweeteners. The data also highlight the potential of using other artificial sweeteners, having assessed the lowest effective concentrations, as food supplements.

Key Words: SGLT1, artificial sweetener, piglet's diet

Physiology and Endocrinology: Feed Intake, Metabolism and Maternal Nutrition

1121 Expression of neuropeptide Y and its receptors as affected by nutrition and leptin infusion in Zebu heifers. J. Diniz-Magalhães, M. V. Carvalho, A. B. S. Machado, R. A. Ribeiro, and L. F. P. Silva*, *Universidade de São Paulo*, *Pirassununga, SP, Brazil*.

Leptin has been proposed to act via NPY in the hypothalamus to modulate the effect of nutrition on sexual maturation. The objective was to evaluate the effect of oLeptin infusion and of high or low energy intake on the expression of neuropeptide Y (NPY), and 2 NPY receptors, NPY-Y1 and NPY-Y2. Thirty 6 prepubertal Nelore heifers, 18 to 20 mo-old, 275.8 ± 17.2kg BW and BCS of 5 ± 0.5 (1 to 9 scale) were randomly assigned to each of 3 treatments (n = 12): H (high energy diet), L (low energy diet), and LL (low energy diet + oLeptin). Diets were formulated to promote weight gain of 0.4 kg/day (groups L and LL) or 1.2 kg/day (H group). Heifers were fed ad libitum once a day, they were weighed and had their BCS evaluated twice weekly. After 21 d of adjustment, heifers in LL group received subcutaneous injections of oLeptin at 4.8µg/kg BW twice a day, for 56 d. Groups H and L received similar injections of 2mL saline solution. Age at puberty was considered to be the age on first detection of a corpus luteum by twice weekly transrectal ultrasonography, confirmed by plasma concentrations of progesterone of >1ng/ml. Twenty 4 heifers were slaughtered at the time of puberty for harvesting of the hypothalamus. Total RNA was extracted with Trizol, treated with DNaseI and reverse transcribed to cDNA. Expression of transcripts of NPY, NPY-Y1 and NPY-Y4 was quantified by real-time PCR. Changes in gene expression were calculated by relative quantification with the ΔΔCt method, using the gene ribosomal protein L-19 as the reference gene. There was no effect of leptin administration on expression of NPY ($P = 0.70$), NPY-Y1 ($P = 0.72$) and NPY-Y4 ($P = 0.96$) at the time of puberty. However, high energy intake reduced expression of NPY-Y1 ($P = 0.02$), without affecting expression of the other 2 genes. Downregulation of NPY-Y1 could indicate lower sensibility of the hypothalamus to NPY action. NPY is a well known inhibitor of puberty therefore this result indicates that a reduction in NPY-Y1 expression could permit attainment of puberty at a younger age in Zebu heifers.

Key Words: *Bos indicus*, hypothalamus, puberty

1122 Blocking µ-opioid receptors alters short-term feed intake and oro-sensorial preferences of weaned calves. C. Montoro*[1], I. Ipharraguerre[2], and A. Bach[1,3], [1]*Ruminant Production, IRTA*, *Caldes de Montbui, Barcelona, Spain*, [2]*LUCTA S.A.*, *Barcelona, Spain*, [3]*ICREA*, *Barcelona, Spain*.

In rats and humans, opioids play a role in controlling short-term regulation of feed intake through oro-sensorial reward mechanisms. Thirty-four Holstein calves (BW = 86.5 ± 1.73kg, age = 77 ± 0.6 d) were housed in individual pens and submitted to 4 treatments to determine whether naloxone, a µ-opioid receptor antagonist, affects feed intake and oro-sensorial preferences in weaned calves. The study was conducted in 2 periods with 17 animals per period. Treatments followed a 2 × 2 factorial arrangement combining a fasted (FA) or fed (FE) state with an i.v. injection of saline (0.9% NaCl) solution (S) or naloxone (1 mg/kg of BW; N). Each factor combination involved 8 animals, except FA-S and FE-N which had 9 calves. All calves were offered a double choice of the same feed unflavored or flavored with a sweetener (Luctarom SFS-R, Lucta) *ad libitum*. Feed consumption was recorded every 60 min during 6 h (from 0800 to 1400) following the morning feed offer. Data were log-transformed and analyzed using a mixed-effects model with repeated measures. Calves in the FE-N group tended ($P = 0.10$) to consume less concentrate (3.97 ± 0.398 log g/h) than FE-S (4.86 ± 0.422 log g/h), FA-N (5.30 ± 0.422 log g/h), and FA-S (5.07 ± 0.398 log g/h). Furthermore, S calves showed a preference for the sweetened feed ($P < 0.05$) whereas N calves did not show any preference (Table 1). These data suggest that µ-opioid receptors are involved in short-term feed intake regulation by mediating oro-sensorial feed preferences and may interact with energy-mediated mechanisms in regulating the amount of feed consumed.

Table 1. Feed consumption rate (log of g/h) as affected by treatments

Treatment	Unflavored concentrate	Sweetened concentrate	P-value
FA-S	4.78±0.417	5.36±0.42	0.02
FA-N	5.31±0.442	5.29±0.44	0.93
FE-S	4.36±0.442	5.36±0.44	<0.001
FE-N	4.14±0.417	3.79±0.42	0.15

Key Words: taste, intake, regulation

1123 Evidence that nesfatin-1 is a satiety factor in the pig and that the hypothalamus controls its expression in adipose tissue. C. A. Lents*[1], C. R. Barb[2], G. J. Hausman[2], L. Lee-Rutherford[2], C. J. Rogers[1], N. L. Heidorn[1], R. S. Cisse[1], and M. J. Azain[1], [1]*University of Georgia*, *Athens,* [2]*USDA-ARS Richard B. Russell Agriculture Research Center*, *Athens, GA*.

Two experiments (Exp) were conducted to test if nesfatin-1 is part of the adipose tissue-hypothalamic loop regulating appetite and energy balance of the pig. In Exp 1, prepuberal gilts were adapted to a twice-daily feeding schedule (0800 and 1600 h) and received intracerebroventricular (i.c.v.) injection of 100 µg of either recombinant human leptin or nesfatin-1 (nearly equal mass to leptin) in 0.9% saline. Control animals received 0.9% saline alone (n = 4/group). Four hours after i.c.v. injection, feeders were placed in all pens (1600 h) for determination of cumulative intake at 4, 20, 44, and 68 h after feed presentation. Food consumption of nesfatin-1 treated pigs was suppressed ($P < 0.01$) during the first 20 h compared with saline controls (0.54 ± 0.3 and 3.15 ± 0.3 kg, respectively), but was not different from leptin-treated pigs (1.04 ± 0.3 kg). Although food intake of nesfatin-1 and leptin-treated pigs was increasing ($P < 0.05$) after 20 h, it was still less ($P < 0.001$) at 68 h than that observed for saline-treated pigs (4.04, 4.50 and 8.76 ± 0.31 kg for nesfatin-1, leptin and saline, respectively). Subcutaneous (SC) adipose in the pig is innervated by hypothalamic neurons that are sensitive to secreted adipokines. Nesfatin-1 is proposed to work through the melanocortin 3/4 receptor (MC3/4R) pathway, which when activated alters gene expression in fat. In Exp II, gilts received i.c.v. injection of 10 µg of the MC3/4R agonist NDP-MSH or 0.9% saline alone (n = 9/group). Pigs were sacrificed 24 h later and SC adipose tissue was collected for isolation of RNA. Abundance of mRNA for nesfatin was quantified with real-time RT-PCR. Relative differences in expression were calculated by the REST procedure with 18S rRNA as the reference control. mRNA for nesfatin in SC adipose tissue of NDP-MSH treated pigs was reduced 1.7 fold ($P = 0.05$) compared with saline-treated pigs. We conclude that nesfatin-1 is a satiety factor in the pig and that activation of the MC3/4R pathway suppresses expression of nesfatin-1, which may be mediated by sympathetic neuronal outflow to adipose tissue.

Key Words: nesfatin-1, feed intake, swine

1124 Endocannabinoid and PPARα signaling gene network expression in liver of peripartal cows fed two levels of dietary energy prepartum. M. J. Khan*, D. E. Graugnard, and J. J. Loor, *University of Illinois*, *Urbana.*

Fatty acid ethanolamides (FAE) have anorexic and anti-inflammatory properties and are endogenous ligands for cannabinoid receptors subtype 1 (CNR1) or 2 (CNR2). Some FAE mediate peripheral metabolic effects in non-ruminants through the activation of PPARα. Because of the potential for endogenous FAE to mediate inflammation and satiety at the level of the liver, we sought to establish the longitudinal mRNA expression of *CNR1*, *CNR2*, *PPARA*, *FAAH*, *ASAH*, several PPARα targets (*CPT1A*, *ANGPTL4*, *FGF21*), and *RXRA* in cows (n = 14/diet) assigned to a control (high-straw, S; NEL = 1.34 Mcal/kg) or moderate-energy (ME; NEL = 1.62 Mcal/kg) diet during the dry period and until parturition. A percutaneous liver biopsy was collected at −14, 7, 14, and 30 d relative to parturition for transcript profiling via quantitative PCR. Normalized/log-transformed data were analyzed using ANOVA. Estimated prepartal energy balance (EBAL) in cows fed ME was greater ($P < 0.05$) and averaged 159% of requirements compared with 102% in cows fed S. However, EBAL during the first week postpartum tended ($P = 0.10$) to be lower in cows fed ME (83% vs. 89% of requirements) which had greater ($P = 0.06$) serum NEFA (560 vs. 351 mEq/L). *CNR2* expression remained high (diet × time $P < 0.05$) with ME by d 7 after which it decreased to levels similar to cows fed S. Following a decrease from −14 to 7 d, *PPARA* and RXRA increased ($P < 0.05$) gradually through 14 d regardless of diet. However, cows fed ME had overall greater ($P < 0.05$) *RXRA*. The PPARα targets *ANGPTL4* (3-fold) and FGF21 (20-fold) increased dramatically between −14 and 7 d in cows fed ME (diet × time $P < 0.05$). Thereafter, expression of both genes declined and reached lowest levels at 30 d regardless of prepartal diet. Whereas *CPT1A* decreased between −14 and 7 d and then reached peak expression by 30 d with S, expression increased gradually between −14 and 14 d with ME (diet × time $P < 0.05$). Preliminary results revealed a potential role of negative EBAL and high NEFA induced by prepartal energy overfeeding on endocannabinoid signaling and PPARα activation.

Key Words: metabolism, inflammation, transition cow

1125 Endoplasmic reticulum (ER) stress gene network expression in liver of peripartal cows fed two levels of dietary energy prepartum. M. J. Khan*, D. E. Graugnard, and J. J. Loor, *University of Illinois*, *Urbana*.

X-box binding protein 1 (XBP1) is a key regulator of the mammalian unfolded protein response or ER stress response. We examined expression of genes associated with the ER stress response in cows assigned (14/diet) to a control (high-straw, S; NEL = 1.34 Mcal/kg) or moderate-energy (ME; NEL = 1.62 Mcal/kg) diet prepartum and until parturition. A percutaneous liver biopsy was collected at −14, 7, 14, and 30 d relative to parturition for transcript profiling via quantitative PCR. Normalized/log-transformed data were analyzed by ANOVA. Estimated prepartal energy balance (EBAL) in cows fed ME was greater ($P < 0.05$) and averaged 159% of requirements compared with 102% in cows fed S. However, EBAL during the first week postpartum tended ($P = 0.10$) to be lower in cows fed Me (83% vs. 89% of requirements) which had greater ($P = 0.06$) serum NEFA (560 vs. 351 mEq/L). *XBP1* was 185% greater at −14 d in cows fed S and increased 24% by d 7 postpartum (diet × day $P < 0.05$) after which it decreased close to prepartal levels by 14 d but still was 93% greater in cows fed S vs. ME. There was a diet × time effect ($P < 0.05$) for the expression of *EIF2AK3*, a kinase induced by ER stress leading to a halt of translation, due to a decrease between −14 and 7 d in cows fed S which also had greater (25%) *EIF2AK3* at −14 d. *EIF2AK3* returned to prepartal levels by 14 through 30 d. The stress-induced transcription factor DDIT3 decreased ($P < 0.05$) between −14 and 7 d regardless of prepartal diet after which it remained below prepartal values. Expression of stearoyl-CoA desaturase (*SCD*), whose downregulation in rodent liver leads to robust ER stress, was lower at −14 d with S but increased by 4-fold at 7 d leading to a diet × time effect ($P < 0.05$). There was no change in *SCD* between −14 and 7 d in cows fed ME, but expression increased gradually to peak values at 30 d. Despite differences in EBAL and NEFA postpartum, preliminary results indicated moderate effects of prepartal energy level on ER stress at calving potentially driven the by marked upregulation of *SCD* postpartum.

Key Words: transition cow, metabolism, transcriptomics

1126 Effects of a hyperinsulemic euglycemic clamp administered during heat stress or pair feeding on plasma ghrelin concentrations of lactating dairy cattle. S. E. Cossel*, M. E. Field, M. V. Skrzypek, S. R. Sanders, L. H. Baumgard, R. P. Rhoads, and M. L. Rhoads, *University of Arizona*, *Tucson*.

The objective of this study was to measure the effects of a hyperinsulinemic euglycemic clamp (HEC) on plasma ghrelin (GHR) concentrations during heat stress (HS) or pair feeding (PF). Lactating Holstein dairy cows (n = 11; 136 ± 8 DIM; 560 ± 32 kg BW) were housed in environmentally controlled chambers and assigned to 1 of 2 treatment groups. During period 1 (9 d), both groups were maintained in thermal neutral (TN) conditions (18°C; 20% RH) and fed ad libitum. During period 2 (9 d), cows were exposed to: 1) HS (n = 6; cyclical temperatures; 31.1–38.9°C; 20% RH) with ad libitum feed or 2) TN conditions while being PF to match the intake of the HS cows (n = 5). On d 8 of each period, 7 control (CON) blood samples were collected at 30-min intervals for each group. On d 9 of each period, a HEC was conducted and 7 blood samples were collected at 30-min intervals beginning 240 min after the administration of an insulin bolus. Rectal temperatures (RT) and respiration rates (RR) increased during the HS period compared with the TN period (39.7 ± 0.1 vs. 38.3 ± 0.1°C; $P < 0.01$ and 90 ± 2 vs. 38 ± 2; $P < 0.01$, respectively), while DMI decreased (15.1 ± 0.4 vs. 19.75 ± 0.4 kg; $P < 0.01$). The RT and RR of PF animals did not differ from TN conditions, while DMI decreased as designed. Plasma GHR concentrations were not affected by HS or PF alone (CON-HS or CON-PF vs. CON-TN concentrations). Likewise, mean plasma GHR concentrations in CON samples were similar to those from the HEC during the TN and HS treatments. In contrast to the HS group, PF cows had lower mean plasma GHR concentrations during the HEC compared with CON (187.2 ± 53.9 vs. 336.6 ± 53.9 pg/mL, respectively; $P < 0.01$). During the HEC of both the HS and PF treatments, plasma GHR concentrations increased from the beginning to the end of the sampling period ($P < 0.03$ and $P < 0.01$, respectively). Thus, regardless of similar feed intake, profiles of plasma GHR concentrations differed between PF and HS cows.

Key Words: ghrelin, dairy, glucose

1127 Effects of heat stress on insulin action in lactating Holstein cows. M. V. Skrzypek*[1], R. P. Rhoads[1], S. R. Sanders[1], K. Flann[1], L. Cole[1], J. W. Perfield[2], M. R. Waldron[2], and L. H. Baumgard[3], [1]*University of Arizona*, *Tucson,* [2]*University of Missouri*, *Columbia,* [3]*Iowa State University*, *Ames*.

Multiparous cows (n = 12; parity = 2; 136 ± 8 DIM, 560 ± 32 kg BW) housed in climate chambers were fed a TMR consisting primarily of alfalfa hay and steam-flaked corn and subjected to 2 experimental periods

(P): 1) thermoneutral (TN) conditions (18°C, 20% humidity) with ad libitum intake for 9d and 2) heat-stress (HS) conditions (cyclical temperature 31.1–38.9°C, 20% humidity: min THI = 73, max THI = 80.5) and ad libitum intake (n = 6) or pair-fed (PF in TN conditions, n = 6) for 9d. Rectal temperature (Tr) and respiration rate (RR) were measured thrice daily at 0430, 1200 and 1630h. To evaluate insulin sensitivity, an 8-h hyperinsulinemic-euglycemic clamp (HEC) was performed on d9 of P1 and P2. The HEC was a primed, continuous infusion of bovine insulin (3.8 μg/kg BW/h followed by 2 μg/kg BW/h) and euglycemia maintained by varying intrajugular exogenous glucose infusion rates. During P2, HS cows had ($P < 0.01$) a 1.48°C increase in Tr and a 2.4-fold increase in RR compared with PF cows. HS reduced ($P < 0.01$) DMI by 8 kg/d and by design PF cows had similar intake reductions. Milk yield was decreased similarly (30%) in HS and PF cows and both groups entered into a similar (−4.5 Mcal/d) calculated negative energy balance during P2. Compared with P1 ($P < 0.05$), basal glucose levels increased (5%) in PF cows but decreased (5%) in HS cows. Basal NEFA levels increased (34%, $P < 0.01$) in PF cows compared with P1, but did not change from P1 to P2 in HS cows. The HEC increased ($P < 0.01$) plasma insulin levels similarly for both treatments during both periods (0.6 vs. 5.9 ng/ml). The overall rate of glucose infusion (ROI) to maintain euglycemia during the HEC did not differ between treatments, but was markedly reduced (29%; $P < 0.01$) during P2. Compared with P1, the ratio of ROI to basal glucose concentration decreased (21%; $P < 0.01$) in PF cows, but did not differ in HS cows during P2. Because a comparable ROI was needed to maintain a smaller blood glucose pool in HS cows, the HEC data imply HS cows have greater glucose disposal as a result of enhanced insulin action.

Key Words: heat stress, insulin

1128 The effect of insulin glargine on the metabolism of lactating Holstein cows. L. A. Winkelman*, D. M. Barbano, M. E. Van Amburgh, and T. R. Overton, *Cornell University*, *Ithaca, NY*.

Two studies were conducted to determine the effects of an insulin analog, insulin glargine (SRI) (Lantus , Sanofi-Aventis), on metabolism of lactating Holstein cows. In study one, 16 multiparous cows (213 ± 10 DIM) were divided into 2 groups and randomly assigned to one of 4 treatments (control, 0.1 IU SRI/kg BW (L), 0.2 IU/kg BW (M), and 0.4 IU/kg BW (H)). Subcutaneous (SQ) injections of SRI or water were given at 0900 h. Cows were fed hourly and milked at 1500, 2300, and 0700 h. Blood samples were taken hourly via jugular catheter for 24 h after treatment injections. Administration of increasing doses of SRI resulted in a linear ($P = 0.004$) decrease in plasma glucose (66.0, 62.3, 61.0, 54.1 mg/dl glucose for control, L, M, and H doses, respectively). Endogenous insulin secretion decreased linearly ($P = 0.028$) with SRI dose (1.04, 0.88, 0.79, 0.64 ng/ml for control, L, M, and H doses, respectively). In study 2, 3 multiparous cows (101 ± 22 DIM) fitted with indwelling intercostal arterial and mammary vein catheters were used to determine effects of SRI in a 2-period crossover design. Periods lasted 4 d with a 2 d washout in between periods. In period one, 2 cows received 0.15 IU/kg BW of SRI, 2x/d at 12-h intervals, while the remaining cow was a control. Treatments were reversed in period 2. On d 4 of each period, simultaneous blood samples were taken from the arterial and venous catheters hourly for 12 h. Dry matter intake, milk yield, and all major milk components, except lactose, were not different ($P > 0.10$). Lactose content ($P = 0.094$) and yield ($P = 0.091$) were higher for the control treatment. Casein content and yield did not differ between treatments ($P > 0.10$), but whey content ($P = 0.012$) and yield ($P = 0.015$) were higher for SRI. Arterial and venous glucose were lower ($P < 0.10$) for SRI (arterial: 63.1, 56.9 mg/dl for control vs. SRI, respectively; venous: 45.4, and 40.7 mg/dl for control vs. SRI, respectively). Based on these studies, insulin glargine is able to lower plasma glucose across different doses and its effect on milk protein composition warrants further research.

Key Words: insulin, glucose

1129 The effects of maternal obesity and overnutrition on ovine fetal adipose tissue lipid composition. N. M. Long*[1,2], D. C. Rule[2], P. W. Nathanielsz[3], and S. P. Ford[1,2], [1]*Center for the Study of Fetal Programming*, *University of Wyoming, Laramie,* [2]*Department of Animal Science*, *University of Wyoming, Laramie,* [3]*Department of Obstetrics and Gynecology*, *University of Texas Health Sciences Center, San Antonio*.

The effects of maternal obesity and overnutrition on fetal adiposity and adipose tissue composition were evaluated. Multiparous ewes were allotted by BW and age and fed either 100% of NRC recommendations (Control; C) or 150% of NRC (Obese; OB) from d 60 before conception until necropsy on d 135 of gestation. Fetal body weights and fetal adipose depot weights were recorded. Fatty acid (FA) composition of perirenal, pericardial, and subcutaneous (SC) adipose tissue of 7 male twin fetuses per group was determined by GLC. Data were analyzed using the GLM procedure of SAS. Fetal BW tended to be reduced ($P = 0.08$), and eviscerated weight (EFW) was lower ($P = 0.05$) for fetuses from OB than C ewes (4.78 ± 0.23 vs. 5.40 ± 0.25 kg and 3.56 ± 0.18 vs. 4.12 ± 0.18 kg, respectively). Pericardial and perirenal adipose tissue weight as a % of EFW was greater ($P < 0.05$) in fetuses from OB than C ewes (0.195 ± 0.001 vs. 0.191 ± 0.001%; 0.81 ± 0.01 vs. 0.68 ± 0.01%, respectively). 12th rib fat thickness was greater ($P < 0.01$) in fetuses from OB than C ewes (0.9 ± 0.1 vs. 0.5 ± 0.1 mm). Total FA concentrations were greater ($P < 0.01$) in the perirenal adipose tissue of OB fetuses than C fetuses (913.4 ± 29.8 vs. 731.6 ± 29.8 mg/g tissue). Concentrations of 18:0, 18:1 c-9 and 18:1 c10/c11 in perirenal adipose tissue were greater ($P < 0.05$) in fetuses from OB than C ewes. Only 18:1 c-9 was greater ($P < 0.05$) in pericardial adipose tissue of fetuses from OB than C ewes. Total FA in SC adipose tissue tended to be greater ($P = 0.09$) in fetuses from OB than C ewes (114.5 ± 24.9 vs. 50.0 ± 24.9 mg/g tissue). Concentrations of 16:0, 18:1 c-9, and 20:4 n-6 were greater ($P < 0.03$) in SC adipose tissue from fetuses of OB than C ewes. Maternal obesity resulted in greater fetal adiposity and altered FA composition of adipose tissue in late gestation which could lead to permanent alteration in adipose tissue function.

Key Words: maternal obesity, fatty acid composition, adipose tissue

1130 Influence of metabolizable protein supplementation during late gestation on vasoreactivity of maternal and fetal placental arteries in sheep. L. A. Lekatz*[1], M. L. Van Emon[2], P. K. Shukla[3], S. T. O'Rourke[3], C. S. Schauer[2], K. M. Carlin[1], and K. A. Vonnahme[1], [1]*Center for Nutrition and Pregnancy, Department of Animal Sciences, North Dakota State University*, *Fargo,* [2]*Hettinger Research Extension Center, North Dakota State University*, *Hettinger,* [3]*Department of Pharmaceutical Sciences, North Dakota State University*, *Fargo*.

To examine the effects of metabolizable protein (MP) intake during late gestation on the vasoreactivity of placental arteries, 18 pregnant ewes received 100% (CON), 75% (LOW), or 125% (HIGH) of MP requirement from d 100 to 130 of gestation. On d 130, several caruncular (CAR) and cotyledonary (COT) arteries from placentomes of similar size and in close proximity to the umbilicus were selected for vasoreactivity studies. Arterial rings were suspended in organ chambers filled with 25 mL of physiological salt solution aerated with a mixture

of 95% O_2 and 5% CO_2 and kept at 38.6°C. Optimal tension was found by progressively stretching the rings until the contractile response to KCl (20 mM) was maximal. The presence or absence of endothelium was verified by testing the ability of bradykinin (BK; 10^{-7} M) to produce endothelium-dependent relaxation during contraction evoked by norepinephrine (10^{-6} M). Contractile dose response curves (DRC) were obtained by contracting with increasing concentrations of KCl and phenylephrine (PE). Rings were contracted with U46619 (10^{-8} M) and the DRC to either BK or sodium nitroprusside (SNP) was obtained in endothelium intact and endothelium removed rings, respectively. There was no effect on the KCl DRC in CAR arteries ($P \geq 0.36$). KCl exhibited a treatment × dose interaction in COT arteries where arteries from CON and LOW ewes were more ($P = 0.01$) sensitive to KCl compared with arteries from HIGH ewes. There was no effect of PE in CAR or COT ($P \geq 0.12$) arteries. There was no effect on either BK or SNP in CAR ($P \geq 0.56$) arteries. The COT arteries from CON and LOW ewes tended ($P = 0.09$) to be more sensitive to BK compared with arteries from HIGH ewes; however, there was no effect of SNP in these arteries ($P = 0.87$). This indicates that BK-induced vasodilation in COT arteries cannot solely be explained by a nitric oxide donor. Perhaps the vasodilator action of BK is through downstream affects of an endothelial derived hyperpolarizing factor and/or prostacyclin. Further analyses are needed to determine how protein supplementation impacts vascular function in the placenta.

1131 Maternal nutrient restriction (NR) upregulates phosphoenolpyruvate carboxykinase (PEPCK) expression in the livers of aged female offspring. L. Zhang*[1], Y. Ma[1], N. Tuersunjiang[1], L. A. George[1], S. P. Ford[1], and P. W. Nathanielsz[2], [1]*Center for the Study of Fetal Programming*, *Univ. of Wyoming, Laramie,* [2]*Center for Pregnancy and Newborn Research*, *Univ. of Texas Health Sciences Center, San Antonio*.

Undernutrition often occurs in pregnant ruminants under range conditions. Maternal NR during pregnancy is linked to offspring insulin resistance and metabolic disease. In 2003, ewes carrying singleton fetuses were fed a control (C, 100% NRC recommendations) or NR (50% NRC) diet from 28 to 78d of gestation. After d78, all ewes were fed 100% NRC until lambing. C and NR lambs were managed together and assigned to this study in 2009, when female offspring of NR (n = 4) and C (n = 4) ewes were subjected to ad lib feeding for 12 wks. As previously reported (George et al., Ann. Mtg. Soc. Gynecol. Invest, 2010, abstract), feed efficiency, weight gain, glucose clearance and insulin resistance were greater ($P < 0.05$) in ewes from NR dams. After the feeding trial, ewes were necropsied, the liver quickly removed and tissue from the left lobe frozen in liquid nitrogen. Protein and mRNA expression of PEPCK and glucose-6-phosphatase (G6Pase) were quantified via Western blotting and Real-time PCR. Additional liver tissue was placed in a tissue cassette, fixed with paraformaldehyde and paraffin embedded for immunohistochemistry. Both mRNA and protein expression of PEPCK were elevated ($P < 0.05$) in NR vs C ewe offspring (4.6 ± 0.9 vs 1.9 ± 0.6 and 0.8 ± 0.1 vs 0.5 ± 0.1 arbitrary units, respectively). In contrast, no differences were observed between C and NR groups in G6Pase at the mRNA or protein levels (2.1 ± 0.7 vs 2.2 ± 0.3 and 0.6 ± 0.1 vs 0.6 ± 0.03 arbitrary units, respectively). PEPCK and G6Pase binding was localized to the cytoplasm of hepatic cells. Enhanced gluconeogenesis was associated with the greater glucose clearance index, weight gain and feed efficiency in these aged NR offspring during ad lib feeding. Further, lower insulin sensitivity in NR offspring may impair suppression of hepatic gluconeogenesis, fitting with the upregulation of PEPCK observed in this study.

Key Words: maternal undernutrition, aged offspring, liver glucoconeogenesis

1132 Maternal nutrient restriction (NR) from early to mid-gestation increases pancreatic β-cell number at mid-gestation but pancreatic weight and β-cell numbers are reduced by late-gestation. L Zhang*[1], L. A. George[1], S. P. Ford[1], and P. W. Nathanielsz[2], [1]*Center for the Study of Fetal Programming*, *Univ. of Wyoming, Laramie,* [2]*Center for Pregnancy and Newborn Research*, *Univ. of Texas Health Sciences Center, San Antonio*.

Both maternal obesity (MO) and NR are associated with increased rates of obesity and diabetes in offspring. We reported that MO in ewes results in increased fetal pancreatic β-cell numbers at mid-gestation, but reduced β-cell numbers by late gestation. Here we compare these data to a sheep model of early to midgestation maternal NR. Multiparous ewes were assigned to a control group (C, 100% NRC recommendations) or an NR group (50% NRC) from 28 to 78 d of gestation (dG). A subgroup of ewes was necropsied on 78 dG (C = 5, NR = 5), and the rest (C = 5, NR = 5) were fed 100% NRC from 78 to 135 dG and necropsied. A fetal blood sample was collected for insulin quantitation, and the fetal pancreas weighed and the splenic end paraffin embedded for determination of β-cell numbers per unit area. At 78 dG, NR fetal weight was lower ($P < 0.05$) than C fetuses (230.7 ± 10.3 vs. 312.0 ± 22.6 g). While no difference was observed in pancreatic weight on 78 dG, β-cell numbers per unit area islet tissue, were increased ($P < 0.05$) in NR versus C fetuses (134.9 ± 11.4 vs. 89.8 ± 9.9). No treatment difference in fetal weight was observed on d135 which averaged 4034.1 g, however, pancreatic weights of d135 NR fetuses were lower ($P < 0.05$) than those from C fetuses (2.8 ± 0.2 vs. 3.8 ± 0.3 g). The β-cell numbers were also markedly decreased ($P < 0.01$) in d135 fetuses from NR versus C ewes (113.3 ± 4.7 vs. 187.3 ± 19.3). Blood insulin levels from all d78 fetuses were below assay sensitivity, whereas on 135 dG concentrations were lower ($P = 0.07$) in fetuses from NR versus C ewes (1.8 ± 0.2 vs. 4.8 ± 1.4 mIU/L). These results suggest that maternal NR from early to midgestation, like MO, initial increased pancreatic growth and β-cell numbers, but lead to reductions in pancreatic growth and β-cell numbers by late gestation, possibly leading to pancreatic dysfunction in postnatal life.

Key Words: maternal nutrient restriction, fetal pancreatic development, sheep

1133 Effects of supplementing transition cow diets with different levels of dietary glycerol on performance, efficiency, and blood metabolites. J. Boyd*[2], J. Bernard[1], and J. West[1], [1]*The University of Georgia*, *Tifton,* [2]*US Dairy Forage Research Center*, *Madison, WI.*

A study was conducted to determine the effects of dietary glycerol on dry matter intake (DMI), milk yield and components, blood metabolites, and efficiency in the transition cow. The study was conducted from Feb. to Oct. of 2008 using 48 cows (25 primiparous and 23 multiparous). The study ran from 3wk prepartum to 8wk postpartum with a randomized block design using a 2 × 2 factorial. Treatments were prepartum control and postpartum control (CC); prepartum control and postpartum 400g/h/d glycerol (CG); prepartum 200g/h/d glycerol and postpartum control (GC); prepartum 200g/h/d glycerol and postpartum 400g/h/d glycerol (GG). Cows were assigned to treatment by previous or predicted production values, parity, and estimated calving date. Diets were corn silage based and balanced to be isocaloric and isonitrogenous. Data was analyzed using Proc MIXED of SAS with contrasts and 2 and 3 way interactions. Postpartum DMI ($P = 0.15$) was 16.1, 17.3, 18.7, and 16.7 kg/d (±0.81) for CC, CG, GC, and GG respectively. Milk yield ($P = 0.59$) was 32.4, 34.4, 35.0, and 34.8(±1.70) for CC, CG, GC, and GG respectively. Milk protein percentage ($P = 0.08$) was 3.4%, 3.9%, 3.8%, and 4.0% (±0.18) for CC, CG, GC, and GG respectively. Efficiency defined as (ECM/DMI) [$P = 0.15$] was 2.11, 2.09, 1.98, and 2.25 (±0.08) for CC, CG, GC, and GG respectively. No statistical effect on serum glucose (average 66.1 mg/dl) or blood urea N (average 15.2 mg/dl) was observed. Non-esterified fatty acids and B-hydroxybutyrate concentrations were not affected by treatment averaging 0.62 mEq/L and 8.0 mg/dl respectively. The inclusion of glycerol in the diet resulted in a numerical improvement in milk yield and components compared with CC. GG resulted in a numerical improvement on efficiency compared with CC, CG, and GC. Researchers observed that the use of dietary glycerol as an energy source may be useful in improving production and efficiency in the transition cow though further research is needed to determine the optimum levels.

Key Words: transition cow, glycerol, efficiency

1134 The influence of *Bacillus pumilus* 8G-134 on milk production of dairy cows in early lactation. J. D. Ferguson*[1], Z. Wu[1], D. W. Remsburg[1], and K. Mertz[2], [1]*University of Pennsylvania, School of Veterinary Medicine*, *Kennett Square,* [2]*Danisco Animal Nutrition*, *Waukesha, WI.*

The usage of direct-fed microbials (DFM) has become common in the dairy industry, but questions regarding their value remain prevalent. The efficacy of 3 different DFM feeding regimens on lactation performance was determined. Forty Holsteins (24 multiparous) were randomly assigned to one of 4 dietary treatments for the last 2 wk prepartum and the first 22 wk postpartum. The treatments included a placebo (CO), a *Propionibacterium* DFM prepartum followed by a *Lactobacillus* DFM postpartum (PL), and a DFM comprised of *Bacillus pumilus* 8G-134 offered at 5×10^9 (BL) or 1×10^{10} (BH) CFU/d. The TMR was the same for all treatments and fed to treatment groups once a day to 5% refusal. The treatment products were top dressed daily. Daily samples of TMR and orts were collected from each group and analyzed monthly. Cows were milked twice a day, and milk from AM and PM milking was analyzed for composition once a week. Milk production was compared between treatments using the Mixed Model Procedure of SAS. Group DMI was similar among treatments. Milk yield was higher for BL and BH than for CO and PL, and milk fat content was higher for PL, BL, and BH than for CO. The increase in milk yield with *B. pumilus* 8G-134 and the increase in milk fat for all DFM treatments indicate the benefits of these DFM.

Table 1. Lactation performance of dairy cows receiving different direct-fed microbials

Item	CO	PL	BL	BH	SEM	P
Milk, kg/d	33.8[a]	33.3[a]	35.5[b]	35.1[b]	0.6	0.04
Milk fat, %	3.57[a]	3.82[b]	3.81[b]	3.88[b]	0.08	0.05
Milk proten, %	2.89	2.91	2.88	2.90	0.03	0.92
MUN, mg/dl	10.9	11.2	11.2	11.2	0.3	0.91
SCC, log	5.9[a]	6.4[a]	5.0[b]	5.0[b]	0.3	0.01

[a,b]Means with different superscripts in a row were different ($P < 0.05$).

Key Words: direct-fed microbials, milk production, dairy cow

1135 Utilization of wet brewers grains as a replacement for corn silage in lactating dairy cow diets. C. L. Mahnken*, B. J. Bradford, T. G. Rozell, and M. J. Brouk, *Kansas State University*, *Manhattan.*

Eight primiparous (192 DIM) and 4 multiparous (191 DIM) mid-lactation Holstein cows were used to evaluate replacing corn silage (CS) and soybean meal with a blend of wet brewers grains (WBG) and cracked corn on a short-term basis. Milk production, composition, DMI and production efficiency were evaluated. Cows were allotted to a 4 × 4 Latin Square with 3 replications blocked by parity, days in milk and energy corrected milk (ECM). Four diets were evaluated; 0 WBG (0% WBG and 24% CS of diet DM), 12 WBG (12% WBG and 12% CS), 18 WBG (18% WBG and 6% CS), and 24 WBG (24% WBG and 0% CS). Crude protein and starch levels were balanced between diets by varying the levels of cracked corn and soybean meal. Fifteen day periods were used, d11–15 were designated for collection. Orts were collected daily and TMR was fed at 5 to 10% above previous day's intake. Cows were milked 3x/day and milk weights recorded at every milking. Milk samples, body weights and BCS were taken −2 and −1d pre-trial to obtain baseline data and d14 and 15 of each period. During collection, TMR and orts were taken d1, 3 and 5. Fecal grab samples were taken d12–15 at 8 h intervals and advanced 2 h every 24 h period to account for diurnal variation. Dry matter intake was similar ($P = 0.21$) among treatments (20.3, 20.8, 20.9 and 21.2 kg/cow) for 0 WBG, 12 WBG, 18 WBG AND 24 WBG respectively, however CP intake of 24 WBG was greatest ($P = 0.03$) while 0 WBG was lowest. NDF intake was lower for 0 WBG compared with all other treatments and 24 WBG was higher than 12 WBG ($P = 0.005$). Dietary fat intake was different ($P < 0.001$) across all treatments, increasing with WBG inclusion. Inclusion of WBG had no effect ($P = 0.19$) on milk production (30.5, 31.5, 31.6 and 32.1 kg/cow), fat percent or amount, protein percent, SNF, lactose or SCC, but protein yield and MUN were lower ($P = 0.04$) with 0 WBG compared with 18 WBG and 24 WBG. Efficiency of production did not differ ($P = 0.86$) among treatments. Results suggest WBG fed in conjunction with grass hay can replace CS in lactating cow diets for a short-term period.

Key Words: by-product, production efficiency, forage replacement

1136 Methane suppressing effect of flaxseed in diets containing hay or silage. Y.-H. Chung*, M. L. He, S. M. McGinn, T. A. McAllister,

and K. A. Beauchemin, *Agriculture and Agri-Food Canada, Research Centre*, *Lethbridge, AB, Canada*.

Including flaxseed (flax) in the diet of cattle can increase n-3 fatty acid content of milk and meat. Our study investigated the potential of flax to reduce enteric methane (CH_4) emissions from cows when added to diets containing hay or silage. Effects of forage type and flax inclusion on ruminal fermentation and apparent nutrient digestibility were also studied. Twelve ruminally cannulated, non-lactating Holstein cows were used in a replicated 4 × 4 Latin Square design with 21-d periods. Experimental diets (50:50 forage to concentrate ratio; DM basis) were formulated as a 2 × 2 factorial using either alfalfa-grass (mostly grass, chopped) mixed hay or barley silage as the forage source with or without 15% (ration DM; provided 5.2% added fat) ground flax as a partial replacement of barley grain. Diets were fed once daily as a total mixed ration. Enteric CH_4 production was measured for 3 d using the sulfur hexafluoride tracer gas technique. Without flax inclusion, cows produced 31, 26 or 29% less ($P \leq 0.5$) CH_4 when fed hay compared with silage (207 vs. 300 g CH_4/head/d, 19.6 vs. 26.4 g CH_4/kg of DMI, or 30.4 vs. 42.9 g CH_4/kg of digestible DMI, respectively). The lower CH_4 emissions per unit of intake from cows fed hay, as compared with those fed silage, may be partially attributable to lower ruminal pH due to sorting of the hay diet. Including flax in the hay diet did not further suppress CH_4 emissions whereas, including flax in the silage diet reduced ($P \leq 0.5$) daily g CH_4 per head by 36% and CH4 production per kg DMI and per kg digestible DMI by 33 and 28%, respectively. Flax inclusion lowered CH_4 emissions of cows fed the silage diet in part by depressing ($P \leq 0.5$) fermentation of ruminal fiber and total tract fiber digestibility, a response not observed with the hay diet. Our study demonstrated that including 15% ground flax in a barley silage-based diet, with an aim of enhancing n-3 fatty acid content of meat, is an effective practice to mitigate enteric CH_4.

Key Words: forage type, flaxseed, enteric methane emissions

1137 Effects of live yeast culture supplementation (*Saccharomyces cerevisiae*) and nutritional management on ruminal pH and fermentation in early lactation dairy cows. R. M. Al Ibrahim*, V. P. Gath, C. McCarney, P. Duffy, and F. J. Mulligan, *University College Dublin*, *Dublin 4, Ireland*.

The aim of this study was to investigate the potential effect of yeast culture (YC) on rumen physiology of dairy cows nutritionally managed to have an abrupt introduction to pasture after calving or a more gradual introduction to pasture. Eight Holstein dairy cows in early lactation fitted with ruminal cannulas were randomly allocated to a 2 × 2 factorial experimental arrangement. Treatments were supplementation with YC (2.5 g/cow/d × 10^9 CFU of *S. cerevisiae*^{1026}/g; supplemented, Y or control, C; n = 4) and nutritional management (abrupt introduction to pasture, AP; or TMR for the first 21 DIM and then gradual introduction to pasture, GP; n = 4). Cows on pasture (perennial ryegrass) were supplemented with pasture lactating compound (±YC) at rate of 3.5 kg DM/cow/d twice daily. Rumen fluid samples were harvested on d 8, 9, 10 and 22, 23, 24 PP to assess volatile fatty acids (VFA), ammonia-N, lactic acid and protozoal count. Internal pH meters were installed in the rumen of cows to continuously monitor rumen pH during the sampling days. Data were analyzed using the Mixed procedure in SAS v 9.1, 2004. A higher total VFA concentration during the both first and second measuring periods was detected in Y group in comparison with C group. Protozoal count was higher ($P = 0.009$) in GP than AP groups during the first measuring period while no effect was detected in the second measuring period. Rumen pH and lactic acid in the first measuring period were not affected by YC supplementation while nutritional management had an effect with higher pH ($P = 0.001$) and lower ($P = 0.007$) lactic acid in GP than AP groups. Whereas, during the second measuring period Y and GP groups had higher pH and lower lactic acid in comparison with C and AP groups. Results suggested that dietary supplementation with YC during early lactation increased the rumen pH and total VFA and decreased lactic acid while the abrupt introduction to pasture after calving reduced the rumen PH and increased lactic acid with no effect on rumen VFA.

Key Words: dairy cows, nutrition changes, yeast culture, rumen fermentation

1138 Effect of supplemental corn dry distiller grains plus solubles on digestibility of steers grazing native range during summer growing season. M. F. Martínez-Pérez[1], D. Calderón-Mendoza[2], N. J. Dupass[1], A. Islas[1], J. Armendariz[1], A. M. Encinias[1], F. Loya-Olguin[2], and S. A. Soto-Navarro*[1], [1]*New Mexico State University*, *Las Cruces,* [2]*Universidad Autónoma de Baja California*, *Mexicali, BC, Mexico*.

Sixteen English-crossbred steers (360 ± 28.9 kg) fitted with ruminal cannulas grazing native range during the summer growing season were used in a completely randomized design to evaluate effects of corn distiller grains plus solubles (DDGS) supplementation level (0, 0.2, 0.4, and 0.6% BW) on forage intake, digestibility, and rumen fermentation characteristics. The experiment was conducted during the first and second weeks of October 2008. Steers grazed a single native range pasture with supplements offered individually once daily at 0700. Forage OM, NDF, CP, and EE intake decreased ($P \leq 0.05$) linearly with increasing DDGS supplementation level. Total CP and EE intake increased ($P < 0.01$) with increasing DDGS supplementation level. Digestibility of OM, CP, and NDF increased (linear; $P < 0.01$) with increasing DDGS supplementation level while digestion of EE increased (linear and cubic effect; $P \leq 0.04$) with increasing DDGS supplementation level (40.81, 54.31, 50.99, and 70.07 ≥ 3.89% for 0, 0.2, 0.4, and 0.6% of BW, respectively). Forage masticate in situ soluble linearly increased ($P < 0.01$) and slowly degradable CP fraction linearly decreased ($P > 0.01$) with increasing DDGS supplementation level. Forage in situ masticate DM and NDF disappearance rate increased (quadratically; $P \leq 0.05$) and DDGS in situ DM disappearance rate increased (linearly; $P > 0.03$) with increasing supplementation levels. Forage and DDGS UIP (% of CP), ruminal pH, and VFA concentration were not affected ($P \geq 0.25$) by DDGS supplementation level. These results indicate that DDGS supplementation improved total CP and EE intake and digestibility of OM, NDF, CP, and EE of steers grazing native range during the forage growing season. Therefore, DDGS represent a viable supplement for cattle grazing native range during the forage growing season when forage has medium or high quality.

Key Words: DDGS supplementation, grazing native range, steers

1139 Effect of replacing grain and silage with wheat distiller grain on intake, digestibility and urine purine derivatives in finishing beef cattle. Y. L. Li*1,2, W. Z. Yang[1], T. A. McAllister[1], and K. A. Beauchemin[1], [1]*Agriculture and Agri-Food Canada, Research Centre*, *Lethbridge, AB, Canada*, [2]*Feed Research Institute, Chinese Academy of Agricultural Sciences*, *Beijing, China*.

Our objective was to evaluate the effects of wheat dried distillers grains′ with solubles (DDGS) when used to partially replace barley grain and forage or to entirely replace forage in the finishing diet of beef cattle. Effects on intake, digestibility, and purine derivatives (PD) in urine (as an indication of microbial protein synthesis) were evaluated. Eight ruminally fistulated Angus heifers were assigned to a replicated 4 × 4

Latin square design with 4 treatments: control, low (25%), med (30%), and high (35%) DDGS (DM basis). The diets consisted of barley silage, barley concentrate, and wheat DDGS in ratios of 15:85:0, 10:65:25, 5:65:30 and 0:65:35 (DM basis), respectively. The dietary contents (% DM) of CP were higher for DDGS diets (mean ± SD, 21.3 ± 1.6) than for the control (11.5) diet, but all diets had similar NDF contents (mean ± SD, 23.2 ± 1.1). DMI (kg/d) was lower ($P < 0.01$) for the high DDGS diet (7.9) than for other 3 diets (9.1). Increasing DDGS content of diets linearly reduced ($P < 0.01$) starch intake. Total digestibility (% intake) of DM quadratically ($P < 0.01$) changed with the highest digestibility for high DDGS (79) and the lowest for low DDGS (76). There were linear ($P < 0.01$) increases in the total digestibilities of CP, NDF and starch with increasing DDGS and decreasing silage in the diet. Total excretion of PD (mmol/d) quadratically ($P = 0.02$) increased with the highest excretion for low (282) and med DDGS (295) diets and the lowest for control (231). It was concluded that partially replacing barley grain and silage with wheat DDGS improved total digestibilities of CP and NDF, as well as microbial protein synthesis. Entirely removing silage from a finishing diet may improve feed efficiency due to lower DMI and higher digestibility, but further work is needed to determine whether the risk of acidosis is also increased.

Key Words: wheat DDGS, intake, digestibility

1140 Feeding wheat distillers grains compared with corn distillers grains in diets for lactating dairy cows: Effect on milk production and rumen fermentation. M. M. Abdelqader* and M. Oba, *University of Alberta*, *Edmonton, AB, Canada*.

In western Canada, dried distillers grains with soluble (DDGS) is produced from mixtures of corn and wheat at variable ratios, and used as a source of dietary crude protein. The objective of this study was to determine the effect of feeding corn DDGS (CDG), wheat DDGS (WDG), and a 50:50 mixture of both (CWDG) on dry matter intake, milk production, milk composition, and feed efficiency of dairy cows in mid-lactation. Sixteen multiparous and 16 primiparous lactating Holstein cows were used in a replicated 4 × 4 Latin square with 3-wk periods. Dietary treatments were a control diet containing canola meal as the primary protein source (CON) and diets containing CDG, WDG, or CWDG. The treatment protein sources supplied 35% of dietary crude protein, and all diets were formulated for similar protein (17.9%) and fat (4.5%) contents. Dry matter intake tended to be higher when cows were fed WDG diet compared with CDG (25.4 vs. 22.9 kg/d; $P = 0.08$), but milk yield was not affected by treatment and averaged at 36.3 kg/d. As such, feeding CDG tended to increase feed efficiency compared with WDG (milk yield / dry matter intake; 1.64 vs. 1.45; $P = 0.08$). However, no differences in DMI and milk yield were observed between CON and diet containing DDGS. Furthermore, concentrations of milk fat, protein, lactose, and milk urea nitrogen were not affected by treatment, and averaged at 3.59%, 3.11%, 4.54%, and 10.7 mg/dL, respectively. Rumen pH was not affected by dietary treatment and averaged at 6.19. However; cows fed CDG had lower ($P = 0.03$) NH3-N concentration in the rumen compared with those fed the WDG and CWDG diet (9.4 vs. 12.9 and 12.5 mg/dL, respectively). In conclusion, regardless type of grain source, DDGS can be used as an alternative protein source in diets for lactating dairy cows, but type of grain from which DDGS is produced may affect feed efficiency.

Key Words: corn DDGS, wheat DDGS, feed efficiency

1141 *Megasphaera elsdenii* effects on adaptation to concentrate diets. L. K. Thompson*[1], P. H. Henning[2], and J. S. Drouillard[1], [1]*Kansas State University*, *Manhattan*, [2]*MS-Biotech*, *Centurion, South Africa*.

Crossbred (n = 80; 408 ± 66 kg initial BW) steers were used in a randomized complete block experiment to evaluate effects of oral dosing of *Megasphaera elsdenii* strain NCIMB 41125 (ME). Cattle fed forage diets for 3 wk after arrival were allotted to factorialized treatments consisting of step-up regimen (17 or 8 d) and oral drenching with a placebo or 10^{11} cfu ME. Diets consisted of alfalfa hay and steam-flaked corn, with 36 mg/kg monensin. The 17-d regimen used 5 diets (45, 35, 25, 15, and 6% roughage) with diet changes on d 5, 9, 13, and 17. The 8-d regimen used 3 diets (45, 25, and 6% roughage) with diet changes on d 4 and 8. On d 1, steers were weighed, orally dosed with ME or Placebo, placed in individual pens, and fed ad libitum for 63 d. Feed offered and refused were measured daily to determine daily DMI. On d 64, cattle were consolidated into pens of 10 animals each (2 pens/treatment) and fed until harvest on d 95. ME cattle maintained more consistent intakes ($P = 0.07$) during the initial 3 d of concentrate feeding compared with Placebo cattle. ME cattle tended to have greater ADG in the first 63 d ($P = 0.11$), particularly with the accelerated step-up (interaction, $P = 0.11$). HCW increased ($P = 0.10$) with ME, but were not affected by step-up regimen or the interaction between ME and step-up regimen. Liver abscess rates tended ($P = 0.14$) to be greater for cattle on the accelerated step-up. A single oral dose of *Megasphaera elsdenii* strain NCIMB 41125 can be used effectively to transition cattle from forage to high-grain diets in 8 d.

Table 1. Effects of *Megasphaera elsdenii* on intake and carcass characteristics

Item	17d/-ME	17d/+ME	8d/-ME	8d/+ME	SEM
DMI d 1-3, kg/d	2.87	3.46	2.83	4.13	0.791
DMI d 1-3 CV, %†	117	102	119	84	14
DMI d 1-63, kg/d	8.23	8.74	8.40	8.41	0.223
Liver abscess, %	4.7	5.5	20.1	9.7	6.6
HCW, kg†	334	338	324	335	4.4

†Main effect of ME, P ≤ 0.10.

Key Words: *Megasphaera elsdenii*, intake, feedlot

1142 Effects of adding a mycotoxin-sequestering agent on milk aflatoxin M1 concentration and the performance and immune response of dairy cattle fed an aflatoxin B1-contaminated diet. O. C. M. Queiroz*, A. T. Adesogan, C. R. Staples, J. Hun, M. Garcia, L. F. Greco, and L. J. Oliveira, *Department of Animal Sciences, University of Florida*, *Gainesville*.

The objective was to examine effects of adding 2 doses of a montmorillonite-based mycotoxin adsorbent on milk aflatoxin M1 (AFM1) concentrations and the performance and innate immune response of dairy cows fed an aflatoxin B1 (AFB1)-contaminated diet. Eight lactating cows were used in an experiment with a duplicated 4 × 4 Latin square design with 12-d periods. Treatments included the following: 1) Control diet (C); 2) Toxin diet (T) containing C and 75 μg/kg of AFB1; 3) Low-clay (LC) diet containing T and 0.2% Calibrin A (Amlan International, Chicago, IL); and 4) High-clay diet (HC) containing T and 1% Calibrin A. Milk production and DMI were recorded daily, and milk was sampled twice daily on d 5, 9, 10, 11, and 12 in each period. Blood samples were collected on d 5 and 9 of each period. The model included treatment, square and period effects and significance was declared at $P < 0.05$. Dietary treatments did not affect DMI, milk yield, or feed efficiency.

Feeding T instead of C tended to reduce 3.5% FCM yield (19.0 vs. 20.8 kg/d; $P = 0.08$, SE = 0.79) and reduced milk fat yield (0.67 vs. 0.74 kg/d; SE = 0.03) and milk protein concentration (3.28 vs 3.36%; SE = 0.03). Concentrations of AFM1 in milk of cows fed the T and LC diets were similar (0.63 and 0.65 μg/kg) and greater than those of cows fed the HC diet (0.48 μg/kg; SE = 0.04), but cows fed C had trace levels (0.03 μg/kg; SE = 0.04). Haptoglobin concentration was greater (22.0 vs. 14.4; SE = 1.9) and β2-integrin expression (220 vs. 130; $P = 0.1$; SE = 32) tended to be greater in cows fed diet T instead of C, but values for cows fed LC, HC and C did not differ. Feeding HC or LC instead of T prevented the increased innate immune response and decreased FCM yield caused by T, but milk AFM1 concentration was only reduced by feeding HC instead of T.

Key Words: mycotoxin adsorbent, aflatoxin, immunity

1143 The effect of rumen-protected methionine and choline on productive performance of Holstein dairy cows. M. Ardalan*, M. Dehghan-Banadaky, and K. Rezayazdi, *Department of Animal Science, University College of Agriculture and Natural Resources, University of Tehran*, *Karaj, Iran*.

Forty Holstein dairy cows in their first and second lactation were used in a lactation study from 4-week prepartum through 10-week postpartum to investigate the effect of feeding ruminally protected sources of methionine and choline on productive performance of Holstein dairy cows. Cows (10 cows per treatment = 6 cows in 1st lactation and 4 cows in 2nd lactation) were housed in individual tie stalls. Animals were randomly assigned to receive one of the following treatments in a 2 × 2 factorial design 4-week before their expected calving dates, using block randomization based on parity: 18 g/d of rumen-protected methionine product (RPM), 60 g/d of rumen-protected choline product (RPC), 18 g/d of RPM + 60 g/d of RPC, or neither supplement (control). The repeated measurements of milk yield and composition were analyzed as a linear mixed model (Proc Mixed) with the best fitted covariance structure of SAS. The statistical model included the fixed effects of treatment, parity, time (week of lactation), treatment × time, and the random effect of cow within treatment and parity. The error covariance structure used for the repeated measures was the first-order heterogeneous autoregressive structure. The supplementation of RPC significantly affected milk yield, FCM, and ECM across lactation weeks ($P < 0.05$). The actual milk yield, FCM, and ECM were greater for RPC-fed cows than other treatment groups ($P < 0.05$). The RPM and RPC have significant effects on the lactose percentage of milk across lactation weeks, but the treatments did not significantly affect fat and protein percentages of milk. Also, RPC significantly affected fat, protein, and lactose yields of milk across lactation weeks ($P < 0.05$). There was a significant interaction effect of RPM × RPC for lactose percentage of milk ($P < 0.05$). In general, the RPM × RPC × time had not any significant effect on milk yield and composition. The results of this study indicated the positive effect of RPC supplementation on the productive performance of dairy cows.

Key Words: rumen-protected methionine, rumen-protected choline, productive performance

Ruminant Nutrition Symposium: Acidosis: New Insights Into the Persistent Problem

1144 Role of fermentation acid absorption in the regulation of ruminal pH. J. R. Aschenbach*[1], G. B. Penner[2], F. Stumpff[3], and G. Gäbel[4], [1]*University of Veterinary Medicine Vienna*, *Vienna, Austria*, [2]*University of Saskatchewan*, *Saskatoon, Canada*, [3]*Free University of Berlin*, *Berlin, Germany*, [4]*University of Leipzig*, *Leipzig, Germany*.

Diets with high energy density are rapidly fermented to acids (short chain fatty acids, SCFA; lactic acid) within the rumen. The resulting release of protons can constitute a challenge to the ruminal ecosystem and animal health. Health upsets resulting from acidogenic diets are classified as subacute and acute acidosis based on the degree of ruminal pH dysregulation. While increased acid production is a nutritionally desired effect of increased concentrate feeding, the accumulation of protons in the rumen is not. Consequently, mechanisms of proton removal and their quantitative importance are of major interest. From the 1950′s, salivary buffers (bicarbonate, phosphate) have been identified as important mechanisms for ruminal proton removal. However, it appears that a larger proportion of protons is removed from the rumen by transport processes across the ruminal epithelium. Proceeding initially from exclusively diffusional absorption of fermentation acids, several protein-dependent mechanisms have been discovered over the last 2 decades. Although the molecular identity of these proteins is mostly uncertain, acetate absorption proceeds to a major part via acetate-bicarbonate exchange in addition to another nitrate-sensitive, bicarbonate-independent transport mechanism and lipophilic diffusion. Propionate and butyrate also show partially bicarbonate-dependent transport modes. In sheep, susceptibility to subacute ruminal acidosis was positively related to the efficiencies of protein-mediated acetate uptake and diffusional butyrate uptake. The latter seemed attributable to high rates of butyrate metabolism in the epithelial cells. Finally, SCFA absorption also accelerates urea transport via UT-B into the rumen which via ammonium recycling may remove protons from the rumen to the blood.

Key Words: nutrient absorption, ruminal acidosis, short chain fatty acids

1145 Molecular adaptation of ruminal epithelia to highly fermentable diets. G. B. Penner*[1], M. A. Steele[2], and B. W. McBride[2], [1]*University of Saskatchewan*, *Saskatoon, Canada*, [2]*University of Guelph*, *Guelph, Ontario, Canada*.

Feeding highly fermentable diets to ruminants is one strategy to increase energy intake. However, the increase in short-chain fatty acid (SCFA) production and reduced ruminal pH associated with highly fermentable diets imposes a metabolic challenge to the ruminal epithelia. In response to greater SCFA supply, the ruminal epithelia respond with coordinated actions of altered cell function and proliferation. While the proliferative response is well documented, emerging evidence at the mRNA level indicates that temporal changes in epithelial cell function is the initial response. It is not surprising that gene expression analysis has identified pathways involved in fatty acid metabolism, ion transport, and intracellular homeostasis to be the pathways dominantly affected during adaptation and following adaptation to a highly fermentable diet. It is widely acknowledged that intraepithelial metabolism of SCFA, particularly butyrate, helps to maintain the concentration gradient between the cytosol and lumen thereby facilitating absorption. Current data suggests that for butyrate metabolism, 3-hydroxy-3-methyglutaryl-CoA synthase 1 is the regulatory point with transient up and downregulation during diet adaptation. Interestingly, rate-limiting enzymes involved in cholesterol biosynthesis appear to be downregulated during diet adaptation. In addition to nutrient transport and utilization, genes involved in the maintenance of tight cell junctions and induction of the inflammatory response have been identified as differentially expressed genes during adaptation to highly fermentable diets. This may have important implications on ruminal epithelial barrier function and the inflammatory response associated with subacute ruminal acidosis.

Key Words: adaptation, gene expression, rumen epithelia

1146 Animal productivity and health responses to hind-gut acidosis. T. F. Gressley*[1], M. B. Hall[2], and L. E. Armentano[3], [1]*University of Delaware*, *Newark*, [2]*US Dairy Forage Research Center*, *Madison, WI*, [3]*University of Wisconsin*, *Madison*.

Microbial fermentation of carbohydrates in the large intestine of dairy cattle is responsible for 5 to 10% of total tract carbohydrate digestion. When dietary, animal, and/or environmental factors contribute to abnormal, excessive flow of fermentable carbohydrates to the large intestine, hind-gut acidosis can occur. Hind-gut acidosis is characterized by increased rates of production of volatile fatty acids (VFA) including lactic acid, decreased digesta pH, and damage to gut epithelium as evidenced by the appearance of mucin casts in feces. In parallel to ruminal disorders, it is possible that hindgut acidosis can also be classified as acute or sub-acute. In the more severe situations, hind-gut acidosis is characterized by an inflammatory response; the resulting breach of the barrier between animal and digesta may contribute to laminitis and other disorders. In a research setting, hind-gut acidosis has been evaluated using pulse-dose or continuous abomasal infusions of varying amounts of fermentable carbohydrates. Continuous low dose infusions of pectin or fructans (1 kg/d) into lactating cows resulted in decreased diet digestibility, increased intake variation, decreased milk fat percentage, decreased milk urea N concentration, and increased fecal N output, without affecting fecal pH or VFA. Pulse dose fructan infusions (1 g/kg BW) into steers resulted in watery feces, decreased fecal pH, and increased fecal VFA, without causing an inflammatory response. Daily 12 h abomasal infusions of a high dose of starch (~4 kg/d) have also induced hind-gut acidosis as indicated by decreased fecal pH and watery feces. Evidence of hind-gut acidosis has also been noted on farms as detected by fecal signs of excessive fermentation (watery or foamy appearance) or of epithelial damage (presence of mucin casts). In summary, hind-gut acidosis occurs as a result of relatively high rates of large intestinal fermentation, likely as a result of digestive dysfunction in other parts of the gut. A better understanding of the relationship of this disorder to other animal health disorders is needed.

Key Words: acidosis, hind-gut

1147 Bovine endotoxicosis: Does acidosis cause inflammatory responses? P. H. Andersen*, *Copenhagen University*, *Copenhagen, Denmark.*

Endotoxins (LPS) are structural parts of the gram-negative bacteria membrane and belong to the group of pathogen-associated molecular patterns (PAMP), that are instantly recognized by the innate immune system. LPS and gram-negative bacteria are generally present in the rumen of cattle, and it is now widely accepted, that the LPS concentration increases when grain is added to the diet. LPS in even very minute amounts (10 ng per kg BW) elicit an inflammatory response in cattle.

Clinical and biochemical signs such as decreased GI motility, anorexia, increased concentrations of acute phase proteins, leukocytosis and leukopenia appear in endotoxicosis as well as in acute ruminal acidosis. In cattle, fever is not a consistent sign of endotoxicosis. If ruminitis is present, the ruminal barrier may become leaky. In experimentally induced acute ruminal acidosis, increased amounts of LPS can be detected in the portal vein and sometimes also in the systemic circulation. Controversy exists whether this is the case also in cows with subclinical ruminal acidosis. However, concentrations of the acute phase protein serum amyloid A increase in subclinical ruminal acidosis, and results from recent in vitro experiments have shown that the permeability of the rumen epithelium to LPS increases in the presence of LPS and low pH. Whether the inflammatory signs detected in ruminal acidosis may be ascribed to the occurrence of ruminitis, to the consequences of increased translocation of LPS from the inflamed rumen epithelium to the portal blood system, or to combination of these, is however not yet entirely clear. Interestingly, large variations in the clinical susceptibility of cattle to LPS are reported from various studies on rumen acidosis and mastitis. Cows may be divided into "moderate" and "severe" responders. The detoxifying capacity of the macrophages in the liver may play a role, but the causative factors are far from elucidated. It is suggested that further investigation of the response of cattle to LPS or other PAMP challenges may provide a basis for the identification of indicators of robustness or health.

Key Words: endotoxin, ruminal acidosis, inflammation

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